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(54) Title: **STAT6 ACTIVATION GENE**

(57) Abstract: Proteins having activity that promotes STAT6 activation, which are used for diagnosing, treating or preventing diseases associated with the excessive activation or inhibition of STAT6 are provided. Using a STAT6 response reporter plasmid, cDNA encoding a protein capable of promoting STAT6 activation was cloned from the cDNA library constructed from human lung fibroblasts and the like, and the DNA sequence and the deduced amino acid sequence are determined. The protein, the DNA encoding the protein, a recombinant vector containing the DNA, and a transformant containing the recombinant vector are useful for screening a substance inhibiting or promoting STAT6 activation.

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DESCRIPTION

STAT6 ACTIVATION GENE

TECHNICAL FIELD

The present invention relates to a protein capable of promoting STAT6 activation, a DNA sequence encoding the protein, a method for obtaining the DNA, a recombinant vector containing the DNA, a transformant containing the recombinant vector, and an antibody which reacts with the protein. The present invention also relates to use of the protein, DNA or antibody of the invention in the diagnosis, treatment or prevention of diseases associated with the excessive activation or inhibition of STAT6. The present invention also relates to a method for screening a substance capable of inhibiting or promoting STAT6 activation by using the protein, DNA, recombinant vector and transformant.

BACKGROUND ART

Mosmann et al. advocated that helper T cells (the term will be abbreviated as "Th" hereinafter) which play an important role in immune response, should be classified into two different subsets (J. Immunol. (1986) 136:2348-2357). They classified these cells into two types of cell, Th1 and Th2, based on their cytokine-production pattern. Th1 cell produces interleukin 2 (IL-2), interferon γ (IFN- γ), tumor necrosis factor β (TNF- β) etc., which are referred to as Th1 type cytokines, and activates cell-mediated immunity, for example, in viral infection. On the other hand, Th2 cell produces interleukin 4 (IL-4), interleukin 5 (IL-5), interleukin 10 (IL-10), interleukin 13 (IL-13) etc., which are referred to as Th2 type cytokines, and is involved in humoral immunity such as antibody production in case of an infection of intracellular cytozoic microorganisms such as parasites or an exposure to an antigen/allergen. Thus, the idea of classifying various immune responses in a body depending on Th cell types to comprehend disease immune responses in view of the balance between Th1 and Th2 cells, has emerged, and a concept of Th1/Th2 diseases has also been suggested.

Since Th2 produces a number of cytokines involved in allergic reaction, hyperactive

Th2 is considered to cause allergic disease such as asthma or the like.

IL-4 is an immunomodulatory cytokine which is secreted from activated T lymphocytes, basocytes and mast cells. IL-4 induces proliferation of B cells and production of IgE and IgG1 as well as activation and proliferation of mast cells. It also induces gene expression of VCAM-1 which functions when a basocyte adheres to a vascular endothelial cell and infiltrates into tissues. Furthermore, IL-4 has been shown to play an important role in differentiation into a Th2 cell and proliferation and differentiation of a hemopoietic progenitor cell.

IL-13 is a cytokine which is secreted from activated T lymphocytes, mast cells, basocytes, NK cells, and dendritic cells. It has approximately 30% sequence identity to IL-4 and shows IL-4-like activity against monocyte/macrophage and B cell. However, IL-13 does not act on T cells.

Binding of IL-4 and IL-13 with their receptors on the cell surface activates intracellular tyrosine kinase, transmitting signals into the cell via tyrosine phosphorylation of some intracellular proteins. Recent developments in molecular biology have elucidated a signaling mechanism from the IL-4 receptor, and major intracellular transducer molecules have been identified. Among them, STAT6 has been found to be an important molecule.

STAT6 is a member of a STAT (Signal transducer and Activator of Transcription) family. STAT is a transcription factor which functions depending on stimulations downstream of various cytokine receptors and growth factor receptors. In mammals, seven types, STAT1, 2, 3, 4, 5a, 5b, and 6 have been identified so far. Binding of a ligand such as a cytokine with its receptor activates a receptor-associated tyrosine kinase referred as JAK family, and the activated JAK phosphorylates the tyrosine residues of the receptor itself, thereby causing activation of the STAT molecule. The activation of STAT6 molecule forms dimers and moves to the nucleus promptly, inducing gene expression.

JAK is activated via a IL-4 and a IL-13 receptor, and tyrosines on the receptors are phosphorylated. Subsequently, STAT6 binds to phosphorylated tyrosine residues of the receptors via SH2 domain, and STAT6 per se is tyrosine phosphorylated and forms homodimers, then moves to a nucleus. The genes which are known to be a target gene of

STAT6 include germline epsilon, CD23, MHC (Major Histocompatibility Complex) class II antigen, STAT6 gene, etc.

Recently, STAT6 defective mouse has been created and the physiological roles of STAT6 have been examined. The fact that, in the STAT6 defective mouse, the major functions of IL-4 and IL-13 are all disturbed has demonstrated that STAT6 is an important molecule in signal transduction of IL-4 and IL-13. Further, it was demonstrated that Th2 reactions are disturbed and little Th2 type cytokine was produced in said mouse, and therefore it was demonstrated that STAT6 is also an essential molecule in Th2 cell differentiation. Thus, STAT6 has been proved to be an important molecule in induction of allergic reaction.

In this context, the inhibition of function or activation of STAT6 may specifically inhibit the function of IL-4 and IL-13, repressing allergic disease, inflammatory or immunological diseases. Thus, the protein involved in STAT6 activation is a promising target for medicaments against diseases caused or characterized by allergic disease, autoimmunity or inflammation [see e.g., Proc. Natl. Acad. Sci. USA 95, 172-177 (1998), Science 282, 2258-2261 (1998), Science 282, 2261-2263 (1998), J. Exp. Med. 183, 109-117 (1996), J. Immunol. 160, 4004-4009 (1998), J. Immunol. 160, 1581-1588 (1998)].

Extracellular information is converted into a certain signal, which passes through the cell membrane and goes through the cytoplasm to the nucleus, where it regulates the expression of the target gene and causes cell responses. Therefore the elucidation of the mechanism of intracellular signal transduction from extracellular stimuli to STAT6 activation is of very important significance, because it provides very important means of developing new medicaments or therapies against allergic diseases, autoimmune diseases and diseases exhibiting inflammatory symptoms.

It is considered, however, that the signal transduction pathway from a certain cell stimulus to STAT6 activation includes the existence of some other molecules which regulate and control the pathway in addition to JAK kinase and STAT molecule. Therefore it is desirable for more efficient drug discovery to identify the transmitters which play a key role in the pathway, and to focus research on the transmitters to establish a new drug-screening method. However, apart from JAK/STAT molecules, most of the mechanism of the signaling

pathway via STAT6 remains unknown, and the identification of new signaling molecules and elucidation of the STAT6 activation mechanism are desired.

DISCLOSURE OF THE INVENTION

The object of the present invention is to identify a new gene and protein capable of promoting STAT6 activation, and to provide a method of use of them in medicaments, diagnostics and therapy. That is, an object of the present invention is to provides a new protein capable of promoting STAT6 activation, a DNA sequence encoding the protein, a recombinant vector containing the DNA, a transformant containing the recombinant vector, a process for producing the protein, an antibody directed against the protein or a peptide fragment thereof, and a process for producing the antibody.

Another object of the present invention is to provides a method for screening a substance capable of inhibiting or promoting STAT6 activation by using the protein, DNA, recombinant vector and transformant, a kit for the screening, a substance capable of inhibiting or promoting STAT6 activation obtainable by the screening method or the screening kit, a process for producing the substance, a pharmaceutical composition containing a substance capable of inhibiting or promoting STAT6 activation, etc.

The present inventors have intensively studied to solve the above objects. As a result, the present inventors have succeeded in constructing a full-length cDNA library by using the oligo-capping method; establishing a gene function assay system by expression cloning using NIH3T3 cells; and isolating a new DNA (cDNA) encoding a protein having a function of promoting STAT6 activation by using the assay system. This new DNA molecule induced promotion of STAT6 activation by its expression in NIH3T3 cells. This result shows that this new DNA is a signal transduction molecule involved in promotion of STAT6 activation. Thus, the present invention has been completed.

That is, the present invention provides the followings:

- (1) A purified protein of the following (a) or (b):
 - (a) a protein that consists of an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46,

48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182 and 184; and

(b) a protein that promotes STAT6 activation and consists of an amino acid sequence having at least one amino acid deletion, substitution or addition in an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182 and 184.

(2) A purified protein that promotes STAT6 activation and comprises an amino acid sequence having at least 95% identity to the protein according to (1) over the entire length thereof.

(3) An isolated polynucleotide which comprises a nucleotide sequence encoding a protein of the following (a) or (b):

(a) a protein that consists of an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182 and 184; and

(b) a protein that promotes STAT6 activation and consists of an amino acid sequence having at least one amino acid deletion, substitution or addition in an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182 and 184.

(4) An isolated polynucleotide comprising a nucleotide sequence of any of the following (a) to (c):

(a) a nucleotide sequence represented by any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181 and 183;

(b) a nucleotide sequence which encodes a protein that promotes STAT6 activation, and which hybridizes with a polynucleotide having a nucleotide sequence complementary to the nucleotide sequence of (a) under stringent conditions; and

(c) a nucleotide sequence which encodes a protein that promotes STAT6 activation, and which consists of a nucleotide sequence having at least one nucleotide deletion, substitution or addition in a nucleotide sequence of any of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181 and 183.

(5) An isolated polynucleotide comprising a nucleotide sequence of any of the following (a) to (c):

(a) a nucleotide sequence represented by a coding region of any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181 and 183;

(b) a nucleotide sequence which encodes a protein that promotes STAT6 activation, and which hybridizes with a polynucleotide having a nucleotide sequence complementary to the nucleotide sequence of (a) under stringent conditions; and

(c) a nucleotide sequence which encodes a protein that promotes STAT6 activation, and which

consists of a nucleotide sequence having at least one nucleotide deletion, substitution or addition in a coding region of a nucleotide sequence of any of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181 and 183.

(6) An isolated polynucleotide comprising a nucleotide sequence which encodes a protein that promotes STAT6 activation and has at least 95% identity to the polynucleotide according to (3) over the entire length thereof.

(7) An isolated polynucleotide comprising a nucleotide sequence which encodes a protein that promotes STAT6 activation and has at least 95% identity to the polynucleotide according to (4) or (5) over the entire length thereof.

(8) A purified protein encoded by the polynucleotide according to any one of (3) to (7).

(9) A recombinant vector which comprises a polynucleotide according to any one of (3) to (7).

(10) A agent for gene therapy which comprises the recombinant vector according to (9) as an active ingredient.

(11) A transformant which comprises the recombinant vector according to (9).

(12) A membrane of the transformant according to (11) which has the protein according to (1) or (2), which is a membrane protein.

(13) A process for producing a protein according to (1), (2) or (8) comprising the steps of;
(a) culturing a transformant according to (11) under conditions providing expression of the protein according to (1), (2) or (8); and
(b) recovering the protein from the culture product.

(14) A process for diagnosing a disease or susceptibility to a disease related to expression or activity of the protein of (1), (2) or (8) in a subject comprising the steps of:

(a) determining the presence or absence of a mutation in the gene encoding said protein in the genome of said subject; and/or

(b) analyzing the amount of expression of said gene in a sample derived from said subject.

(15) A method for screening compounds which inhibit or promote STAT6 activation, which comprises the steps of:

- (a) preparing a transformant by introducing a gene encoding a protein that promotes STAT6 activation according to (1), (2) or (8) and a gene encoding a signal which can detect STAT6 activation into a cell;
- (b) culturing the transformant under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;
- (c) measuring the signal which can detect STAT6 activation; and
- (d) selecting a candidate compound which can change the signal amount as compared with the case of the absence of candidate compounds, as a compound which inhibit or promote STAT6 activation.

(16) A method for screening compounds which inhibit or promote STAT6 activation, which comprises the steps of:

- (a) preparing a transformant by introducing a gene encoding a protein that promotes STAT6 activation according to (1), (2) or (8) into a cell;
- (b) culturing the transformant under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;
- (c) measuring an activity of STAT6; and
- (d) selecting a candidate compound which can change the activity of STAT6 as compared with the case of the absence of candidate compounds, as a compound which inhibit or promote STAT6 activation.

(17) A compound which inhibits or promotes STAT6 activation, which is selected by the method for screening according to (15) or (16).

(18) A process for producing a pharmaceutical composition, which comprises the steps of:

- (a) preparing a transformant by introducing a gene encoding a protein that promotes STAT6 activation according to (1), (2) or (8) and a gene encoding a signal which can detect STAT6 activation into a cell;
- (b) culturing the transformant under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;

- (c) measuring the signal which can detect STAT6 activation;
 - (d) selecting a candidate compound which can change the signal amount as compared with the case of the absence of candidate compounds, as a compound which inhibit or promote STAT6 activation; and
 - (e) producing a pharmaceutical composition which comprises a compound selected in the step of (d).
- (19) A process for producing a pharmaceutical composition, which comprises the steps of:
- (a) preparing a transformant by introducing a gene encoding a protein that promotes STAT6 activation according to (1), (2) or (8) into a cell;
 - (b) culturing the transformant under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;
 - (c) measuring an activity of STAT6;
 - (d) selecting a candidate compound which can change the activity of STAT6 as compared with the case of the absence of candidate compounds, as a compound which inhibit or promote STAT6 activation; and
 - (e) producing a pharmaceutical composition which comprises a compound selected in the step of (d).
- (20) A kit for screening a compound which inhibits or promotes STAT6 activation, which comprises:
- (a) a transformant comprising a gene encoding a protein that promotes STAT6 activation according to (1), (2) or (8) and a gene encoding a signal which can detect promotion of STAT6 activation; and
 - (b) reagents for measuring the signal.
- (21) A monoclonal or polyclonal antibody or a fragment thereof, which recognizes the protein according to (1), (2) or (8).
- (22) The monoclonal or polyclonal antibody or a fragment thereof according to (21), which inhibits the activity of promoting STAT6 activation by the protein according to (1), (2) or (8).
- (23) A process for producing a monoclonal or polyclonal antibody according to (21) or

(22), which comprises administering the protein according to (1), (2) or (8) or epitope-bearing fragments thereof to a non-human animal as an antigen.

(24) An antisense oligonucleotide having a sequence complementary to a part of the polynucleotide according to any one of (3) to (7), which prevents the expression of a protein which promotes STAT6 activation.

(25) A ribozyme or deoxyribozyme capable of inhibiting STAT6 activation, which has an action of cleavage of RNA that encodes the protein according to (1), (2) or (8) or an action of cleavage of RNA that encodes a protein which is involved in a route leading to STAT6 activation.

(26) A double strand RNA having a sequence corresponding to a part of the nucleotide sequence according to any one of (3) to (7), which inhibits expression of a protein that promotes STAT6 activation.

(27) A method for treating a disease associated with STAT6 activation, which comprises administering to a subject a compound screened by the process according to (15) or (16), and/or a monoclonal or polyclonal antibody or a fragment thereof according to (21) or (22), and/or an antisense oligonucleotide according to (24), and/or a ribozyme or deoxyribozyme according to (25), and/or a double strand RNA according to (26) in an effective amount to treat a disease selected from the group consisting of allergic diseases, inflammation, autoimmune diseases, diabetes, hyperlipidemia, infectious disease and cancers.

(28) A pharmaceutical composition produced by the process according to (18) or (19) for inhibiting or promoting STAT6 activation.

(29) The pharmaceutical composition according to (28) for the treatment and/or prevention of allergic diseases, inflammation, autoimmune diseases, diabetes, hyperlipidemia, infectious disease and/or cancers.

(30) A method of treating allergic diseases, inflammation, autoimmune diseases, diabetes, hyperlipidemia, infectious disease or cancers, which comprises administering a pharmaceutical composition produced by the process according to (18) or (19) to a patient suffering from a disease associated with STAT6 activation.

(31) A pharmaceutical composition according to (28) for the treatment and/or prevention

of Th1 hyperactive diseases.

(32) A method of treating Th1 hyperactive diseases, which comprises administering a pharmaceutical composition produced by the process according to (18) or (19) to a patient suffering from a disease related to inhibition of STAT6 activation.

(33) A pharmaceutical composition which comprises a monoclonal or polyclonal antibody or a fragment thereof according to (21) or (22) as an active ingredient.

(34) A pharmaceutical composition which comprises an antisense oligonucleotide according to (24) as an active ingredient.

(35) A pharmaceutical composition which comprises a ribozyme or deoxyribozyme according to (25) as an active ingredient.

(36) A pharmaceutical composition or a gene therapy agent, which comprises a double strand RNA according to (26) or a vector capable of expressing said double strand RNA, an active ingredient.

(37) The pharmaceutical composition according to any one of (33) to (35) for the treatment and/or prevention of a disease which is selected from the group consisting of allergic diseases, inflammation, autoimmune diseases, diabetes, hyperlipidemia, infectious disease and/or cancers.

(38) A computer-readable medium on which a sequence data set has been stored, said sequence data set comprising at least one of nucleotide sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181 and 183, and/or at least one amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182 and 184.

(39) A method for calculating identity to other nucleotide sequences and/or amino acid sequences, which comprises comparing data on a medium according to (38) with data of said other nucleotide sequences and/or amino acid sequences.

(40) An insoluble substrate to which polynucleotides comprising all or part of the nucleotide sequences selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181 and 183 are fixed.

(41) An insoluble substrate to which polypeptides comprising all or a part of the amino acid sequences selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182 and 184, are fixed.

The contents of the specifications and/or drawings of Japanese Patent Applications Nos.2002-164257, 2002-377326 and 2003-137505, U.S. Provisional Applications Nos.60/385912 and 60/436, 467 and U.S. Provisional Application filed on May 16, 2003, which form the bases of priority of the instant application, are incorporated herein.

BEST MODE FOR CARRYING OUT THE INVENTION

At first, in order to further clarify the basic feature of the present invention, the present invention is explained by following how the present invention is completed. In order to obtain a new gene having a function of promoting STAT6 activation, the following experiments were carried out as shown in the examples.

First, using the oligo-capping method, a full-length cDNA was produced from mRNA prepared from normal human lung fibroblasts (purchased from Sanko Junyaku Co., Ltd.),

ATDC5 cells (purchased from RIKEN Gene Bank) and the like, and a full-length cDNA library was constructed in which the cDNA was inserted into the vector pME18S-FL3 (GenBank Accession AB009864). Next, the cDNA library was introduced into *E. coli* cells, and plasmid preparation was carried out per clone. Then, a reporter plasmid containing a STAT6 response sequence upstream of DNA encoding luciferase (e.g., *J. Biol. Chem.* 275, 26500-26506 (2000), *J. Exp. Med.* 190, 1837-1848 (1999), *J. Immunol.* 150, 5408-5417 (1993), *J. Immunol.* 157, 2058-2065 (1996)) and the above full-length cDNA plasmid were cotransfected into NIH3T3 cells (Dainippon Pharmaceutical). After 48 hours of culture followed by slightly weak stimulation with mouse IL-4, luciferase activity was measured at a time of 6 hours thereafter, and the plasmid with significantly increased luciferase activity compared to that of a control experiment (vector pME18S-FL3 is introduced into a cell in place of a full-length cDNA) was selected (the selected plasmid showed a 3-fold or more increase in luciferase activity compared to that of the control experiment), and the entire nucleotide sequence of the cDNA cloned into the plasmid was determined. The protein encoded by the cDNA thus obtained shows that this protein is a signal transduction molecule involved in promotion of STAT6 activation.

The present invention is described in detail below.

In the present invention, the phrase "promote(s) STAT6 activation" means that direct or indirect activation of STAT6 (including induction of STAT6 activation) occurs when a gene is introduced into a suitable cell and the protein encoded by the gene is excessively expressed, without physiological stimuli; and/or that further direct or indirect promotion (including induction of promotion of STAT6 activation) of normal levels of STAT6 activation occurs, in the case where, after the gene is introduced into a suitable cell and the protein encoded by the gene is excessively expressed, a physiological stimulus is introduced to the cell. Activation of STAT6 can be measured, for example, by an assay using an STAT6 dependant reporter gene. In the assay, activation of STAT6 can be detected by an increase in reporter activity compared to control cells (cells into which the reporter gene and a null vector were introduced). Increase in reporter activity is preferably by a factor of 1.5 or more, more preferably by a factor of 3 or more, and still more preferably by a factor of 6 or more.

Reporter activity can be measured by cloning a polynucleotide (e.g. cDNA) encoding the protein to be expressed into a suitable expression vector, co-transfecting the expression vector and a STAT6 dependant reporter plasmid into a suitable cell, and after culturing for a certain period, then measuring reporter activity. Or, after co-transfecting and culturing for a certain period, a stimulant is added followed by culturing, and then the reporter activity is measured. Suitable expression vectors are well known to those skilled in the art, examples of which include pME18S-FL3, pcDNA3.1 (Invitrogen). The reporter gene can be one which enables a person skilled in the art to easily detect the expression thereof, and examples include a gene encoding luciferase, chloramphenicol acetyl transferase, or β -galactosidase. Use of a gene encoding luciferase is most preferable, and examples of an STAT6 dependent reporter plasmid include luciferase reporter plasmid N4 x 8-luc which has a STAT6 response sequence. Suitable cells include cells which exhibit an STAT6 activation response to stimulation by IL-4, IL-13 and the like. Examples include NIH3T3 cells. Cell culture and introduction of genes into cells (transfection) can be performed and optimized by a person skilled in the art by known techniques.

As a preferable method, NIH3T3 cells are inoculated on 10% FBS (Fetal Bovine Serum)-containing IMDM medium in a 96-well cell culture plate to a final cell density of 1×10^4 cells/well, and cultured for 24 hours at 37°C, in the presence of 5% CO₂. Then, the luciferase reporter plasmid N4 x 8-luc which has a STAT6 response sequence, and the expression vector are cotransfected into the cells in a well using FuGENE 6 (Roche). After 48 hours of culture at 37°C, in the presence of 5% CO₂, mouse IL-4 (Immuno Biological Laboratories Co., Ltd.) is added to a final concentration of 0.5ng/ml. After culturing for further 6 hours, promoting activity for STAT6 activation is then measured by measuring luciferase activity using a long term luciferase assay system, Picagene LT2.0 (Toyo Ink Mfg). For example, luciferase activity can be measured using PerkinElmer's Wallac ARVOTMST 1420 MULTILABEL COUNTER. The method for gene introduction by FuGENE6, and measurement of luciferase activity by Picagene LT2.0 can be performed respectively according to the attached protocols. In a method of gene introduction with a 96-well plate using FuGENE6, the amount of FuGENE6 per 1 well is suitably 0.3 to 0.5 μ l, preferably 0.3

μ l; the amount of N4 x 8-luc reporter plasmid is suitably 50 to 100ng, preferably 100ng; and the amount of expression vector is suitably 50 to 100ng, preferably 100ng. An ability (action) to promote STAT6 activation refers to an ability to increase the reporter activity (luciferase activity) relative to the control experiment (for cells into which the reporter gene and a null vector were introduced). Increase in reporter activity is preferably by a factor of 1.5 or more, more preferably by a factor of 3 or more, and still more preferably by a factor of 6 or more.

Related to the amino acid sequences of 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182 and 184, the present invention provides the following proteins:

- (a) proteins which comprise the above amino acid sequence;
- (b) polypeptides having one of the above amino acid sequences;
- (c) proteins which promote STAT6 activation and consist of an amino acid sequence having 1 or several (preferably a few) amino acid deletion, substitution or addition in the above amino acid sequences;
- (d) proteins which promote STAT6 activation and comprises an amino acid sequence, which has at least 95% identity, preferably at least 97-99% identity, to the above amino acid sequences over the entire length thereof:

“Identity” used herein means a relationship between two or more protein sequence or two or more nucleotide sequences, as determined by comparing the sequences, as known in the art. In the art, “identity” also means the degree of sequence relatedness between protein or nucleotide sequences, as determined by the match between protein or nucleotide sequences, as the case may be, as determined by the match between strings of such sequences. “Identity” and “similarity” can be readily calculated by known methods. Preferred methods to determine identity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in publicly available computer

programs. "Identity" can be determined by using, for example, the BLAST program (for example, Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ., J. Mol. Biol., 215:p403-410(1990), Altschul SF, Madden TL, Schaffer AA, Zhang Z, Miller W, Lipman DJ., Nucleic Acids Res. 25:p3389-3402 81997)), however methods of determining identity are not limited to this. Where software such as BLAST is used, it is preferable to use default values.

The main initial conditions generally used in a BLAST search are as follows, but are not limited to these. An amino acid substitution matrix is a matrix numerically representing the degree of analogy of each pairing of each of the 20 types of amino acid, and normally the default matrix, BLOSUM62, is used. The theory of this amino acids substitution matrix is shown in Altschul S.F., J. Mol. Biol. 219: 555-565 (1991), and its applicability to DNA sequence comparison is shown in States D. J., Gish W., Altschul S.F., Methods, 3: 66-70 (1991). In this case, optimal gap cost is determined empirically and in the case of BLOSUM62, preferably parameters, Existence 11, Extension 1 are used.

The expected value (EXPECT) is the threshold value concerning statistical significance for a match with a database sequence, and the default value is 10.

As one example, a protein having, for example, 95% or more sequence identity to the amino acid sequence of SEQ ID NO: 2 may have an amino acid sequence that includes up to 5 amino acid changes per 100 amino acids of the amino acid sequence of SEQ ID NO: 2. In other words, a protein having 95% or more amino acid sequence identity to a subject amino acid sequence, may have amino acids up to 5% of the total number of amino acids within the subject sequence, deleted or substituted by other amino acids, or amino acids up to 5% of the total number of amino acids within the subject sequence may be inserted within the subject sequence. These changes within the subject sequence, may exist at the amino terminus or the carboxy terminus of the subject sequence, or may form one or more groups of changes.

The Examples described below demonstrate that the protein consisting of an amino acid sequence of the above SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162,

164, 166, 168, 170, 172, 174, 176, 178, 180, 182 or 184 is capable of promoting STAT6 activation.

Related to the nucleotide sequences of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181 and 183, the present invention further provides the following isolated polynucleotides:

- (a) polynucleotides of any of the above sequences;
- (b) polynucleotides comprising a nucleotide sequence, which has at least 95% identity, preferably 97-99% identity, to any of the above sequences, and which encodes a protein which acts to promote STAT6 activation;
- (c) a polynucleotide which has a nucleotide sequence that encodes a protein, wherein the protein has an amino acid sequence having at least 95% identity, preferably at least 97-99% identity, to the amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182 or 184 and acts to promote STAT6 activation.

Polynucleotides which are identical or substantially identical to a nucleotide sequence contained in the above nucleotide sequence may be used as hybridization probes to isolate full-length cDNA or genomic clones encoding proteins of the present invention or cDNA and genomic clones of other genes that have a high sequence similarity to the above sequences, or as primers for a nucleic acid amplification reactions. Typically, these nucleotide sequences are 70% identical, preferably 80% identical, more preferably 90% identical, most preferably 95% identical to the above sequences. The probes or primers will generally comprises at least 15 nucleotides, preferably 30 nucleotides and may have 50 nucleotides. Particularly preferred probes will have between 30 and 50 nucleotides. Particularly preferred primers have

between 20 and 25 nucleotides.

The polynucleotide of the present invention may be either in the form of a DNA such as cDNA, a genomic DNA obtained by cloning or synthetically produced, or may be in the form of RNA such as mRNA. The polynucleotide may be single-stranded or double-stranded. The double-stranded polynucleotides may be double-stranded DNA, double-stranded RNA or DNA:RNA hybrid. The single-stranded polynucleotide may be sense strand also known as coding strand or antisense strand also known as non-coding strand.

Those skilled in the art can prepare a protein having the same activity that promotes STAT6 activation as the protein having an amino acid sequence represented by SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182 or 184 by means of appropriate substitution of an amino acid in the protein using known methods. One such method involves using conventional mutagenesis procedures for the DNA encoding the protein. Another method is, for example, site-directed mutagenesis (e.g., Mutan-Super Express Km Kit from Takara Shuzo Co., Ltd.). Mutations of amino acids in proteins may also occur in nature. Thus, the present invention also includes a mutated protein which is capable of promoting STAT6 activation and which has at least one amino acid deletion, substitution or addition compared to the protein having an amino acid sequence represented by SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182 or 184, as well as DNA encoding the protein. The number of mutation of amino acid is preferably 1 to 10, more preferably 1 to 5, most preferably 1 to 3.

The substitutions of amino acids are preferably conservative substitutions, specific examples of which are substitutions within the following groups: (glycine, alanine), (valine,

isoleucine, leucine), (aspartic acid, glutamic acid), (asparagine, glutamine), (serine, threonine), (lysine, arginine) and (phenylalanine, tyrosine). Based on the nucleotide sequences (e.g., a polynucleotide of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181 and 183) encoding a protein consisting of an amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182 or 184, or fragments thereof, those skilled in the art can routinely isolate a DNA with a high sequence similarity to these nucleotide sequences by using hybridization techniques and the like, and obtain proteins having the same activity that promotes STAT6 activation as the protein having of an amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182 or 184. Thus, the present invention also includes a protein that promotes STAT6 activation and comprises an amino acid sequence having a high identity to the amino acid sequence of above SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182 or 184. "High identity" refers to an amino acid sequence having an identity of at least 95%, preferably at least 97-99% over the entire length of an amino acid sequence represented by above SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70,

72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182 or 184.

The proteins of the present invention may be natural proteins derived from any human or animal cells or tissues, chemically synthesized proteins, or proteins obtained by genetic recombination techniques. The protein may or may not be subjected to post-translational modifications such as sugar chain addition or phosphorylation.

Examples of the protein encoded by the gene of the present invention includes secretory proteins (growth factors, cytokines, hormones, etc.), protein modifying enzymes (protein phosphorylases, protein dephosphorylases, proteases, etc), intranuclear proteins (intranuclear receptors, transcription factors) and membrane proteins. Membrane proteins include receptors, cellular adhesion molecules, ion channels, transporters, etc. Where the protein is a membrane protein, a compound selected by the below-described screening is more useful as a medical compound research tool since it is expected to easily migrate into a cell or give signal transduction into a cell.

The present invention also includes a polynucleotide encoding the above protein of the present invention. Examples of nucleotide sequences encoding a protein consisting of an amino acid sequence of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182 or 184 include nucleotide sequences of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181 and 183. The DNA includes cDNA, genomic DNA, and chemically synthesized DNA. In accordance with the degeneracy of the genetic code, at least one nucleotide in the nucleotide sequence encoding a protein consisting of an amino acid sequence

of SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182 or 184, can be substituted with other nucleotides without altering the amino acid sequence of the protein produced from the gene. Therefore, the DNA sequences of the present invention also include nucleotide sequences altered by substitution based on the degeneracy of the genetic code. Such DNA sequences can be synthesized using known methods.

The DNA of the present invention includes a DNA which encodes a protein capable of promoting STAT6 activation and hybridizes under stringent conditions with the DNA of the above nucleotide sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181 or 183 or complementary nucleotide sequence thereof. Stringent conditions are apparent to those skilled in the art, and can be easily attained in accordance with various laboratory manuals such as T. Maniatis et al., *Molecular Cloning A Laboratory Manual*, and Cold Spring Harbor Laboratory 1982, 1989.

That is, "stringent conditions" refer to overnight incubation at 37°C in a hybridization solution containing 30% formamide, 5 x SSC (0.75 M NaCl, 75mM trisodium citrate), 5 x Denhardt's solution, 0.5% SDS, 100µg/ml denatured, sheared salmon sperm DNA) followed by washing (three times) in 2 x SSC, 0.1% SDS for 10 minutes at room temperature, then followed by washing (two times) in 1 x SSC, 0.1% SDS for 10 minutes at 37°C (low stringency). Preferred stringent conditions are overnight incubation at 42°C in a hybridization solution containing 40% formamide, followed by washing (three times) in 2 x SSC, 0.1% SDS for 10 minutes at room temperature, then followed by washing (two times) in 0.2 x SSC, 0.1% SDS for 10 minutes at 42°C (moderate stringency). More preferred stringent conditions are overnight incubation at 42°C in a hybridization solution containing 50%

formamide, followed by washing (three times) in 2 x SSC, 0.1% SDS for 10 minutes at room temperature, followed by washing (two times) in 0.2 x SSC, 0.1% SDS for 10 minutes at 50°C (high stringency). The DNA sequence thus obtained must encode a protein capable of promoting STAT6 activation.

The present invention also includes a polynucleotide comprising a nucleotide sequence which encodes a protein capable of promoting STAT6 activation and has a high sequence similarity to the nucleotide sequence of the polynucleotide according to above item (3), (4) or (5). Typically these nucleotide sequences are 95% identical, preferably 97% identical, most preferably at least 99% identical to the nucleotide sequence of the polynucleotide according to above item (3), (4) or (5) over the entire length thereof.

The above DNA of the present invention can be used to produce the above protein using recombinant DNA techniques. In general, the DNA and peptide of the present invention can be obtained by:

- (A) cloning the DNA encoding the protein of the present invention;
- (B) inserting the DNA encoding the entire coding region of the protein or a part thereof into an expression vector to construct a recombinant vector;
- (C) transforming a host with the recombinant vector thus constructed; and
- (D) culturing the obtained host to express the protein or its analogue, and then purifying it by column chromatography.

General procedures necessary to handle DNA and recombinant hosts (e.g., *E. coli*) in the above steps are well known to those skilled in the art, and can be easily carried out in accordance with various laboratory manuals such as T. Maniatis et al., *supra*. All the enzymes, reagents, etc., used in these procedures are commercially available, and unless otherwise stated, such commercially available products can be used according to the use conditions specified by the manufactures' instructions to attain completely its objects. The above steps (A) to (D) can be further illustrated in more details as follows.

Techniques for cloning the DNA encoding the protein of the present invention in the above step (A) include, in addition to the methods described in the specification of the present application, PCR amplification using a synthetic DNA having a portion of the nucleotide

sequence of the present invention (e.g., SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181 or 183), as a primer, and selection of the DNA inserted into a suitable vector by hybridization with a labeled DNA fragment encoding a partial or full coding region of the protein of the present invention or a labeled synthetic DNA. Another technique involves direct amplification from total RNAs or mRNA fractions prepared from cells or tissues, using the reverse transcriptase polymerase chain reaction (RT-PCR method). As a DNA inserted into a suitable vector, for example, a commercially available library (e.g., from CLONTECH and STRATAGENE) can be used. Techniques for hybridization are normally used in the art, and can be easily carried out in accordance with various laboratory manuals such as T. Maniatis et al., *supra*. Depending on the intended purpose, the cloned DNA encoding the protein of the present invention can be used as such or if desired after digestion with a restriction enzyme or addition of a linker. The DNA thus obtained may have a nucleotide sequence of SEQ ID NO: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181 or 183, or may be a polynucleotide of above items (3) to (7). The DNA to be inserted into an expression vector in the above step (B) may be a full-length cDNA encoding the above full-length protein or a DNA fragment thereof, or may be a DNA fragment constructed so that it expresses a part thereof.

Thus, the present invention also provides a recombinant vector, which comprises the above DNA. The expression vector capable of expressing the protein of the present invention can be produced, for example, by excising the desired DNA fragment from the DNA encoding the protein of the present invention, and ligating the DNA fragment downstream of a promoter in a suitable expression vector.

Expression vectors for use in the present invention may be any vectors derived from prokaryotes (e.g., *E. coli*), yeast, fungi, insect viruses and vertebrate viruses. The vectors should be selected to be compatible with hosts. Suitable combinations of host – expression vector systems are selected depending on the desired expression product.

When bacteria are used as hosts, plasmid vectors compatible with these bacteria are generally used as replicable expression vectors for recombinant DNA molecules. For example, the plasmids pBR322 and pBR327 can be used to transform *E. coli*. Plasmid vectors normally contain an origin of replication, a promoter, and a marker gene conferring upon a recombinant DNA a phenotype useful for selecting the cells transformed with the recombinant DNA. Example of such promoters include lactose promoter and tryptophan promoter. Examples of such marker genes include an ampicillin resistance gene, and a tetracycline resistance gene. Examples of suitable expression vectors include the plasmids pUC18 and pUC19 in addition to pBR322, pBR327.

In order to express the DNA of the present invention in yeast, for example, YEpl24 can be used as a replicable expression vector. The plasmid YEpl24 contains the URA3 gene, which can be employed as a marker gene. Examples of promoters in expression vectors for yeast cells include promoters of genes of 3-phosphoglycerate kinase, glyceraldehyde-3-phosphate dehydrogenase, alcohol dehydrogenase and the like.

Examples of promoters and terminators for use in expression vectors to express the DNA of the present invention in fungal cells include promoters and terminators derived from genes for phosphoglycerate kinase (PGK), glyceraldehyde-3-phosphate dehydrogenase (GAPD), actin and the like. Examples of suitable expression vectors include the plasmids pPGACY2 and pBSFAHY83.

Examples of promoters for use in expression vectors to express the DNA of the present invention in insect cells include a polyhedrin promoter and P10 promoter. Examples of expression vector suitable for insect cells include baculovirus.

Recombinant vectors used to express the DNA of the present invention in animal cells normally contain functional sequences to regulate genes, an origin of replication, a promoter to be placed upstream of the DNA of the present invention, a polyadenylation site and a

transcription termination sequence. Such functional sequences, which can be used to express the DNA of the present invention in cells, can be obtained from viruses and viral substances.

Examples of such functional sequences include an SR α promoter, SV40 promoter, LTR promoter, CMV (cytomegalovirus) promoter and HSV-TK promoter. Among them, a CMV promoter and SR α promoter can be preferably used. As promoters to be placed inherently upstream of the gene encoding the protein of the present invention, any promoters can be used so long as they are suitable for use in the above host-vector systems. Examples of origins of replication include foreign origins of replication, for example, those derived from viruses such as adenovirus, polyoma virus and SV40 virus. When vectors capable of integration into host chromosomes are used as expression vectors, origins of replication of the host chromosomes may be employed.

Examples of suitable expression vectors include the plasmids pSV2-dhfr (ATCC 37146), pBPV-1(9-1) (ATCC 37111), pcDNA3.1 (INVITROGEN) and pME18S-FL3.

The present invention also provides a transformant which comprises the above recombinant vector. Microorganisms or cells transformed with the recombinant vector of the present invention can be selected from remaining untransformed parent cells based on at least one phenotype conferred by the recombinant vector. Phenotypes can be conferred by inserting at least one marker gene into the recombinant vector. Marker genes naturally contained in replicable vectors can be employed. Examples of marker genes include drug resistance genes such as neomycin resistance genes, and genes encoding dihydrofolate reductase.

As hosts for use in the above step (C), any of prokaryotes (e.g., *E. coli*), microorganisms (e.g., yeast and fungi) as well as insect and animal cells can be used so long as such hosts are compatible with the expression vectors used. Examples of such microorganisms include *Escherichia coli* strains such as *E. coli* K12 strain 294 (ATCC 31446), *E. coli* X1776 (ATCC 31537), *E. coli* C600, *E. coli* JM109 and *E. coli* B strain; bacterial strains belonging to the genus *Bacillus* such as *Bacillus subtilis*; intestinal bacteria other than *E. coli*, such as *Salmonella typhimurium* or *Serratia marcescens*; and various strains belonging to the genus *Pseudomonas*. Examples of yeast include *Saccharomyces cerevisiae*,

Schizosaccharomyces pombe, and Pichia pastoris. Examples of fungi include Aspergillus nidulans, and Acremonium chrysogenum (ATCC 11550).

As insect cells, for example, Spodoptera frugiperda (Sf cells), High FiveTM cells derived from eggs of Trichoplusia, etc., can be used when the virus is AcNPV. Examples of animal cells include HEK 293 cells, COS-1 cells, COS-7 cells, Hela cells, and Chinese hamster ovary (CHO) cells. Among them, CHO cells and HEK 293 cells are preferred. When animal cells are used as hosts, combinations of expression vectors and hosts to be used vary with experimental objects. According to such combinations, two types of expression (i.e. transient expression and constitutive expression) can be included.

"Transformation" of microorganisms and cells in the above step (C) refers to introducing DNA into microorganisms or cells by forcible methods or phagocytosis of cells and then transiently or constitutively expressing the trait of the DNA in a plasmid or an intra-chromosome integrated form. Those skilled in the art can carry out transformation by known methods [see e.g., "Idenshi Kougaku Handbook (Genetic Engineering Handbook)", an extra issue of "Jikken Igaku (Experimental Medicine)", YODOSHA CO., LTD.]. For example, in the case of animal cells, DNA can be introduced into cells by known methods such as DEAE-dextran method, calcium-phosphate-mediated transfection, electroporation, lipofection, etc. For obtaining cells which stably express the protein of the present invention using animal cells, there is a method in which selection can be carried out by clonal selection of the animal cells containing the chromosomes into which the introduced expression vectors have been integrated. For example, transformants can be selected using the above selectable marker as an indication of successful transformation. In addition, the animal cells thus obtained using the selectable marker can be subjected to repeated clonal selection to obtain stable animal cell strains highly capable of expressing the protein of the present invention. When a dihydrofolate reductase (DHFR) gene is used as a selectable marker, one can culture animal cells while gradually increasing the concentration of methotrexate (MTX) and select the resistant strains, thereby amplifying the DNA encoding the protein of the present invention together with the DHFR gene to obtain animal cell strains having higher levels of expression.

The above transformant can be cultured under conditions which permit the expression

of the DNA encoding the protein of the present invention to produce and accumulate the protein of the present invention. In this manner, the protein of the present invention can be produced. Thus, the present invention also provides a process for producing a protein, which comprises culturing a transformant comprising the isolated polynucleotide according to above item (3) to (7) under conditions providing expression of the encoded protein and recovering the protein from the culture (namely, cell itself or culture medium).

The above transformant can be cultured by methods known to those skilled in the art (see e.g., "Bio Manual Series 4", YODOSHA CO., LTD.). For example, animal cells can be cultured by various known animal cell culture methods including attachment culture such as Petri dish culture, multitray type culture and module culture, attachment culture in which cells are attached to cell culture carriers (microcarriers), or suspension culture in which productive cells themselves are suspended. Examples of medium for use in the culture include medium commonly used for animal cell culture, such as D-MEM and RPMI 1640.

In order to separate and purify the protein of the present invention from the above culture, suitable combinations of per se known separation and purification methods can be used. Examples such methods include methods based on solubility, such as salting-out and solvent precipitation; methods based on the difference in charges, such as ion-exchange chromatography; methods mainly based on the difference in molecular weights, such as dialysis, ultrafiltration, gel filtration and SDS-polyacrylamide gel electrophoresis; methods based on specific affinity, such as affinity chromatography; methods based on the difference in hydrophobicity, such as reverse phase high performance liquid chromatography; and methods based on the difference in isoelectric points, such as isoelectric focusing. For example, a protein of the present invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxyapatite chromatography and lectin chromatography. Preferably, high performance liquid chromatography is employed for purification. Well known techniques for refolding proteins may be employed to regenerate active conformation when the polypeptide is denatured during intracellular synthesis, isolation

or purification.

The protein of the present invention can also be produced as a fusion protein with another protein. These fusion proteins are also included within the present invention. For the expression of such fusion proteins, any vectors can be used so long as the DNA encoding the protein can be inserted into the vectors and the vectors can express the fusion protein. Examples of proteins to which a polypeptide of the present invention can be fused include glutathione S-transferase (GST) and a hexa-histidine sequence (6 x His). The fusion protein of the protein of the present invention with another protein can be advantageously purified by affinity chromatography using a substance with an affinity for the fusion partner protein. For example, fusion proteins with GST can be purified by affinity chromatography using glutathione as a ligand.

When the protein of the present invention is a membrane protein, a transformant into which DNA encoding the protein of the present invention has been introduced can express the protein on its membrane. The membrane which is prepared from such transformants and contains the protein of the present invention is also included within the present invention. As used herein, "membrane of a cell" includes cell membrane, and membrane of cell organelle. The membrane of a cell can be prepared by a method known to those skilled in the art. For example, cells are collected from the culture where transformants are cultured, and suspended in a suitable buffer. Then, the cells are lysed by a homogenizer or by vortex after addition of glassbeads. The obtained solution is centrifuged to remove uncrushed cells and the like, and the supernatant is ultracentrifuged under a suitable condition, and the obtained precipitate is suspended in a buffer to prepare a membrane fraction. The condition for ultracentrifugation can be suitably selected depending on the type of membrane and the like.

The present invention also provides a protein capable of inhibiting the activity of the protein of the present invention. Examples of such proteins include antibodies, or other proteins that bind to active sites of the protein of the present invention, thereby inhibiting the expression of their activity.

The present invention also relates to an antibody that reacts with the protein of the present invention or a fragment thereof, and to production of such an antibody. More

preferably, the present invention relates to an antibody that specifically react with the protein of the present invention or a fragment thereof, and to production of such an antibody. As used herein, "specifically" means that cross-reactivity is low, more preferably cross-reactivity is not present.

The antibody of the present invention is not specifically limited so long as it can recognize the protein of the present invention. Examples of such antibodies include polyclonal antibodies, monoclonal antibodies and their fragments, single chain antibodies and humanized antibodies. Antibody fragments can be produced by known techniques. Examples of such antibody fragments include, but not limited to, F(ab')₂ fragments, Fab' fragments, Fab fragments and Fv fragments. For example, a monoclonal or polyclonal antibody can be produced by administering the protein according to above item (1) or (2) or epitope-bearing fragments as an antigen to a non-human animal. The antibody against the protein of the present invention can be produced by using the protein of the present invention or a peptide thereof as an immunogen according to per se known process for producing antibodies or antisera. Such methods are described, for example, in "Shin Idenshi Kougaku Handbook (New Genetic Engineering Handbook)", the third edition, an extra issue of "Jikken Igaku (Experimental Medicine)", YODOSHA CO., LTD.

In the case of polyclonal antibodies, for example, the protein of the present invention or a peptide thereof can be injected to animals such as rabbits to produce antibodies directed against the protein or peptide, and then their blood can be collected. The polyclonal antibodies can be purified from the blood, for example, by ammonium sulfate precipitation or ion-exchange chromatography, or by using the affinity column on which the protein has been immobilized.

In the case of monoclonal antibodies, for example, animals such as mice are immunized with the protein of the present invention, their spleen is removed and homogenized to obtain spleen cells, which are then fused with mouse myeloma cells by using a reagent such as polyethylene glycol. From the resulting fused cells (i.e. hybridoma), the clone producing the antibody directed against the protein of the present invention can be selected. Then, the resulting clonal hybridoma can be implanted intraperitoneally into mice, the ascitic fluid

recovered from the mice. The resulting monoclonal antibody can be purified, for example, by ammonium sulfate precipitation or ion-exchange chromatography, or by using the affinity column on which the protein has been immobilized.

When the resulting antibody is used to administer to humans, it is preferable to use a humanized antibody or human antibody in order to reduce its immunogenicity. These humanized antibodies or human antibodies can be produced using transgenic mice or other mammals. For a general review of humanized antibodies, see, for example, Morrison, S.L. et al., Proc. Natl. Acad. Sci. USA, 81:6851-6855 (1984); Jones, P.T. et al., Nature 321:522-525 (1986); Hiroshi Noguchi, Igaku no Ayumi (J. Clin. Exp. Med.) 167:457-462 (1993); Takashi Matsumoto, Kagaku to Seibutsu (Chemistry and Biology) 36:448-456 (1998). Humanized chimeric antibodies can be produced by linking a V region of a mouse antibody to a C region of a human antibody. Humanized antibodies can be produced by substituting a sequence derived from a human antibody for a region other than a complementarity-determining region from a mouse monoclonal antibody.

In addition, human antibodies can be directly produced in the same manner as the production of conventional monoclonal antibodies by immunizing the mice whose immune systems have been replaced with human immune systems. These antibodies can be used to isolate or to identify clones expressing the protein or to purify the protein of the present invention from a cell extract or transformant producing the protein of the present invention. These proteins can also be used to construct ELISA, RIA (radioimmunoassay) and western blotting systems. These assay systems can be used for diagnostic purposes for detecting an amount of the protein of the present invention present in a body sample in a tissue or a fluid in the blood of an animal, preferably human. For example, these antibodies can be used for diagnosis of a disease characterized by undesirable activation of STAT6 resulting from (expression) abnormality of the protein of the present invention, such as allergic disease, inflammation, autoimmune disease, diabetes, hyperlipidemia, infection (for example, HIV infection), cancer and the like. In order to provide a basis for diagnosis of a disease, a standard value must be established regarding the expression of the protein of the present invention. However, this is a well-known technique to those skilled in the art. For example,

a method of calculating the standard value comprises binding a body fluid or a cell extract of normal individual of a human or an animal to an antibody against the protein of the present invention under a suitable condition for the complex formation, detecting the amount of the antibody-protein complex by chemical or physical means and then calculating the standard value for the normal sample using a standard curve prepared from a standard solution containing a known amount of an antigen (the protein of the present invention). The presence of a disease can be confirmed by deviation from the standard value obtained by comparison of the standard value with the value obtained from a sample of an individual latently suffering from a disease associated with the protein of the present invention. These antibodies can also be used as reagents for studying functions of the protein of the present invention.

The antibody of the present invention can be used as a medicament as mentioned below. When the antibody of the present invention is used as a medicament, it is preferred to use an antibody capable of inhibiting the activity of promoting STAT6 activation possessed by the present invention (that is, neutralizing antibody).

The antibodies of the present invention can be purified and then administered to patients characterized by undesirable activation of STAT6 resulting from (expression) abnormality of the protein of the present invention, such as allergic disease, inflammation, autoimmune disease, diabetes, hyperlipidemia, infection (such as HIV infection), cancer and the like. Thus in another aspect, the present invention is a pharmaceutical composition which comprises the above antibody as an active ingredient, and a method for therapy and/or prevention using the antibody of the present invention. In such pharmaceutical compositions of the present invention, the active ingredient may be combined with other therapeutically or preventively active ingredients or inactive ingredients (e.g., conventional pharmaceutically acceptable carriers or diluents such as immunogenic adjuvants) and physiologically non-toxic stabilizers and excipients. The resulting combinations can be sterilized by filtration, and formulated into vials after lyophilization or into various dosage forms in stabilized and preservable aqueous preparations.

Administration to a patient can be intra-arterial administration, intravenous

administration and subcutaneous administration, which are well known to those skilled in the art. The dosage range depends upon the weight and age of the patient, route of administration and the like. Suitable dosages can be determined by those skilled in the art. The antibody of the present invention exhibits therapeutic activity by inhibiting the promotion of STAT6 activation mediated by the protein of the present invention.

The DNA of the present invention can also be used to isolate, identify and clone other proteins involved in intracellular signal transduction processes. For example, the DNA sequence encoding the protein of the present invention can be used as a "bait" in yeast two-hybrid systems (see e.g., Nature 340:245-246 (1989)) to isolate and clone the sequence encoding a protein ("prey") which can associate with the protein of the present invention. In a similar manner, it can be determined whether the protein of the present invention can associate with other cellular proteins (e.g., STAT6, JAK1). In another method, proteins which can associate with the protein of the present invention can be isolated from cell extracts by immunoprecipitation [see e.g., "Shin Idenshi Kougaku Handbook (New Genetic Engineering Handbook)", an extra issue of "Jikken Igaku (Experimental Medicine)", YODOSHA CO., LTD.] using antibodies directed against the protein of the present invention. In still another method, the protein of the present invention can be expressed as a fusion protein with another protein as described above, and immunoprecipitated with an antibody directed against the fusion protein to isolate a protein which can associate with the protein of the present invention.

The present invention provides a process for diagnosing a disease or susceptibility to a disease related to expression or activity of the protein of present invention in a subject comprising the steps of:

- (a) determining the presence or absence of a mutation in the gene encoding said protein in the genome of said subject; and/or
- (b) analyzing the amount of expression of said protein in a sample derived from said subject.

The diagnostic assays offer a process for diagnosing diseases or determining a susceptibility to the diseases through detection of mutation in a gene for the protein of the present invention which has an activity of promoting STAT6 activation. In addition, such

diseases may be diagnosed by analyzing expression level of the gene in a sample derived from a subject at protein or mRNA level, and detecting an abnormally decreased or increased level of the expression.

Determination of the presence or absence of a mutation in the gene encoding the protein of the present invention which has an activity of promoting STAT6 activation, may involve RT-PCR using a part of the nucleotide sequences of genes as a primer, followed by conventional DNA sequencing to detect the presence or absence of the mutation. PCR-SSCP [Genomics 5:874-879 (1989); "Shin Idenshi Kougaku Handbook (New Genetic Engineering Handbook)", an extra issue of "Jikken Igaku (Experimental Medicine)", YODOSHA CO., LTD.] can also be used to determine the presence or absence of the mutation.

Decreased or increased expression of a gene in a sample can be measured at the RNA level using any of the methods well known in the art for the quantitation of polynucleotides, for example, nucleic acid amplification methods such as RT-PCR, and methods such as RNase protection assay, Northern blotting and other hybridization methods. Assay techniques that can be used to determine levels of a protein in a sample derived from a host are well-known to those skilled in the art. Such assay methods include radioimmunoassays, competitive-binding assays, Western blot analysis and ELISA assays. When an expression level is determined at a protein level, the antibody of the present invention mentioned above can be used.

The degree of abnormality of expression level of gene in a sample is not particularly limited. For example, when the level of the expressed protein is 2 or more times, or 1/2 or less, as compared with normal case, the subject may be diagnosed to be a disease. In another example, when the level of the expressed protein is 3 or more times, or 1/3 or less, as compared with normal case, the subject may be diagnosed to be a disease.

The DNA of the present invention can be used to detect abnormality in the DNA or mRNA encoding the protein of the present invention or a peptide fragment thereof. Thus, for example, the DNA of the present invention is useful for gene diagnosis regarding damage, mutations, and reduced, increased or over- expression of the DNA or mRNA.

When the nucleotide sequence encoding the protein of the present invention in a

genome of an individual contains a mutation, the mutation may cause a disease associated with the expression and/or activity of STAT6.

When the amount of the expression of the protein in a sample from an individual is different from the normal value, the abnormal expression of the novel protein of the present invention which has an activity of promoting STAT6 activation may be responsible for diseases associated with the expression and/or activity of STAT6.

The present invention also relates to a method for screening compounds which inhibit or promote STAT6 activation.

It should be noted that compounds that inhibit STAT6 activation, will, as a result of this action, have *in vivo* and *in vitro* activity as a STAT6 inhibiting agent. Also, compounds that promote STAT6 activation, will, as a result of this action, have *in vivo* and *in vitro* activity as a STAT6 activating agent. Consequently, the above screening method is for screening in respect of activity as an inhibiting agent or activating agent of STAT6, and the above compound is a compound having activity as an inhibiting agent or activating agent of STAT6.

The above screening method comprises the following steps:

- (a) preparing a transformant by introducing a gene encoding a protein that promotes STAT6 activation according to the present invention and a gene encoding a signal which can detect STAT6 activation into a cell;
- (b) culturing the transformant under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;
- (c) measuring the signal which can detect STAT6 activation; and
- (d) selecting a candidate compound which can change the signal amount as compared with the case of the absence of candidate compounds, as a compound which inhibit or promote STAT6 activation.

A compound that increases the detectable signal 1.2-fold or higher than normal is preferably isolated or identified as an activator compound, and a compound that decreases the detectable signal 80% or less than normal is preferably isolated or identified as an inhibitor compound.

Examples of genes encoding a signal which can detect promotion of STAT6

activation include reporter genes. Reporter genes are used instead of directly detecting the activation of transcription factors of interest to be tested. The transcriptional activity of a promoter of a gene is analyzed by linking the promoter to a reporter gene and measuring the activity of the product of the reporter gene ("Bio Manual Series 4" (1994), YODOSHA CO., LTD.).

Any peptide or protein can be used so long as those skilled in the art can measure the activity or amount of the expression product (including the amount of the produced mRNA) of the reporter genes. For example, enzymatic activity of chloramphenicol acetyltransferase, β -galactosidase, luciferase, etc., can be measured. Any reporter plasmids can be used to evaluate STAT6 activation so long as the reporter plasmids have an STAT6 recognition sequence inserted upstream of the reporter gene. For example, a sequence derived from the CD23 or germline C epsilon transcription initiation site can be used. Other examples include reporter plasmids described in J. Biol. Chem. 275, 26500-26506 (2000), J. Exp. Med. 190, 1837-1848 (1999), J. Immunol. 150, 5408-5417 (1993), J. Immunol. 157, 2058-2065 (1996).

Any host can be used so long as promotion of STAT6 activation can be detected in the hosts. Preferred hosts are mammalian cells such as NIH3T3 cells, HepG2 cells and the like. Transformation and culture of the cells can be carried out as described above.

In a specific embodiment, the method for screening a compound which inhibits or promotes STAT6 activation comprises culturing the transformant for a certain period of time, adding a certain amount of a test compound, measuring the reporter activity expressed by the cell after a certain period of time, and comparing the activity with that of a cell to which the test compound has not been added. On this occasion, proper stimulation, e.g. addition of IL-4, etc. may be optionally carried out at the same time. The reporter activity can be measured by methods known in the art (see e.g., "Bio Manual Series 4" (1994), YODOSHA CO., LTD.).

Examples of test compounds for the screening include, but not limited to, low molecular weight compounds and peptides. Test compounds may be artificially synthesized compounds or naturally occurring compounds. Test compounds may be a single compound or mixtures. Usable examples includes a library of low molecular weight compounds, a

compound library which was synthesized by combinatorial chemistry, a naturally occurring product containing cells, plants, animals or a part thereof, or an extracted product of such naturally occurring product. When a mixture containing several compounds is used as a test substance for screening, the test substance which shows an activity of inhibiting or promoting STAT6 activation can be further screened to isolate a single substance having the activity. Isolation and purification of a desired compound from a mixture can be carried out by using any known method such as filtration, extraction, washing, drying, concentration, crystallization or various chromatography in combination.

The method for screening according to the present invention can be carried out by the following steps:

- (a) preparing a transformant by introducing a gene encoding a protein that promotes STAT6 activation according to the present invention into a cell;
- (b) culturing the transformant under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;
- (c) measuring an activity of STAT6; and
- (d) selecting a candidate compound which can change the activity of STAT6 as compared with the case of the absence of candidate compounds, as a compound which inhibit or promote STAT6 activation.

In the above method, the amount of mRNA or proteins for genes whose expression is known to be induced by STAT6 activation (e.g., genes for IL-1 Receptor Antagonist, CD23, MHC Class II and STAT6) is measured instead of using a reporter gene assay as a method for detecting a detectable signal. Activated STAT6 can also be quantified by a method for detecting bindings of DNA and protein such as gel mobility shift assay using nuclear extract, etc. Alternatively, phosphorylation of STAT6 can be quantified with cell extracts.

The amount of mRNA can be measured, for example, by northern hybridization, RT-PCR, etc. The amount of proteins can be measured, for example, by using antibodies. The antibodies may be produced by known methods. Commercially available antibodies (from, e.g., Wako Pure Chemical Industries, Ltd.) can also be used.

The present invention further provides a method of producing a pharmaceutical

composition, which comprises the following steps (a) to (e):

- (a) preparing a transformant by introducing a gene encoding a protein that promotes STAT6 activation according to the present invention and a gene encoding a signal which can detect STAT6 activation into a cell;
- (b) culturing the transformant under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;
- (c) measuring the signal which can detect STAT6 activation;
- (d) selecting a candidate compound which can change the signal amount as compared with the case of the absence of candidate compounds, as a compound which inhibit or promote STAT6 activation; and
- (e) producing a pharmaceutical composition which comprises a compound selected in the step of (d).

In the present invention, a pharmaceutical composition may also be produced by the following steps (a) to (e):

- (a) preparing a transformant by introducing a gene encoding a protein that promotes STAT6 activation according to the present invention into a cell;
- (b) culturing the transformant under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;
- (c) measuring an activity of STAT6;
- (d) selecting a candidate compound which can change the activity of STAT6 as compared with the case of the absence of candidate compounds, as a compound which inhibit or promote STAT6 activation; and
- (e) producing a pharmaceutical composition which comprises a compound selected in the step of (d).

In the step (d) of the method of producing a pharmaceutical composition, it is preferable to isolate or identify as an activator compound, a compound that increases said detectable signal 1.2-fold or higher than normal, and to isolate or identify as an inhibitor compound, a compound that decreases said detectable signal 80% or less than normal.

The protein of the present invention may also be used in a method for the

structure-based design of an agonist, antagonist or inhibitor of the protein, by:

- (a) determining in the first instance the three-dimensional structure of the protein;
- (b) deducing the three-dimensional structure for the likely reactive or binding site(s) of an agonist, antagonist or inhibitor;
- (c) synthesising candidate compounds that are predicted to bind to or react with the deduced binding or reactive site; and
- (d) testing whether the candidate compounds are indeed agonists, antagonists or inhibitor.

The present invention also provides a compound which is selected by the above screening method. This compound has an activity of inhibiting or promoting STAT6 activation. More specifically, this compound has an activity of inhibiting or promoting STAT6 activation which is promoted by the protein of the present invention.

Since the compounds obtained by the above screening methods have an activity of inhibiting or promoting STAT6 activation, they are useful as therapeutic or preventive pharmaceuticals for the treatment of diseases resulting from unfavorable activation or inactivation of STAT6.

When obtainment of a salt of the compounds is desired, a compound which is obtained in the form of a salt can be purified as it is. A compound which is obtained in the free form can be converted into a salt by isolating and purifying a salt obtained by dispersing or dissolving the compound into a suitable solvent and then adding a desired acid or base. Examples of a step to optimize the compounds or salts thereof obtained by the method of the present invention as a pharmaceutical composition, include methods of formulating according to ordinary processes such as the following. The above compounds or their pharmaceutically acceptable salts in an amount effective as an active ingredient, and pharmaceutically acceptable carriers can be mixed. A form of formulation suitable for the mode of administration is selected. A composition suitable for oral administration includes a solid form such as tablet, granule, capsule, pill and powder, and solution form such as solution, syrup, elixir and dispersion. A form useful for parenteral administration includes sterile solution, dispersion, emulsion and suspension. The above carriers include, for example, sugars such as gelatin, lactose and glucose, starches such as corn, wheat, rice and maize, fatty

acids such as stearic acid, salts of fatty acids such as calcium stearate, magnesium stearate, talc, vegetable oil, alcohol such as stearyl alcohol and benzyl alcohol, gum, and polyalkylene glycol. Examples of such liquid carriers include generally water, saline, sugar solution of dextrose and the like, glycols such as ethylene glycol, propylene glycol and polyethylene glycol.

The present invention provides a kit for screening a compound which inhibits or promotes STAT6 activation. The kit comprises: (a) a transformant comprising a gene encoding a protein that promotes STAT6 activation according to the present invention and a gene encoding a signal which can detect promotion of STAT6 activation; and (b) reagents for measuring the signal. The kit comprises reagents necessary for screening compounds which inhibits or promotes STAT6 activation.

In another aspect, the present invention relates to a diagnostic kit which comprises:

- (a) a polynucleotide of the present invention having a nucleotide sequence represented by any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181 and 183;
- (b) a polynucleotide having a nucleotide sequence complementary to that of (a);
- (c) a protein of the present invention having an amino acid sequence represented by any one of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182 and 184, or a fragment thereof; or
- (d) an antibody to a protein of the present invention of (c).

A diagnostic kit comprising at least any one of (a) to (d) is useful for diagnosing a disease or susceptibility to a disease such as allergic disease, inflammation, autoimmune diseases, diabetes, hyperlipidemia, infectious diseases (e.g., HIV infection) and cancers.

Because STAT6 is involved in a wide variety of pathological conditions such as

allergic disease, inflammation, autoimmune diseases, diabetes, hyperlipidemia, cancers and viral infections, it is an attractive target for drug design and therapeutic intervention. Many experiments show that the inhibition of STAT6 activity may have significant physiological effects [see e.g., Nature 380, 627-630 (1996), Nature 380, 630-633 (1996), Immunity 4, 313-319 (1996), J. Immunol. 157, 3220-3222 (1996), Immunity 8, 255-264 (1998), J. Exp. Med. 187, 939-948 (1998), J. Exp. Med. 187, 1537-1542 (1998)].

The finding of the new protein described herein capable of promoting STAT6 activation has provided a new method for inhibiting an abnormal STAT6 function.

The present invention also relates to use of a compound which inhibits the function of the protein capable of promoting STAT6 activation described above, for inhibiting STAT6 activation. The compound obtained by the above screening method, which inhibits STAT6 activation, is useful as a medicament to treat or prevent diseases characterized by undesirable activation of STAT6, such as allergic disease, inflammation, autoimmune diseases, diabetes, hyperlipidemia, infectious diseases (e.g., HIV infection) and cancers.

On the other hand, since STAT6 activation promotes differentiation into Th2 cells, there is also a possibility of reducing symptoms of or treating Th1 hyperactive diseases, for example, organ-specific autoimmune diseases such as multiple sclerosis and insulin-dependent diabetes mellitus, and rheumatism. Thus, the compound obtained by the above screening method, which promotes STAT6 activation, is useful as a medicament to treat or prevent these diseases.

In addition, the gene encoding the protein of the present invention is useful for gene therapy to treat various diseases such as cancers, autoimmune diseases, diabetes, hyperlipidemia, allergy diseases and inflammatory response. "Gene therapy" refers to administering into the human body a gene or a cell into which a gene has been introduced. The protein of the present invention and the DNA encoding the protein can also be used for diagnostic purposes. Thus, the present invention provides a agent for gene therapy which comprises a gene encoding the protein of the present invention.

When a gene encoding the protein of the present invention is used for a agent for gene therapy, a technique of RNA interference (RNAi) mentioned below may be applied. Thus,

the present invention provides a vector for gene therapy which expresses double strand RNA having a gene sequence encoding the protein of the present invention.

The form of the agent for gene therapy is not particularly limited, but includes a pharmaceutical composition which comprises an expression vector containing a gene of the present invention in a pharmaceutical carrier of physiological buffer. The pharmaceutical carrier may contain suitable stabilizer (for example, nuclease inhibitor), chelate agent (for example, EDTA), and/or other auxiliary agent. Alternatively, the agent for gene therapy of the present invention may be provided as a complex of an expression vector containing a gene of the present invention and a liposome. The agent for gene therapy may be applied using a catheter. For example, the agent for gene therapy of the present invention can be directly injected into a blood vessel of patient and the like.

The dosage of the agent for gene therapy of the present invention should be selected depending on the conditions such as age, sex, body weight and symptom of patient, and administration route, and is generally about $1 \mu\text{g/kg}$ to about 1000 mg/kg , more preferably about $10 \mu\text{g/kg}$ to about 100 mg/kg , as an amount of DNA (which is an effective ingredient) per one administration for adult. The number of administration is not particularly limited.

The compound obtained by the screening method of the present invention or a salt thereof can be formulated into the above pharmaceutical compositions (e.g., tablets, capsules, elixirs, microcapsules, sterile solutions and suspensions) according to conventional procedures. The formulations thus obtained are safe and of low toxicity, and can be administered, for example, to humans and mammals (e.g., rats, rabbits, sheep, pigs, cattle, cats, dogs and monkeys). Administration to patients can be carried out by methods known in the art, such as intra-arterial injection, intravenous injection and subcutaneous injection. The dosage may vary with the weight and age of the patient as well as a mode of administration, but those skilled in the art can appropriately select suitable dosages. When the compound can be encoded by DNA, the DNA can be inserted into a vector for gene therapy, and gene therapy can be carried out. Thus, the present invention relates to a medicament which comprises a compound which inhibits or promotes STAT6 activation as an active ingredient.

In addition, the above compound is useful as a medicament to treat or prevent

diseases characterized by undesirable activation of STAT6, such as allergic disease, inflammation, autoimmune diseases, diabetes, hyperlipidemia, viral diseases, infectious diseases and cancers. Thus, the present invention also relates to a pharmaceutical composition for allergic disease, inflammation, autoimmune diseases, diabetes, hyperlipidemia, viral diseases, cancers, etc., which comprises the above compound. Specifically, the pharmaceutical composition is useful as a therapeutic and prophylactic drug against, for example, rheumatoid arthritis, osteoarthritis, systemic lupus erythematosus, diabetes, sepsis, asthma, allergic rhinitis, ischemic heart diseases, inflammatory intestinal diseases, subarachnoid hemorrhage, viral hepatitis and AIDS.

The present invention also relates to the use of the above-mentioned compound for manufacturing a medicament for the treatment and/or prevention of allergic disease, inflammation, autoimmune diseases, diabetes, hyperlipidemia, viral diseases, cancers, etc.

The present invention also provides an antisense oligonucleotide against the polynucleotide of any one of above items (3) to (7). An antisense oligonucleotide refers to an oligonucleotide complementary to the target gene sequence. The antisense oligonucleotide can inhibit the expression of the target gene by inhibiting RNA functions such as translation to proteins, transport to the cytoplasm and other activity necessary for overall biological functions. In this case, the antisense oligonucleotide may be RNA or DNA. The DNA sequence of the present invention can be used to produce an antisense oligonucleotide capable of hybridizing with the mRNA transcribed from the gene encoding the protein of the present invention. It is known that an antisense oligonucleotide generally has an inhibitory effect on the expression of the corresponding gene (see e.g., Saibou Kougaku Vol.13, No.4 (1994)). The oligonucleotide containing an antisense coding sequence against a gene encoding the protein of the present invention can be introduced into a cell by standard methods. The oligonucleotide effectively blocks the translation of mRNA of the gene encoding the protein of the present invention, thereby blocking its expression and inhibiting undesirable activity.

The antisense oligonucleotide of the present invention may be a naturally occurring oligonucleotide or its modified form [see e.g., Murakami & Makino, Saibou Kougaku Vol.13, No.4, p.259-266 (1994); Akira Murakami, Tanpakushitsu Kakusan Kouso (PROTEIN,

NUCLEIC ACID AND ENZYME) Vol.40, No.10, p.1364-1370 (1995), Tunenari Takeuchi et al., Jikken Igaku (Experimental Medicine) Vol. 14, No. 4 p85-95(1996)]. Thus, the oligonucleotide may have modified sugar moieties or inter-sugar moieties. Examples of such modified forms include phosphothioates and other sulfur-containing species used in the art. According to several preferred embodiments of the present invention, at least one phosphodiester bond in the oligonucleotide is substituted with the structure which can enhance the ability of the composition to permeate cellular regions where RNA with the activity to be regulated is located.

Such substitution preferably involves a phosphorothioate bond, a phosphoramidate bond, methylphosphonate bond, or a short-chain alkyl or cycloalkyl structure. The antisense oligonucleotide may also contain at least some modified base forms. Thus, it may contain purine and pyrimidine derivatives other than naturally occurring purine and pyrimidine. Similarly, the furanosyl moieties of the nucleotide subunits can be modified so long as the essential purpose of the present invention is attained. Examples of such modifications include 2'-O-alkyl and 2'-halogen substituted nucleotides. Examples of modifications in sugar moieties at their 2-position include OH, SH, SCH₃, OCH₃, OCN or O(CH₂)_nCH₃, wherein n is 1 to about 10, and other substituents having similar properties. All the analogues are included in the scope of the present invention so long as they can hybridize with the mRNA of the gene of the present invention to inhibit functions of the mRNA.

The antisense oligonucleotide of the present invention contains about 3 to about 50 nucleotides, preferably about 8 to about 25 nucleotides, more preferably about 12 to about 20 nucleotides. The antisense oligonucleotide of the present invention can be produced by the well-known solid phase synthesis technique. Devices for such synthesis are commercially available from some manufactures including Applied Biosystems. Other oligonucleotides such as phosphothioates can also be produced by methods known in the art.

The antisense oligonucleotide of the present invention is designed to hybridize with the mRNA transcribed from the gene of the present invention. Those skilled in the art can easily design an antisense oligonucleotides based on a given gene sequence (For example, Murakami and Makino: Saibou Kougaku Vol. 13 No.4 p259-266 (1994), Akira Murakami:

Tanpakushitsu Kakusan Kousho (PROTEIN, NUCLEIC ACID AND ENZYME) Vol. 40 No.10 p1364-1370 (1995), Tunenari Takeuchi et al., Jikken Igaku (Experimental Medicine) Vol. 14 No. 4 p85-95 (1996)). Recent study suggests that antisense oligonucleotides which are designed in a region containing 5' region of mRNA, preferably, the translation initiation site, are most effective for the inhibition of the expression of a gene. The length of the antisense oligonucleotides is preferably 15 to 30 nucleotides and more preferably 20 to 25 nucleotides. It is important to confirm no interaction with other mRNA and no formation of secondary structure in the oligonucleotide sequence by homology search. The evaluation of whether the designed antisense oligonucleotide is functional or not can be determined by introducing the antisense oligonucleotide into a suitable cell and measuring the amount of the target mRNA, for example by northern blotting or RT-PCR, or the amount of the target protein, for example by western blotting or fluorescent antibody technique, to confirm the effect of expression inhibition.

Another method includes the triple helix technique. This technique involves forming a triple helix on the targeted intra-nuclear DNA sequence, thereby regulating its gene expression, mainly at the transcription stage. The antisense oligonucleotide is designed mainly in the gene region involved in the transcription and inhibits the transcription and the production of the protein of the present invention. Such RNA, DNA and oligonucleotide can be produced using known synthesizers.

The antisense oligonucleotide may be introduced into the cells containing the target nucleic acid sequence by any of DNA transfection methods such as calcium phosphate method, electroporation, lipofection, microinjection, or gene transfer methods including the use of gene transfer vectors such as viruses. An antisense oligonucleotide expression vector can be prepared using a suitable retrovirus vector, then the expression vector can be introduced into the cells containing the target nucleic acid sequence by contacting the vector with the cells in vivo or ex vivo.

The DNA of the present invention can be used in the antisense RNA/DNA technique or the triple helix technique to inhibit vascularization mediated by the protein of the present invention.

The antisense oligonucleotide against the gene encoding the protein of the present invention is useful as a medicament to treat or prevent diseases characterized by undesirable activation of STAT6, such as allergic disease, inflammation, autoimmune diseases, diabetes, hyperlipidemia, infectious diseases (e.g., HIV infection) and cancers. Thus, the present invention also provides a pharmaceutical composition which comprises the above antisense oligonucleotide as an active ingredient. The antisense oligonucleotide of the present invention can also be used to detect such diseases using northern hybridization or PCR.

The present invention also provides a ribozyme or deoxyribozyme which inhibits STAT6 activation. A ribozyme and deoxyribozyme is an RNA capable of recognizing a nucleotide sequence of a nucleic acid and cleaving the nucleic acid (see e.g., Hiroshi Yanagawa, "Jikken Igaku (Experimental Medicine) Bioscience 12: New Age of RNA). The ribozyme or deoxyribozyme can be produced so that it cleaves the selected target RNA (e.g., mRNA encoding the protein of the present invention). Based on the nucleotide sequence of the DNA encoding the protein of the present invention, the ribozyme or deoxyribozyme specifically cleaving the mRNA of the protein of the present invention can be designed. Such ribozyme or deoxyribozyme has a complementary sequence to the mRNA for the protein of the present invention, complementarily associates with the mRNA and then cleaves the mRNA, which results in reduction or entire loss of the expression of the protein of the present invention. The level of the reduction of the expression is dependent on the level of the ribozyme or deoxyribozyme expression in the target cells.

There are two types of ribozyme or deoxyribozyme commonly used: a hammerhead ribozyme and a hairpin ribozyme. In particular, hammerhead ribozymes or deoxyribozymes have been well studied regarding their primary and secondary structure necessary for their cleavage activity, and those skilled in the art can easily design the ribozymes nucleotided solely on the nucleotide sequence information for the DNA encoding the protein of the present invention [see e.g., Iida et al., Saibou Kougaku Vol.16, No.3, p.438-445 (1997); Ohkawa & Taira, Jikken Igaku (Experimental Medicine) Vol.12, No.12, p.83-88 (1994)]. It is known that the hammerhead ribozymes or deoxyribozymes have a structure consisting of two recognition sites (recognition site I and recognition site II forming a chain complementary to

target RNA) and an active site, and cleave the target RNA at the 3' end of its sequence NUX (wherein N is A or G or C or U, and X is A or C or U) after the formation of a complementary pair with the target RNA in the recognition sites. In particular, the sequence GUC (or GUA) has been found to have the highest activity [see e.g., Koizumi, M. et al., Nucl. Acids Res. 17:7059-7071 (1989); Iida et al., Saibou Kougaku Vol.16, No.3, p.438-445 (1997); Ohkawa & Taira, Jikken Igaku (Experimental Medicine) Vol.12, No.12, p.83-88 (1994); Kawasaki & Taira, Jikken Igaku (Experimental Medicine) Vol.18, No.3, p.381-386 (2000)].

Therefore the sequence GTC (or GTA) is searched out, and a ribozyme is designed to form several, up to 10 to 20 complementary base pairs around that sequence. The suitability of the designed ribozyme can be evaluated by checking whether the prepared ribozyme can cleave the target mRNA in vitro according to the method described for example in Ohkawa & Taira, Jikken Igaku (Experimental Medicine) Vol.12, No.12, p.83-88 (1994). The ribozyme can be prepared by methods known in the art to synthesize RNA molecules.

Alternatively, the sequence of the ribozyme can be synthesized on a DNA synthesizer and inserted into various vectors containing a suitable RNA polymerase promoter (e.g., T7 or SP6) to enzymatically synthesize an RNA molecule in vitro. Such ribozymes can be introduced into cells by gene transfer methods such as microinjection. Another method involves inserting DNA encoding a ribozyme into a suitable expression vector and introducing the vector into cell strains, cells or tissues. Suitable vectors can be used to introduce the ribozyme into a selected cell. Examples of vectors commonly used for such purpose include plasmid vectors and animal virus vectors (e.g., retrovirus, adenovirus, herpes or vaccinia virus vectors). Such ribozymes have an activity of inhibiting promotion of STAT6 activation mediated by the protein of the present invention.

According to the present invention, a double-stranded RNA is provided, which inhibits function of STAT6 activation.

The introduction of the double-stranded RNA into a cell enables the specific degradation of mRNA corresponding to the sequence of the RNA, and the degradation suppresses gene expression. Recently, this phenomenon, referred to as RNA interference (RNAi), has been revealed. One example of a method using RNAi is a method for

introducing an artificially synthesized small interfering RNA (siRNA) into a cell. siRNA is a double-stranded RNA of 19 to 25 base pairs which is mentioned as an important trigger to induce RNAi phenomena. With regard to the 19-to-25-nucleotide sequence in a suitable region of the sequence of a gene encoding the protein of the present invention, a sense RNA (wherein DNA sequence is substituted by RNA sequence) and an antisense RNA (having a sequence complementary to the sense RNA) are synthesized to prepare siRNA, and the siRNA is introduced into a cell by lipofection using, for example, fugene6, thereby enabling the use of RNAi.

In addition to the introduction of synthesized siRNA, a method that is also effective has been recently and gradually unveiled, which comprises: incorporating the 19-to-25-nucleotide sequence in a suitable region of the sequence of a gene encoding the protein of the present invention and a sequence complementary thereto into a plasmid; and temporarily expressing siRNA in the cell. More specifically, for example, pSilencer siRNA Expression Vector available from Ambion can be used (Morita Takashi et al., Protein, Nucleic Acid and Enzyme, Vol.4 No.14 p. 1939-p. 1945 (2001); Sugimoto Asako, Kagaku to Seibutu (Chemistry and Biology), Vol.40 No.11 pp.713-718).

The present invention provides also a method for obtaining a novel gene having a function. More specifically, there is provided a method which comprises constructing a full-length cDNA library by using the oligo-capping method, and detecting the presence of a protein having a function by using a signal factor. An example of such a signal factor is a reporter gene.

Methods using a cDNA library containing a lot of non-full-length cDNAs are inefficient in obtaining many genes (cDNAs) having functions. Therefore libraries with a high ratio of the number of the full-length cDNA clones to the total number of the clones are necessary. "Full-length cDNA" refers to a complete DNA copy of mRNA from a gene. The cDNA libraries produced using the oligo-capping method contain full-length cDNA clones in a ratio of 50 to 80%, namely, a 5 to 10-fold increase in full-length cDNA clones compared to the cDNA libraries produced by prior art methods (Sumio Sugano, the monthly magazine BIO INDUSTRY Vol.16, No.11, p.19-26). Full-length cDNA clones are essential for protein

expression in functional analyses of genes, and full-length cDNA clones themselves are very important materials for activity measurement. Thus, cloning of full-length cDNA is essential for functional analyses of genes. Sequencing of the cDNA not only provides important information for establishing the primary sequence of the protein encoded by the cDNA, but also reveals the entire exon sequence. Thus, the full-length cDNA provides valuable information for identifying a gene, such as information for determining the primary sequence of a protein, exon-intron structure, the transcription initiation site of mRNA, the location of a promoter, etc.

The construction of full-length cDNA libraries by the oligo-capping method can be carried out, for example, according to the method described in "Shin Idenshi Kougaku Handbook (New Genetic Engineering Handbook)", the third edition (1999), an extra issue of "Jikken Igaku (Experimental Medicine)", YODOSHA CO., LTD. In the present invention, the oligo-capping method involves substituting a cap structure with a synthetic oligo sequence by using BAP, TAP and an RNA ligase, as described in Suzuki & Sugano, "Shin Idenshi Kougaku Handbook (New Genetic Engineering Handbook)", the third edition (1999), an extra issue of "Jikken Igaku (Experimental Medicine)", YODOSHA CO., LTD.

The reporter gene indicative of the presence of a protein having a function contains one or more suitable expression regulation sequence portion to which a protein factor such as a transcriptional factor can bind, and a structural gene portion which allows the measurement of the activation of the proteins factor. The structural gene portion may encode any peptide or protein so long as those skilled in the art can measure the activity or amount of its expression product (including the amount of the mRNA produced). For example, polynucleotides which encode chloramphenicol acetyltransferase, β -galactosidase, luciferase, etc., and the like can be used and their enzymatic activity measured. Examples of reporter genes indicative of the presence of a protein having a function include the STAT6 reporter genes described herein, as well as reporter genes containing a CREB (cAMP responsive element binding protein) binding sequence or AP-1 (activator protein-1) binding sequence at the expression regulation sequence region of the reporter genes.

For example, if a gene capable of activating CREB is to be obtained, a

CREB-dependent reporter plasmid and a full-length cDNA clone produced by the oligo-capping method can be cotransfected into cells, and a plasmid having increased reporter activity can be selected from the cells to attain the purpose. If a gene capable of inhibiting CREB is to be obtained, a CREB-dependent reporter plasmid and a full-length cDNA clone produced by the oligo-capping method can be cotransfected into cells, and a plasmid having decreased reporter activity can be selected from the cells to attain the purpose. These procedures may be carried out in the presence of a certain stimulus to the cells. The cDNA to be transfected into the cells may be a single clone or multiple clones which may be transfected simultaneously. One example of such methods of the present invention is described in the Examples of the present specification in detail. Alternatively, a screening system for obtaining a gene capable of inhibiting STAT6 activation can also be constructed. A gene capable of inhibiting STAT6 activation can be obtained by cotransfecting a full-length cDNA and a reporter gene into cells, stimulating the cells by IL-4, IL-13 or the like, and selecting a clone having subnormally increased reporter activity. However, by suitably preparing a reporter gene, a gene encoding a protein capable of activating various physiological active factors (for example, NF- κ B, MAP kinases, vasularization factors, various transcription factors) can be obtained in addition to a gene encoding a protein capable of promoting STAT6 activation.

To obtain the novel gene of the present invention, either an in vitro system or a cell-based system, preferably a cell-based system, is used. Examples of such cells include cells of prokaryotes such as E. coli, microorganisms such as yeast and fungi, as well as insects and animals. Preferred examples include animal cells, in particular, 293-EBNA cells and NIH3T3 cells.

Further, because the cDNA of the present invention is full-length, its 5' end sequence is the transcription initiation site of the corresponding mRNA. Therefore the cDNA sequence can be used to identify the promoter region of the gene by comparing the cDNA with the genomic nucleotide sequence. Genomic nucleotide sequences are available from various databases when the sequences have been deposited in the databases. Alternatively, the cDNA can also be used to clone the desired sequence from a genomic library, for example, by

hybridization, and determine its nucleotide sequence. Thus, by comparing the nucleotide sequence of the cDNA of the present invention with a genomic sequence, the promoter region of the gene located upstream the cDNA can be identified. In addition, the promoter fragment thus identified can be used to construct a reporter plasmid for evaluating the expression of the gene. In general, the DNA fragment spanning 2kb (preferably 1kb) upstream from the transcription initiation site can be inserted upstream of the reporter gene to produce the reporter plasmid. The reporter plasmid can be used to screen for a compound which enhances or reduces the expression of the gene. For example, such screening can be carried out by transforming a suitable cell with the reporter plasmid, culturing the transformant for a certain period of time, adding a certain amount of a test compound, measuring the reporter activity expressed by the cell after a certain period of time, and comparing the activity with that of a cell to which the test compound has not been added. These methods are also included in the scope of the present invention.

The present invention also relates to a computer-readable medium on which a sequence data set has been stored, said sequence data set comprising at least one of nucleotide sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181 and 183, and/or at least one amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182 and 184.

In another aspect, the present invention relates to a method for calculating a homology, which comprises comparing data on the above medium with data of other nucleotide sequences. Thus, the gene and amino acid sequence of the present invention

provide valuable information for determining their secondary and tertiary structure, e.g., information for identifying other sequence having a similar function and high homology. These sequences are stored on the computer-readable medium, then a database is searched using data stored in a known macromolecule structure program and a known search tool such as GCG program package (Devereux, J. et al, Nucleic Acids Research 12(1):387 (1984)). In this manner, a sequence in a database having a certain homology can be easily found.

The computer-readable medium may be any composition of materials used to store information or data. Examples of such media include commercially available flexible disks, tapes, chips, hard disk, compact disks and video disks. The data on the medium allows a method for calculating a homology by comparing the data with other nucleotide sequence data. This method comprises the steps of providing a first nucleotide sequence containing the nucleotide sequence of the present invention for the computer-readable medium, and then comparing the first nucleotide sequence with at least one-second polynucleotide or polypeptide sequence to identify the homology.

The present invention also relates to an insoluble substrate to which polynucleotide comprising all or part of the nucleotide sequences selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181 and 183 are fixed. A plurality of the various polynucleotides which are DNA probes are fixed on a specifically processed solid substrates such as slide glass to form a DNA microarray and then a labeled target polynucleotide is hybridized with the fixed polynucleotides to detect a signal from each of the probes. The data obtained is analyzed and the gene expression is determined.

The present invention further relates to an insoluble substrate to which polypeptides comprising all or part of the amino acid sequences of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112,

114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182 are fixed. By mixing organism-derived cell extract with the insoluble substrate on which these proteins are fixed, it is possible to isolate or identify substances captured on the insoluble substrate that can be expected to be useful in diagnosis or drug development.

EXAMPLES

The following examples further illustrate, but do not limit the present invention.

Example 1: Construction of a full-length cDNA library using the oligo-capping method

(1) Preparation of RNA from human lung fibroblasts (Cryo NHLF)

Human lung fibroblasts (Cryo NHLF: purchased from Sanko Junyaku Co., Ltd.) were cultured according to the attached protocol. After repeating subculturing the cells to obtain fifty 10cm dishes containing the resulting culture, the cells were recovered with a cell scraper. Then, total RNA was obtained from the recovered cells by using the RNA extraction reagent ISOGEN (purchased from NIPPON GENE) according to the manufacture's protocol. Then, poly A⁺ RNA was obtained from the total RNA by using an oligo-dT cellulose column according to Maniatis et al., supra.

(2) Preparation of RNA from mouse ATDC5 cells

ATDC5, a cell strain cloned from mouse EC (embryonal carcinoma) (Atsumi, T. et al.: Cell Diff. Dev., 30: p109-116, (1990)) was repeatedly subcultured to obtain fifty 10cm dishes containing the resultant culture. Thereafter, the cells were collected by using a cell scraper. Then, poly A⁺ RNA was obtained by a method similar to that of (1) above.

ATDC5 cells were cultured in 1:1 mixed medium of HAM F-12 medium (SIGMA) and D-MEM (Dulbecco's Modified Eagle Medium: Sigma) containing 5% Fetal Bovine Serum (Invitrogen), 10 μ g/ml human transferrin (Sigma) and 0.3nmol/l sodium selenite (Wako Junyaku) in the presence of 5% CO₂ at 37°C.

(3) Preparation of RNA from RAW264.7 cells

RAW264.7 cells, a mouse macrophage-like cell strain (ATCC Number TIB-71), were cultured in accordance with an attached protocol. Then, the cells were collected, and

poly A⁺ RNA was obtained in the same way as in the above (1).

(4) Preparation of RNA from HUVEC cells

Human umbilical vein endothelial cells (HUVEC; purchased from Sanko Junyaku Pharmaceutical) were cultured in accordance with an attached protocol, and poly A⁺ RNA was obtained in the same way as in the above (1).

(5) Preparation of RNA from Daudi cells

Daudi cells, a human B lymphoblast strain (ATCC Number CCL-213) were cultured in accordance with an attached protocol. Then, the cells were collected, and poly A⁺ RNA was obtained in the same way as in the above (1).

(6) Preparation of RNA from mouse Th2 (helper T cell type 2) shift cells

A spleen was extracted from female 17 weeks- old BALB/C mouse (purchased from Japan SLC), and the cells were suspended in 1% BSA/PBS, and CD4 positive cells were separated using MACS microbead mouse CD4 (purchased from Miltenyi Biotec) which is a magnetic cell separation system. These CD4 positive cells were cultured in a dish on which anti-CD3 antibody and anti-CD28 antibody (both of which were purchased from Pharmingen) were immobilized in RPMI1640 medium (GIBCO) containing 1ng/ml mouse IL2, 10ng/ml mouse IL4 (both purchased from R&D), 10 μ g/ml anti-IFN γ (purchased from Pharmingen) and 10% FBS (Fetal Bovine Serum: GIBCO) in the presence of 5% CO₂ at 37°C. After 7 days of culturing, the cells were collected, and poly A⁺ RNA was obtained in the same way as in the above (1).

(7) Construction of a full-length cDNA library by the oligo-capping method

A full-length cDNA library was constructed from the above poly A⁺ RNA of human lung fibroblasts, ATDC5 cells, RAW264.7 cells, HUVEC cells, Daudi cells and mouse Th2 shift cells by the oligo-capping method according to the method of Sugano S. et al. [e.g., Maruyama, K. & Sugano, S., *Gene*, 138:171-174 (1994); Suzuki, Y. et al., *Gene*, 200:149-156 (1997); Suzuki, Y. & Sugano, S. "Shin Idenshi Kougaku Handbook (New Genetic Engineering Handbook)", the third edition (1999), an extra issue of "Jikken Igaku (Experimental Medicine)", YODOSHA CO., LTD.].

(8) Preparation of plasmid DNA

The full-length cDNA library constructed as above was transfected into *E. coli* strain TOP 10 by electroporation, then spread on LB agar medium, and incubated overnight at 37°C. Then, using QIAwell 96 Ultra Plasmid Kit (QIAGEN) according to the manufacturer's protocol, the plasmids were recovered from the colonies grown on ampicillin-containing LB agar medium.

Example 2: Cloning of DNA capable of promoting STAT6 activation

(1) Screening of the cDNA encoding the protein capable of promoting STAT6 activation

NIH3T3 cells (purchased from Dainippon Pharmaceutical) were seeded to 1×10^4 cells/100 μ l/well in a 96 well plate in IMDM medium containing 10% FBS, and were cultured for 24 hours at 37°C (in the presence of 5% CO₂). Then, 100ng of luciferase reporter plasmid N4 x 8-luc having a STAT6 response sequence and 2 μ l of the full-length cDNA prepared in above Example 1.(7) were cotransfected into the cells in a well using FuGENE 6 (purchased from Roche) according to the manufacturer's protocol. The luciferase reporter plasmid N4 x 8-luc having the STAT6 response sequence was constructed as follows. With reference to the oligonucleotide sequence to which an activated STAT6 binds specifically, found by Ohmori et al. [J. Immunol. 157, 2058-2065 (1996)], oligonucleotides having the following sequences were synthesized:

5'-TCGAGCTCTTCTTCCCAGGAACTCAATG-3' (SEQ ID NO: 185),

5'-TCGACATTGAGTTCCTGGGAAGAAGAGC-3' (SEQ ID NO: 186)

The synthesized oligonucleotides were dissolved in sterile water to be 1 μ g/ μ l, respectively, mixed in 10 μ l lots, and adjusted the volume to 32 μ l with sterile water. The solution was heated for 5 min at 90°C, and gradually cooled down to room temperature to prepare a double-stranded oligonucleotide solution. The solution was reacted with T4 polynucleotide kinase (Takara Shuzo) according to the attached manual, then the reaction product was purified in a usual manner. Separately, SV40 promoter region of pGL3-Promoter vector (Promega) was replaced by the HSV thymidine kinase promoter sequence (from -50 to +10) with Hind III site and BglII site to construct a vector tk-luc. The aforesaid double-stranded oligonucleotide fragments were inserted into the XhoI site of this tk-luc vector using T4 DNA ligase (GIBCO/BRL). The obtained clones were sequenced according to a usual method, and

clones in which plural oligonucleotide fragments were inserted were selected. A clone with at most 4 inserted fragments was obtained, which was named as N4 x 4-luc. The four-interlinked DNA fragments were excised from the N4 x 4-luc with a XhoI and a BglII site and purified to be inserted into a BamHI and a XhoI site of pBluescript II KS+ (Stratagene). The four-interlinked DNA fragments were excised from this plasmid with KpnI and SpeI and inserted into a KpnI and a NheI site of N4 x 4-luc plasmid to finally obtain N4 x 8-luc.

After transfection, the cells were cultured for 48 hours at 37°C, followed by 6 hours of culture with addition of mouse IL-4 (Immuno-Biological Laboratories) to a final concentration of 0.5ng/ml. The reporter activity of STAT6 (luciferase activity) was measured using long-term luciferase assay system, PIKKA GENE LT2.0 (TOYO INK) according to the attached manufacturer's instructions. The luciferase activity was measured using Wallac ARVO™ST 1420 MULTILABEL COUNTER (Perkin Elmer).

(2) DNA sequencing

The above screening was carried out, and plasmids showing a 3-fold or more increase in luciferase activity compared to that of the control experiment (luciferase activity of the cell into which vacant vector pME18S-FL3 is introduced instead of full-length cDNA) were selected. One pass sequencing was carried out from the 5' end of the cloned cDNA (sequencing primer: 5'-CTTCTGCTCTAAAAGCTGCG-3' (SEQ ID NO: 187)) and from the 3' end (sequencing primer: 5'-CGACCTGCAGCTCGAGCACA-3' (SEQ ID NO: 188)) so that as long sequence as possible is determined. The sequencing was carried out using the reagent Thermo Sequenase II Dye Terminator Cycle Sequencing Kit (Amersham Pharmacia Biotech) or BigDye Terminator Cycle Sequencing FS Ready Reaction Kit (Applied Biosystems) and the device ABI PRISM 377 sequencer or ABI PRISM 3100 sequencer according to the manufacturer's instructions.

(3) Full-length sequencing

The full-length DNA sequences for the 92 new clones which were obtained in the above screening, were determined (SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119,

121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181 and 183). The amino acid sequences of the protein coding regions (open reading frames) were deduced (SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182 and 184).

The results of measurement of STAT6 reporter activity (luciferase activity) of 36 clones among the above obtained clones are shown in Table 1 below. The value of activity shown in Table 1 is a ratio of luciferase activity which was determined by (luciferase activity of the gene of each SEQ ID NO.) / (luciferase activity of pME183-FL3).

Table 1

<u>Nucleotide Sequence</u>	<u>Activity</u>
SEQ ID NO.1	8.5
SEQ ID NO.3	3
SEQ ID NO.7	8.8
SEQ ID NO.11	11.3
SEQ ID NO.17	4.9
SEQ ID NO.21	19.5
SEQ ID NO.25	19.2
SEQ ID NO.31	5.9
SEQ ID NO.37	10.6
SEQ ID NO.41	111.6
SEQ ID NO.51	29
SEQ ID NO.55	57.3
SEQ ID NO.61	76.1
SEQ ID NO.63	9

SEQ ID NO.69	23.5
SEQ ID NO.73	17.6
SEQ ID NO.77	3.5
SEQ ID NO.83	16.7
SEQ ID NO.89	25.3
SEQ ID NO.95	11
SEQ ID NO.99	78
SEQ ID NO.105	17.6
SEQ ID NO.111	8.8
SEQ ID NO.117	7.7
SEQ ID NO.123	4.1
SEQ ID NO.129	3.0
SEQ ID NO.135	12.1
SEQ ID NO.139	7.8
SEQ ID NO.145	8.6
SEQ ID NO.151	6.6
SEQ ID NO.159	57.9
SEQ ID NO.163	9.4
SEQ ID NO.167	7.0
SEQ ID NO.171	22.8
SEQ ID NO.175	4.8
<u>SEQ ID NO.181</u>	<u>17.8</u>

INDUSTRIAL APPLICABILITY

As described above, the present invention provides industrially highly useful proteins capable of promoting STAT6 activity and genes encoding the proteins. The proteins of the present invention and the genes encoding the proteins allow not only screening for compounds useful for treating and preventing diseases associated with the excessive activation or inhibition of STAT6, but also production of diagnostics for such diseases. The genes of the

present invention are also useful as a gene source used for gene therapy.

All publications, patents and patent applications cited herein are incorporated herein in their entirety.

CLAIMS:

1. A purified protein of the following (a) or (b):
 - (a) a protein that consists of an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182 and 184; and
 - (b) a protein that promotes STAT6 activation and consists of an amino acid sequence having at least one amino acid deletion, substitution or addition in an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182 and 184.
2. A purified protein that promotes STAT6 activation and comprises an amino acid sequence having at least 95% identity to the protein according to claim 1 over the entire length thereof.
3. An isolated polynucleotide which comprises a nucleotide sequence encoding a protein of the following (a) or (b):
 - (a) a protein that consists of an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182 and 184; and
 - (b) a protein that promotes STAT6 activation and consists of an amino acid sequence having at least one amino acid deletion, substitution or addition in an amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32,

34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182 and 184.

4. An isolated polynucleotide comprising a nucleotide sequence of any of the following (a) to (c):

(a) a nucleotide sequence represented by any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181 and 183;

(b) a nucleotide sequence which encodes a protein that promotes STAT6 activation, and which hybridizes with a polynucleotide having a nucleotide sequence complementary to the nucleotide sequence of (a) under stringent conditions; and

(c) a nucleotide sequence which encodes a protein that promotes STAT6 activation, and which consists of a nucleotide sequence having at least one nucleotide deletion, substitution or addition in a nucleotide sequence of any of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181 and 183.

5. An isolated polynucleotide comprising a nucleotide sequence of any of the following (a) to (c):

(a) a nucleotide sequence represented by a coding region of any one of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181 and 183;

- (b) a nucleotide sequence which encodes a protein that promotes STAT6 activation, and which hybridizes with a polynucleotide having a nucleotide sequence complementary to the nucleotide sequence of (a) under stringent conditions; and
- (c) a nucleotide sequence which encodes a protein that promotes STAT6 activation, and which consists of a nucleotide sequence having at least one nucleotide deletion, substitution or addition in a coding region of a nucleotide sequence of any of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181 and 183.
6. An isolated polynucleotide comprising a nucleotide sequence which encodes a protein that promotes STAT6 activation and has at least 95% identity to the polynucleotide according to claim 3 over the entire length thereof.
7. An isolated polynucleotide comprising a nucleotide sequence which encodes a protein that promotes STAT6 activation and has at least 95% identity to the polynucleotide according to claim 4 or 5 over the entire length thereof.
8. A purified protein encoded by the polynucleotide according to any one of claims 3 to 7.
9. A recombinant vector which comprises a polynucleotide according to any one of claims 3 to 7.
10. A agent for gene therapy which comprises the recombinant vector according to claim 9 as an active ingredient.
11. A transformant which comprises the recombinant vector according to claim 9.
12. A membrane of the transformant according to claim 11 which has the protein according to claim 1 or 2, which is a membrane protein.
13. A process for producing a protein according to claim 1, 2 or 8 comprising the steps of;
- (a) culturing a transformant according to claim 11 under conditions providing expression of the protein according to claim 1, 2 or 8; and

(b) recovering the protein from the culture product.

14. A process for diagnosing a disease or susceptibility to a disease related to expression or activity of the protein of claim 1, 2 or 8 in a subject comprising the steps of:

(a) determining the presence or absence of a mutation in the gene encoding said protein in the genome of said subject; and/or

(b) analyzing the amount of expression of said gene in a sample derived from said subject.

15. A method for screening compounds which inhibit or promote STAT6 activation, which comprises the steps of:

(a) preparing a transformant by introducing a gene encoding a protein that promotes STAT6 activation according to claim 1, 2 or 8 and a gene encoding a signal which can detect STAT6 activation into a cell;

(b) culturing the transformant under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;

(c) measuring the signal which can detect STAT6 activation; and

(d) selecting a candidate compound which can change the signal amount as compared with the case of the absence of candidate compounds, as a compound which inhibit or promote STAT6 activation.

16. A method for screening compounds which inhibit or promote STAT6 activation, which comprises the steps of:

(a) preparing a transformant by introducing a gene encoding a protein that promotes STAT6 activation according to claim 1, 2 or 8 into a cell;

(b) culturing the transformant under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;

(c) measuring an activity of STAT6; and

(d) selecting a candidate compound which can change the activity of STAT6 as compared with the case of the absence of candidate compounds, as a compound which inhibit or promote STAT6 activation.

17. A compound which inhibits or promotes STAT6 activation, which is selected by the method for screening according to claim 15 or 16.

18. A process for producing a pharmaceutical composition, which comprises the steps of:
- (a) preparing a transformant by introducing a gene encoding a protein that promotes STAT6 activation according to claim 1, 2 or 8 and a gene encoding a signal which can detect STAT6 activation into a cell;
 - (b) culturing the transformant under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;
 - (c) measuring the signal which can detect STAT6 activation;
 - (d) selecting a candidate compound which can change the signal amount as compared with the case of the absence of candidate compounds, as a compound which inhibit or promote STAT6 activation; and
 - (e) producing a pharmaceutical composition which comprises a compound selected in the step of (d).
19. A process for producing a pharmaceutical composition, which comprises the steps of:
- (a) preparing a transformant by introducing a gene encoding a protein that promotes STAT6 activation according to claim 1, 2 or 8 into a cell;
 - (b) culturing the transformant under conditions which permit the expression of the gene in the presence or absence of one or more candidate compounds;
 - (c) measuring an activity of STAT6;
 - (d) selecting a candidate compound which can change the activity of STAT6 as compared with the case of the absence of candidate compounds, as a compound which inhibit or promote STAT6 activation; and
 - (e) producing a pharmaceutical composition which comprises a compound selected in the step of (d).
20. A kit for screening a compound which inhibits or promotes STAT6 activation, which comprises:
- (a) a transformant comprising a gene encoding a protein that promotes STAT6 activation according to claim 1, 2 or 8 and a gene encoding a signal which can detect promotion of STAT6 activation; and
 - (b) reagents for measuring the signal.

21. A monoclonal or polyclonal antibody or a fragment thereof, which recognizes the protein according to claim 1, 2 or 8.
22. The monoclonal or polyclonal antibody or a fragment thereof according to claim 21, which inhibits the activity of promoting STAT6 activation by the protein according to claim 1, 2 or 8.
23. A process for producing a monoclonal or polyclonal antibody according to claim 21 or 22, which comprises administering the protein according to claim 1, 2 or 8 or epitope-bearing fragments thereof to a non-human animal as an antigen.
24. An antisense oligonucleotide having a sequence complementary to a part of the polynucleotide according to any one of claims 3 to 7, which prevents the expression of a protein which promotes STAT6 activation.
25. A ribozyme or deoxyribozyme capable of inhibiting STAT6 activation, which has an action of cleavage of RNA that encodes the protein according to claim 1, 2 or 8 or an action of cleavage of RNA that encodes a protein which is involved in a route leading to STAT6 activation.
26. A double strand RNA having a sequence corresponding to a part of the nucleotide sequence according to any one of claims 3 to 7, which inhibits expression of a protein that promotes STAT6 activation.
27. A method for treating a disease associated with STAT6 activation, which comprises administering to a subject a compound screened by the process according to claim 15 or 16, and/or a monoclonal or polyclonal antibody or a fragment thereof according to claim 21 or 22, and/or an antisense oligonucleotide according to claim 24, and/or a ribozyme or deoxyribozyme according to claim 25, and/or a double strand RNA according to claim 26 in an effective amount to treat a disease selected from the group consisting of allergic diseases, inflammation, autoimmune diseases, diabetes, hyperlipidemia, infectious disease and cancers.
28. A pharmaceutical composition produced by the process according to claim 18 or 19 for inhibiting or promoting STAT6 activation.
29. The pharmaceutical composition according to claim 28 for the treatment and/or prevention of allergic diseases, inflammation, autoimmune diseases, diabetes, hyperlipidemia,

infectious disease and/or cancers.

30. A method of treating allergic diseases, inflammation, autoimmune diseases, diabetes, hyperlipidemia, infectious disease or cancers, which comprises administering a pharmaceutical composition produced by the process according to claim 18 or 19 to a patient suffering from a disease associated with STAT6 activation.
31. A pharmaceutical composition according to claim 28 for the treatment and/or prevention of Th1 hyperactive diseases.
32. A method of treating Th1 hyperactive diseases, which comprises administering a pharmaceutical composition produced by the process according to claim 18 or 19 to a patient suffering from a disease related to inhibition of STAT6 activation.
33. A pharmaceutical composition which comprises a monoclonal or polyclonal antibody or a fragment thereof according to claim 21 or 22 as an active ingredient.
34. A pharmaceutical composition which comprises an antisense oligonucleotide according to claim 24 as an active ingredient.
35. A pharmaceutical composition which comprises a ribozyme or deoxyribozyme according to claim 25 as an active ingredient.
36. A pharmaceutical composition or a gene therapy agent, which comprises a double strand RNA according to claim 26 or a vector capable of expressing said double strand RNA, an active ingredient.
37. The pharmaceutical composition according to any one of claims 33 to 35 for the treatment and/or prevention of a disease which is selected from the group consisting of allergic diseases, inflammation, autoimmune diseases, diabetes, hyperlipidemia, infectious disease and/or cancers.
38. A computer-readable medium on which a sequence data set has been stored, said sequence data set comprising at least one of nucleotide sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165,

167, 169, 171, 173, 175, 177, 179, 181 and 183, and/or at least one amino acid sequence selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182 and 184.

39. A method for calculating identity to other nucleotide sequences and/or amino acid sequences, which comprises comparing data on a medium according to claim 38 with data of said other nucleotide sequences and/or amino acid sequences.

40. An insoluble substrate to which polynucleotides comprising all or part of the nucleotide sequences selected from the group consisting of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181 and 183 are fixed.

41. An insoluble substrate to which polypeptides comprising all or a part of the amino acid sequences selected from the group consisting of SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182 and 184, are fixed.

SEQUENCE LISTING

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<170> PatentIn Ver. 3.1

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cagctctcca tctgcgcgtc tctccgtgaa ccccgtagc ggtgtgcagc cacc atg 177
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5

10

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20

25

30

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 Leu Glu Asp Ala Asp Phe Asp Gly Lys Pro Met Val Leu Val Ala Gly
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 Lys Phe His Ser Leu Lys Pro Lys Leu Leu Glu Ala Leu Asp Glu Met
 370 375 380 385
 ctg acg cac gac atc gcc aag ctc atg ccc ctg ctg cgg cag gag gag 1377
 Leu Thr His Asp Ile Ala Lys Leu Met Pro Leu Leu Arg Gln Glu Glu
 390 395 400
 ctg gag agc acc gag gtg ggc gtg cag ggg ggc gct ttt gag ggc acc 1425
 Leu Glu Ser Thr Glu Val Gly Val Gln Gly Gly Ala Phe Glu Gly Thr
 405 410 415
 cac atg ggc ccg ttt gtg gag cgg gga cct gac gag gcc atg gag gac 1473
 His Met Gly Pro Phe Val Glu Arg Gly Pro Asp Glu Ala Met Glu Asp
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 ggc gag gag ggc tcg gac gac gag gcc gag tgg gtg gtg acc aag gac 1521
 Gly Glu Glu Gly Ser Asp Asp Glu Ala Glu Trp Val Val Thr Lys Asp
 435 440 445
 aag tcc aaa tac gac gag atc ttc tac aac ctg gcg cct gcc gac ggc 1569
 Lys Ser Lys Tyr Asp Glu Ile Phe Tyr Asn Leu Ala Pro Ala Asp Gly
 450 455 460 465
 aag ctg agc ggc tcc aag gcc aag acc tgg atg gtg ggg acc aag ctc 1617

Lys Leu Ser Gly Ser Lys Ala Lys Thr Trp Met Val Gly Thr Lys Leu

470

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ccc aac tca gtg ctg ggg cgc atc tgg aag ctc agc gat gtg gac cgc 1665

Pro Asn Ser Val Leu Gly Arg Ile Trp Lys Leu Ser Asp Val Asp Arg

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490

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gac ggc atg ctg gat gat gaa gag ttc gcg ctg gcc agc cac ctc atc 1713

Asp Gly Met Leu Asp Asp Glu Glu Phe Ala Leu Ala Ser His Leu Ile

500

505

510

gag gcc aag ctg gaa ggc cac ggg ctg ccc gcc aac ctg ccc cgt cgc 1761

Glu Ala Lys Leu Glu Gly His Gly Leu Pro Ala Asn Leu Pro Arg Arg

515

520

525

ctg gtg cca ccc tcc aag cga cgc cac aag ggc tcc gcc gag 1803

Leu Val Pro Pro Ser Lys Arg Arg His Lys Gly Ser Ala Glu

530

535

540

tgagccgggc cccctccca tggccctgct gtggctcccc agctccagtc ggctgcacgc 1863

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ggggtctccc tctcactac cgcagacac cccggtggaa gcatttagag gggaccacgg 1983

gagggacaag gcttctctgt ccgcccttca cacctccggc ctcacgttca cttaggcaca 2043

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tagacaaata catctgccct catggaaggt gacgttccca ggagagggca cctacacagt 2223

cacgcaaaca cactaatt cctggcaggg ccccgagccc ctccctggc tgagcagccc 2283

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ccaggcaaca cctcaaccg gctccatcac atcctcaggt ctcgggacca tggggggctc 2403

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<213> Homo sapiens

<400> 2

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20 25 30

Leu Leu Pro Leu Glu Glu His Tyr Arg Phe Gly Ala Phe His Ser Pro

35	40	45
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Gly Gln Tyr Ser Thr Gly Lys Thr Ser Phe Ile Gln Tyr Leu Leu Glu		
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Gln Glu Val Pro Gly Ser Arg Val Gly Pro Glu Pro Thr Thr Asp Cys		
85	90	95
Phe Val Ala Val Met His Gly Asp Thr Glu Gly Thr Val Pro Gly Asn		
100	105	110
Ala Leu Val Val Asp Pro Asp Lys Pro Phe Arg Lys Leu Asn Pro Phe		
115	120	125
Gly Asn Thr Phe Leu Asn Arg Phe Met Cys Ala Gln Leu Pro Asn Gln		
130	135	140
Val Leu Glu Ser Ile Ser Ile Ile Asp Thr Pro Gly Ile Leu Ser Gly		
145	150	155
Ala Lys Gln Arg Val Ser Arg Gly Tyr Asp Phe Pro Ala Val Leu Arg		
165	170	175
Trp Phe Ala Glu Arg Val Asp Leu Ile Ile Leu Leu Phe Asp Ala His		
180	185	190
Lys Leu Glu Ile Ser Asp Glu Phe Ser Glu Ala Ile Gly Ala Leu Arg		
195	200	205
Gly His Glu Asp Lys Ile Arg Val Val Leu Asn Lys Ala Asp Met Val		
210	215	220
Glu Thr Gln Gln Leu Met Arg Val Tyr Gly Ala Leu Met Trp Ala Leu		
225	230	235
Gly Lys Val Val Gly Thr Pro Glu Val Leu Arg Val Tyr Ile Gly Ser		
245	250	255

Phe Trp Ser Gln Pro Leu Leu Val Pro Asp Asn Arg Arg Leu Phe Glu

260 265 270

Leu Glu Glu Gln Asp Leu Phe Arg Asp Ile Gln Gly Leu Pro Arg His

275 280 285

Ala Ala Leu Arg Lys Leu Asn Asp Leu Val Lys Arg Ala Arg Leu Val

290 295 300

Arg Val His Ala Tyr Ile Ile Ser Tyr Leu Lys Lys Glu Met Pro Ser

305 310 315 320

Val Phe Gly Lys Glu Asn Lys Lys Lys Gln Leu Ile Leu Lys Leu Pro

325 330 335

Val Ile Phe Ala Lys Ile Gln Leu Glu His His Ile Ser Pro Gly Asp

340 345 350

Phe Pro Asp Cys Gln Lys Met Gln Glu Leu Leu Met Ala His Asp Phe

355 360 365

Thr Lys Phe His Ser Leu Lys Pro Lys Leu Leu Glu Ala Leu Asp Glu

370 375 380

Met Leu Thr His Asp Ile Ala Lys Leu Met Pro Leu Leu Arg Gln Glu

385 390 395 400

Glu Leu Glu Ser Thr Glu Val Gly Val Gln Gly Gly Ala Phe Glu Gly

405 410 415

Thr His Met Gly Pro Phe Val Glu Arg Gly Pro Asp Glu Ala Met Glu

420 425 430

Asp Gly Glu Glu Gly Ser Asp Asp Glu Ala Glu Trp Val Val Thr Lys

435 440 445

Asp Lys Ser Lys Tyr Asp Glu Ile Phe Tyr Asn Leu Ala Pro Ala Asp

450 455 460

Gly Lys Leu Ser Gly Ser Lys Ala Lys Thr Trp Met Val Gly Thr Lys

465 470 475 480
 Leu Pro Asn Ser Val Leu Gly Arg Ile Trp Lys Leu Ser Asp Val Asp
 485 490 495
 Arg Asp Gly Met Leu Asp Asp Glu Glu Phe Ala Leu Ala Ser His Leu
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Ser Asp Val Val Ser Leu Pro Arg Gly Arg Phe Arg Cys Cys Leu Cys

10 15 20

aat gtt act aca gcc aac cga ccc agc ctc gat gcc cac ttg aaa ggc 151

Asn Val Thr Thr Ala Asn Arg Pro Ser Leu Asp Ala His Leu Lys Gly

25 30 35

9/617

cgg aag cac cgg gat ttg gtg caa ctc cga gct acc agg aag gca cag 199
 Arg Lys His Arg Asp Leu Val Gln Leu Arg Ala Thr Arg Lys Ala Gln
 40 45 50
 gga ctc cga agt gtg ttt gtc agt ggc ttc ccc agg gat gtg ggt tct 247
 Gly Leu Arg Ser Val Phe Val Ser Gly Phe Pro Arg Asp Val Gly Ser
 55 60 65
 gct cag ctc tct gag tac ttc cag aca ttt ggc cct gtg gcc aat att 295
 Ala Gln Leu Ser Glu Tyr Phe Gln Thr Phe Gly Pro Val Ala Asn Ile
 70 75 80 85
 gtc atg gac aag gac aag ggg gtg ttt gcc atc gtg gag atg gga gac 343
 Val Met Asp Lys Asp Lys Gly Val Phe Ala Ile Val Glu Met Gly Asp
 90 95 100
 ata agt gct cgg gag gct gtc tta tca cag ccc aag cac agc ctt ggg 391
 Ile Ser Ala Arg Glu Ala Val Leu Ser Gln Pro Lys His Ser Leu Gly
 105 110 115
 gga cat gga ctt cga gtc cgg cca agg gag cag aag gag ttc cag agc 439
 Gly His Gly Leu Arg Val Arg Pro Arg Glu Gln Lys Glu Phe Gln Ser
 120 125 130
 cca gct tcc aag tct ccc aaa gga gtg gac tca agt agt cac cag ctg 487
 Pro Ala Ser Lys Ser Pro Lys Gly Val Asp Ser Ser Ser His Gln Leu
 135 140 145
 gtc caa gca ctg gct gag gct gcg gat gtg ggg gcc cag atg gtg aag 535
 Val Gln Ala Leu Ala Glu Ala Ala Asp Val Gly Ala Gln Met Val Lys
 150 155 160 165
 ctt gtg gaa ctg agg gag ttg tct gag gct gag cgg cag ctt cgg aac 583
 Leu Val Glu Leu Arg Glu Leu Ser Glu Ala Glu Arg Gln Leu Arg Asn
 170 175 180

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 Leu Val Val Ala Leu Met Gln Glu Val Phe Thr Ala Phe Phe Pro Gly
 185 190 195
 tgt gtg gtc cat cct ttt ggc tct act gta aat agc ttt gat gtt cat 679
 Cys Val Val His Pro Phe Gly Ser Thr Val Asn Ser Phe Asp Val His
 200 205 210
 ggc tgt gat ctc gac ctc ttc ttg gac atg ggt gat atg gaa gag acc 727
 Gly Cys Asp Leu Asp Leu Phe Leu Asp Met Gly Asp Met Glu Glu Thr
 215 220 225
 gag cca gac cca aag gct cca aag gtt cca gag act tca tcc ttg gac 775
 Glu Pro Asp Pro Lys Ala Pro Lys Val Pro Glu Thr Ser Ser Leu Asp
 230 235 240 245
 tca gcc ctt gct tct tcc ctg gat cct cag gcg ctg gcc tgc acc cca 823
 Ser Ala Leu Ala Ser Ser Leu Asp Pro Gln Ala Leu Ala Cys Thr Pro
 250 255 260
 gct tct cct cta gac tca ctg tct cca act tct gtt caa gag tct gag 871
 Ala Ser Pro Leu Asp Ser Leu Ser Pro Thr Ser Val Gln Glu Ser Glu
 265 270 275
 tcc ctg gac ttt gac acc cca tct tct ctg gca cca cag aca ccc gac 919
 Ser Leu Asp Phe Asp Thr Pro Ser Ser Leu Ala Pro Gln Thr Pro Asp
 280 285 290
 tct gct ttg ggc tct gac act gtc acc tct cct cag tct ctg cct cca 967
 Ser Ala Leu Gly Ser Asp Thr Val Thr Ser Pro Gln Ser Leu Pro Pro
 295 300 305
 gtt tca cca ctg cag gag gac agg aaa gag ggg aaa cag ggg aaa gag 1015
 Val Ser Pro Leu Gln Glu Asp Arg Lys Glu Gly Lys Gln Gly Lys Glu
 310 315 320 325

cta gaa tta gca gaa gaa gcc tca aag gac gag aag gag gag gca gca 1063
 Leu Glu Leu Ala Glu Glu Ala Ser Lys Asp Glu Lys Glu Glu Ala Ala
 330 335 340
 gca gtg tta gag ctg gtg gga tct att ctc cgt ggc tgt gtc cct gga 1111
 Ala Val Leu Glu Leu Val Gly Ser Ile Leu Arg Gly Cys Val Pro Gly
 345 350 355
 gtg tac cga gtc caa act gtg ccc tct gcc cgg cgt cct gtg gtc aag 1159
 Val Tyr Arg Val Gln Thr Val Pro Ser Ala Arg Arg Pro Val Val Lys
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 Phe Cys His Arg Pro Ser Gly Leu His Gly Asp Val Ser Leu Ser Asn
 375 380 385
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 Asp Gly Arg Val Arg Pro Leu Val Tyr Thr Leu Arg Cys Trp Ala Gln
 410 415 420
 cat aat ggg ctg tca gga ggt ggc ccc ctt ctc aat aac tac gcc ttg 1351
 His Asn Gly Leu Ser Gly Gly Gly Pro Leu Leu Asn Asn Tyr Ala Leu
 425 430 435
 acg ttg tta gtg atc tac ttc ctt cag acc aga gac cct cca gta ctt 1399
 Thr Leu Leu Val Ile Tyr Phe Leu Gln Thr Arg Asp Pro Pro Val Leu
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 cct act gtg gcc cag ctt acc cag aga gca ggt gaa ggg gaa cag gta 1447
 Pro Thr Val Ala Gln Leu Thr Gln Arg Ala Gly Glu Gly Glu Gln Val
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gaa gtt gat ggc tgg gac tgt agc ttc cct aag gat gcc tca aga ttg 1495
 Glu Val Asp Gly Trp Asp Cys Ser Phe Pro Lys Asp Ala Ser Arg Leu
 470 475 480 485
 gag ccc agc acc aac gtg gag cct ctc agt tcc ctg ctg gcc cag ttc 1543
 Glu Pro Ser Thr Asn Val Glu Pro Leu Ser Ser Leu Leu Ala Gln Phe
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 505 510 515
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 Arg Glu Gly Arg Pro Leu Met Val Ala Glu Gly Leu Pro Ser Asp Leu
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 Trp Glu Gly Leu Arg Leu Gly Pro Met Asn Leu Gln Asp Pro Phe Asp
 535 540 545
 ctg agt cac aat gtt gca gcc aat gtg acc ggc cgg gtg gct aaa cgt 1735
 Leu Ser His Asn Val Ala Ala Asn Val Thr Gly Arg Val Ala Lys Arg
 550 555 560 565
 ctg cag agc tgt tgt ggg gca gca gcc agt tac tgc cga agt ctc cag 1783
 Leu Gln Ser Cys Cys Gly Ala Ala Ala Ser Tyr Cys Arg Ser Leu Gln
 570 575 580
 tac cag cag cgt tcc tcc cgg ggc cgg gac tgg gga ctg ctc ccg ctt 1831
 Tyr Gln Gln Arg Ser Ser Arg Gly Arg Asp Trp Gly Leu Leu Pro Leu
 585 590 595
 ttg cag ccc agc tcc cct agc tcc ctg ctg tct gcc aag ctc atc ccc 1879
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 600 605 610

tta ccc tct gcc ccc ttt cca cag gtc att atg gct ttg gtg gat gtg	1927
Leu Pro Ser Ala Pro Phe Pro Gln Val Ile Met Ala Leu Val Asp Val	
615 620 625	
tta agg gaa gca cta gga tgc cac ata gaa cag gga acc aag aga cga	1975
Leu Arg Glu Ala Leu Gly Cys His Ile Glu Gln Gly Thr Lys Arg Arg	
630 635 640 645	
cgg tca gaa ggt gcc aga att aaa gac tct ccc ttg gga ggg gtg aac	2023
Arg Ser Glu Gly Ala Arg Ile Lys Asp Ser Pro Leu Gly Gly Val Asn	
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aaa aga cag aga ctt ggt ggg caa gaa aag agc ttc gag gaa ggg aaa	2071
Lys Arg Gln Arg Leu Gly Gly Gln Glu Lys Ser Phe Glu Glu Gly Lys	
665 670 675	
gag gag cca cag gga tgt gca ggg gac cac agt gaa aat gag gta gaa	2119
Glu Glu Pro Gln Gly Cys Ala Gly Asp His Ser Glu Asn Glu Val Glu	
680 685 690	
gaa atg gta ata gag gtt cga gag aca cct cag gac tgg gcc ttg ttg	2167
Glu Met Val Ile Glu Val Arg Glu Thr Pro Gln Asp Trp Ala Leu Leu	
695 700 705	
cac tcg gga cca cca gag gag gag ttg ccc ctg atg act gca aac tgt	2215
His Ser Gly Pro Pro Glu Glu Glu Leu Pro Leu Met Thr Ala Asn Cys	
710 715 720 725	
cta gac aag gca gct gag cat aat ccc atg aaa cct gaa gtg gct gga	2263
Leu Asp Lys Ala Ala Glu His Asn Pro Met Lys Pro Glu Val Ala Gly	
730 735 740	
gaa ggg tct cag ggt gag aca ggg aag gag gca tca cac cca tca tca	2311
Glu Gly Ser Gln Gly Glu Thr Gly Lys Glu Ala Ser His Pro Ser Ser	
745 750 755	

gtg agc tgg cgc tgt gcc ttg tgg cac caa gta tgg cag ggg agg cgg 2359
 Val Ser Trp Arg Cys Ala Leu Trp His Gln Val Trp Gln Gly Arg Arg
 760 765 770
 cgt gcc cgg aga cga tta cag caa caa acc aag gaa gaa ggt aga gga 2407
 Arg Ala Arg Arg Arg Leu Gln Gln Gln Thr Lys Glu Glu Gly Arg Gly
 775 780 785
 ggt ccc acc aca gga gca gag tgg ctg gca atg gaa gct cgt gtg acc 2455
 Gly Pro Thr Thr Gly Ala Glu Trp Leu Ala Met Glu Ala Arg Val Thr
 790 795 800 805
 cag gaa cta aaa gga ccc aat agt gag caa gag agg ccg ccg ggg gag 2503
 Gln Glu Leu Lys Gly Pro Asn Ser Glu Gln Glu Arg Pro Pro Gly Glu
 810 815 820
 ccc ctc ctc agc ttt gtg gca tct gcc tcc cag gct gag cag aca ctc 2551
 Pro Leu Leu Ser Phe Val Ala Ser Ala Ser Gln Ala Glu Gln Thr Leu
 825 830 835
 act gtg gcc cca ctc cag gac tcc caa ggc ctg ttc cct ggt ctt cat 2599
 Thr Val Ala Pro Leu Gln Asp Ser Gln Gly Leu Phe Pro Gly Leu His
 840 845 850
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 His Phe Leu Gln Gly Phe Ile Pro Gln Ala Leu Lys Asn Leu Leu Lys
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Ala His Leu Lys Gly Arg Lys His Arg Asp Leu Val Gln Leu Arg Ala

35 40 45

Thr Arg Lys Ala Gln Gly Leu Arg Ser Val Phe Val Ser Gly Phe Pro

50 55 60

Arg Asp Val Gly Ser Ala Gln Leu Ser Glu Tyr Phe Gln Thr Phe Gly

65 70 75 80

Pro Val Ala Asn Ile Val Met Asp Lys Asp Lys Gly Val Phe Ala Ile

85 90 95

Val Glu Met Gly Asp Ile Ser Ala Arg Glu Ala Val Leu Ser Gln Pro

100 105 110

Lys His Ser Leu Gly Gly His Gly Leu Arg Val Arg Pro Arg Glu Gln

115 120 125

Lys Glu Phe Gln Ser Pro Ala Ser Lys Ser Pro Lys Gly Val Asp Ser

130 135 140

Ser Ser His Gln Leu Val Gln Ala Leu Ala Glu Ala Ala Asp Val Gly

145 150 155 160

Ala Gln Met Val Lys Leu Val Glu Leu Arg Glu Leu Ser Glu Ala Glu

165 170 175

Arg Gln Leu Arg Asn Leu Val Val Ala Leu Met Gln Glu Val Phe Thr

180 185 190

Ala Phe Phe Pro Gly Cys Val Val His Pro Phe Gly Ser Thr Val Asn

195 200 205

16/617

Ser Phe Asp Val His Gly Cys Asp Leu Asp Leu Phe Leu Asp Met Gly
210 215 220
Asp Met Glu Glu Thr Glu Pro Asp Pro Lys Ala Pro Lys Val Pro Glu
225 230 235 240
Thr Ser Ser Leu Asp Ser Ala Leu Ala Ser Ser Leu Asp Pro Gln Ala
245 250 255
Leu Ala Cys Thr Pro Ala Ser Pro Leu Asp Ser Leu Ser Pro Thr Ser
260 265 270
Val Gln Glu Ser Glu Ser Leu Asp Phe Asp Thr Pro Ser Ser Leu Ala
275 280 285
Pro Gln Thr Pro Asp Ser Ala Leu Gly Ser Asp Thr Val Thr Ser Pro
290 295 300
Gln Ser Leu Pro Pro Val Ser Pro Leu Gln Glu Asp Arg Lys Glu Gly
305 310 315 320
Lys Gln Gly Lys Glu Leu Glu Leu Ala Glu Glu Ala Ser Lys Asp Glu
325 330 335
Lys Glu Glu Ala Ala Ala Val Leu Glu Leu Val Gly Ser Ile Leu Arg
340 345 350
Gly Cys Val Pro Gly Val Tyr Arg Val Gln Thr Val Pro Ser Ala Arg
355 360 365
Arg Pro Val Val Lys Phe Cys His Arg Pro Ser Gly Leu His Gly Asp
370 375 380
Val Ser Leu Ser Asn Arg Leu Ala Leu Tyr Asn Ser Arg Phe Leu Asn
385 390 395 400
Leu Cys Ser Glu Met Asp Gly Arg Val Arg Pro Leu Val Tyr Thr Leu
405 410 415
Arg Cys Trp Ala Gln His Asn Gly Leu Ser Gly Gly Gly Pro Leu Leu

420 425 430
Asn Asn Tyr Ala Leu Thr Leu Leu Val Ile Tyr Phe Leu Gln Thr Arg
435 440 445
Asp Pro Pro Val Leu Pro Thr Val Ala Gln Leu Thr Gln Arg Ala Gly
450 455 460
Glu Gly Glu Gln Val Glu Val Asp Gly Trp Asp Cys Ser Phe Pro Lys
465 470 475 480
Asp Ala Ser Arg Leu Glu Pro Ser Thr Asn Val Glu Pro Leu Ser Ser
485 490 495
Leu Leu Ala Gln Phe Phe Ser Cys Val Ser Cys Leu Asp Leu Ser Gly
500 505 510
Ser Leu Leu Ser Leu Arg Glu Gly Arg Pro Leu Met Val Ala Glu Gly
515 520 525
Leu Pro Ser Asp Leu Trp Glu Gly Leu Arg Leu Gly Pro Met Asn Leu
530 535 540
Gln Asp Pro Phe Asp Leu Ser His Asn Val Ala Ala Asn Val Thr Gly
545 550 555 560
Arg Val Ala Lys Arg Leu Gln Ser Cys Cys Gly Ala Ala Ala Ser Tyr
565 570 575
Cys Arg Ser Leu Gln Tyr Gln Gln Arg Ser Ser Arg Gly Arg Asp Trp
580 585 590
Gly Leu Leu Pro Leu Leu Gln Pro Ser Ser Pro Ser Ser Leu Leu Ser
595 600 605
Ala Lys Leu Ile Pro Leu Pro Ser Ala Pro Phe Pro Gln Val Ile Met
610 615 620
Ala Leu Val Asp Val Leu Arg Glu Ala Leu Gly Cys His Ile Glu Gln
625 630 635 640

Gly Thr Lys Arg Arg Arg Ser Glu Gly Ala Arg Ile Lys Asp Ser Pro
645 650 655

Leu Gly Gly Val Asn Lys Arg Gln Arg Leu Gly Gly Gln Glu Lys Ser
660 665 670

Phe Glu Glu Gly Lys Glu Glu Pro Gln Gly Cys Ala Gly Asp His Ser
675 680 685

Glu Asn Glu Val Glu Glu Met Val Ile Glu Val Arg Glu Thr Pro Gln
690 695 700

Asp Trp Ala Leu Leu His Ser Gly Pro Pro Glu Glu Glu Leu Pro Leu
705 710 715 720

Met Thr Ala Asn Cys Leu Asp Lys Ala Ala Glu His Asn Pro Met Lys
725 730 735

Pro Glu Val Ala Gly Glu Gly Ser Gln Gly Glu Thr Gly Lys Glu Ala
740 745 750

Ser His Pro Ser Ser Val Ser Trp Arg Cys Ala Leu Trp His Gln Val
755 760 765

Trp Gln Gly Arg Arg Arg Ala Arg Arg Arg Leu Gln Gln Gln Thr Lys
770 775 780

Glu Glu Gly Arg Gly Gly Pro Thr Thr Gly Ala Glu Trp Leu Ala Met
785 790 795 800

Glu Ala Arg Val Thr Gln Glu Leu Lys Gly Pro Asn Ser Glu Gln Glu
805 810 815

Arg Pro Pro Gly Glu Pro Leu Leu Ser Phe Val Ala Ser Ala Ser Gln
820 825 830

Ala Glu Gln Thr Leu Thr Val Ala Pro Leu Gln Asp Ser Gln Gly Leu
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850
Lys Asn Leu Leu Lys

865

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<222> (67).. (2688)

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Met Ala Ala Val Asp Ser Asp Val Glu Ser Leu Pro Arg Gly

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10

ggg ttc cgc tgc tgc ctc tgc cac gtt act aca gcc aac cga ccc agc 156

Gly Phe Arg Cys Cys Leu Cys His Val Thr Thr Ala Asn Arg Pro Ser

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25

30

ctt gat gcc cac ttg gga ggc aga aag cac cgg cac ctg gta gaa cta 204

Leu Asp Ala His Leu Gly Gly Arg Lys His Arg His Leu Val Glu Leu

35

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45

cga gct gcg aga aag gcc cag gga ctt cga agt gtg ttt gtc agt ggc 252

Arg Ala Ala Arg Lys Ala Gln Gly Leu Arg Ser Val Phe Val Ser Gly

50

55

60

ttt ccc agg gat gtg gat tct gct cag ctc tct gag tac ttc cta gca 300

Phe Pro Arg Asp Val Asp Ser Ala Gln Leu Ser Glu Tyr Phe Leu Ala

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80	85	90	
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Ala Ile Val Glu Met Gly Asp Val Gly Ala Arg Glu Ala Val Leu Ser			
95	100	105	110
cag tcc cag cac agc ctg gga gga cat cgc ctg cgt gtc cgc cca cgg			444
Gln Ser Gln His Ser Leu Gly Gly His Arg Leu Arg Val Arg Pro Arg			
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Glu Gln Lys Glu Phe Gln Ser Pro Ala Ser Lys Ser Pro Lys Gly Ala			
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gcc ccc gac agt cac cag ctg gcc aaa gcg cta gct gag gct gca gac			540
Ala Pro Asp Ser His Gln Leu Ala Lys Ala Leu Ala Glu Ala Ala Asp			
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gtg ggg gca caa atg ata aag ctt gtg ggg ctg agg gag ttg tcc gag			588
Val Gly Ala Gln Met Ile Lys Leu Val Gly Leu Arg Glu Leu Ser Glu			
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gcc gag cgg cag ctt cgc agc cta gtg gtg gcc ctg atg cag gag gtc			636
Ala Glu Arg Gln Leu Arg Ser Leu Val Val Ala Leu Met Gln Glu Val			
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ttc aca gag ttc ttc cct ggc tgt gtg gtc cac cct ttt ggc tct tcc			684
Phe Thr Glu Phe Phe Pro Gly Cys Val Val His Pro Phe Gly Ser Ser			
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Ile Asn Ser Phe Asp Val His Gly Cys Asp Leu Asp Leu Phe Leu Asp			

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cca tcg ctg gac tcg gcc ctg gct tcc cca ctg gac cct caa gcc ctg	828		
Pro Ser Leu Asp Ser Ala Leu Ala Ser Pro Leu Asp Pro Gln Ala Leu			
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gcc tgc acc cca gct tcc cct cca gat tca caa cct cct gct tct ccc	876		
Ala Cys Thr Pro Ala Ser Pro Pro Asp Ser Gln Pro Pro Ala Ser Pro			
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gac ctg ggg aag gcc tcg gaa cta gca gag acc cca aag gag gag aaa	1068		
Asp Leu Gly Lys Ala Ser Glu Leu Ala Glu Thr Pro Lys Glu Glu Lys			
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Cys Val Pro Gly Val Tyr Arg Val Gln Thr Val Pro Ser Ala Arg Arg			

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Pro Ser Asn Leu Trp Glu Gly Leu Arg Leu Gly Pro Leu Asn Leu Gln
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Lys Gly Leu Ser Gly Gly Glu Glu Arg Pro Glu Thr Glu Pro Leu Leu			
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26/617

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740 745 750
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755 760 765
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785 790 795 800
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Leu Leu Pro Leu Glu Glu His Tyr Arg Phe His Glu Phe His Ser Pro

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Ala Leu Glu Asp Ala Asp Phe Asp Asn Lys Pro Thr Val Leu Leu Val

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 Gly Gln Tyr Ser Thr Gly Lys Thr Thr Phe Ile Arg His Leu Ile Glu
 65 70 75 80
 Gln Asp Phe Pro Gly Met Arg Ile Gly Pro Glu Pro Thr Thr Asp Ser
 85 90 95
 Phe Ile Ala Val Met His Gly Pro Thr Glu Gly Val Val Pro Gly Asn
 100 105 110
 Ala Leu Val Val Asp Pro Arg Arg Pro Phe Arg Lys Leu Asn Ala Phe
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 Gly Asn Ala Phe Leu Asn Arg Phe Met Cys Ala Gln Leu Pro Asn Pro
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 Val Leu Asp Ser Ile Ser Ile Ile Asp Thr Pro Gly Ile Leu Ser Gly
 145 150 155 160
 Glu Lys Gln Arg Ile Ser Arg Gly Tyr Asp Phe Ala Ala Val Leu Glu
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 Trp Phe Ala Glu Arg Val Asp Arg Ile Ile Leu Leu Phe Asp Ala His
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 Lys Leu Asp Ile Ser Asp Glu Phe Ser Glu Val Ile Lys Ala Leu Lys
 195 200 205
 Asn His Glu Asp Lys Ile Arg Val Val Leu Asn Lys Ala Asp Gln Ile
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 Glu Thr Gln Gln Leu Met Arg Val Tyr Gly Ala Leu Met Trp Ser Leu
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 Gly Lys Ile Ile Asn Thr Pro Glu Val Val Arg Val Tyr Ile Gly Ser
 245 250 255
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 260 265 270

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Ala Glu Glu Gln Asp Leu Phe Lys Asp Ile Gln Ser Leu Pro Arg Asn

275

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295

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Lys Val His Ala Tyr Ile Ile Ser Ser Leu Lys Lys Glu Met Pro Asn

305

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315

320

Val Phe Gly Lys Glu Ser Lys Lys Lys Glu Leu Val Asn Asn Leu Gly

325

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335

Glu Ile Tyr Gln Lys Ile Glu Arg Glu His Gln Ile Ser Pro Gly Asp

340

345

350

Phe Pro Ser Leu Arg Lys Met Gln Glu Leu Leu Gln Thr Gln Asp Phe

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Ser Lys Phe Gln Ala Leu Lys Pro Lys Leu Leu Asp Thr Val Asp Asp

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Met Leu Ala Asn Asp Ile Ala Arg Leu Met Val Met Val Arg Gln Glu

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Glu Ser Leu Met Pro Ser Gln Val Val Lys Gly Gly Ala Phe Asp Gly

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410

415

Thr Met Asn Gly Pro Phe Gly His Gly Tyr Gly Glu Gly Ala Gly Glu

420

425

430

Gly Ile Asp Asp Val Glu Trp Val Val Gly Lys Asp Lys Pro Thr Tyr

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440

445

Asp Glu Ile Phe Cys Thr Leu Ser Pro Val Asn Gly Lys Ile Thr Gly

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Ala Asn Ala Lys Lys Glu Met Val Lys Ser Lys Leu Pro Asn Thr Val

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475

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 Glu Gly His Glu Leu Pro Ala Asp Leu Pro Pro His Leu Val Pro Pro
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 Ser Lys Arg Arg His Glu Arg Trp Arg Pro Ala Pro His Leu Pro Phe
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Gln Lys Leu Leu Pro Leu Glu Glu His Tyr Arg Phe His Glu Phe His

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tgc ccc gcg ctg gag gac gct gac ttc gac aac aag cct atg gtg ctc 435

Ser Pro Ala Leu Glu Asp Ala Asp Phe Asp Asn Lys Pro Met Val Leu

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Leu Val Gly Gln Tyr Ser Thr Gly Lys Thr Thr Phe Ile Arg His Leu

65 70 75

atc gag cag gac ttc ccg ggg atg cgc atc ggg ccc gag ccc acc acc 531

Ile Glu Gln Asp Phe Pro Gly Met Arg Ile Gly Pro Glu Pro Thr Thr

80 85 90

gac tcc ttc atc gcc gtc atg cac ggc ccc act gag ggc gtg gtg ccg 579

Asp Ser Phe Ile Ala Val Met His Gly Pro Thr Glu Gly Val Val Pro

95 100 105 110

ggc aac gcg ctc gtg gtg gac ccg cgg cgc ccc ttc cgc aag ctc aac 627

Gly Asn Ala Leu Val Val Asp Pro Arg Arg Pro Phe Arg Lys Leu Asn

115 120 125

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 aac ccc gtc ctg gac agc atc agc atc atc gac acc ccc ggg atc ctg 723
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Arg Asn Ala Ala Leu Arg Lys Leu Asn Asp Leu Ile Lys Arg Ala Arg	
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ctg gcc aag gtt cac gcc tac atc atc agc tcc ctc aag aaa gag atg	1203
Leu Ala Lys Val His Ala Tyr Ile Ile Ser Ser Leu Lys Lys Glu Met	
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ccc aat gtc ttt ggt aaa gag agc aaa aag aaa gag ctg gtg aac aac	1251
Pro Asn Val Phe Gly Lys Glu Ser Lys Lys Lys Glu Leu Val Asn Asn	
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Leu Gly Glu Ile Tyr Gln Lys Ile Glu Arg Glu His Gln Ile Ser Pro	
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 Gly Glu Gly Ile Asp Asp Val Glu Trp Val Val Gly Lys Asp Lys Pro
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 aag ctg gag ggc cac gag ctg ccc gcc gac ctg ccc ccg cac ctg gtg 1827
 Lys Leu Glu Gly His Glu Leu Pro Ala Asp Leu Pro Pro His Leu Val
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 Pro Pro Ser Lys Arg Arg His Glu
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<211> 534

<212> PRT

<213> Homo sapiens

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Ala Leu Glu Asp Ala Asp Phe Asp Asn Lys Pro Met Val Leu Leu Val
50 55 60
Gly Gln Tyr Ser Thr Gly Lys Thr Thr Phe Ile Arg His Leu Ile Glu
65 70 75 80
Gln Asp Phe Pro Gly Met Arg Ile Gly Pro Glu Pro Thr Thr Asp Ser
85 90 95
Phe Ile Ala Val Met His Gly Pro Thr Glu Gly Val Val Pro Gly Asn
100 105 110
Ala Leu Val Val Asp Pro Arg Arg Pro Phe Arg Lys Leu Asn Ala Phe
115 120 125
Gly Asn Ala Phe Leu Asn Arg Phe Met Cys Ala Gln Leu Pro Asn Pro
130 135 140
Val Leu Asp Ser Ile Ser Ile Ile Asp Thr Pro Gly Ile Leu Ser Gly
145 150 155 160
Glu Lys Gln Arg Ile Ser Arg Gly Tyr Asp Phe Ala Ala Val Leu Glu
165 170 175
Trp Phe Ala Glu Arg Val Asp Arg Ile Ile Leu Leu Phe Asp Ala His
180 185 190

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Lys Leu Asp Ile Ser Asp Glu Phe Ser Glu Val Ile Lys Ala Leu Lys
 195 200 205
 Asn His Glu Asp Lys Ile Arg Val Val Leu Asn Lys Ala Asp Gln Ile
 210 215 220
 Glu Thr Gln Gln Leu Met Arg Val Tyr Gly Ala Leu Met Trp Ser Leu
 225 230 235 240
 Gly Lys Ile Ile Asn Thr Pro Glu Val Val Arg Val Tyr Ile Gly Ser
 245 250 255
 Phe Trp Ser His Pro Leu Leu Ile Pro Asp Asn Arg Lys Leu Phe Glu
 260 265 270
 Ala Glu Glu Gln Asp Leu Phe Lys Asp Ile Gln Ser Leu Pro Arg Asn
 275 280 285
 Ala Ala Leu Arg Lys Leu Asn Asp Leu Ile Lys Arg Ala Arg Leu Ala
 290 295 300
 Lys Val His Ala Tyr Ile Ile Ser Ser Leu Lys Lys Glu Met Pro Asn
 305 310 315 320
 Val Phe Gly Lys Glu Ser Lys Lys Lys Glu Leu Val Asn Asn Leu Gly
 325 330 335
 Glu Ile Tyr Gln Lys Ile Glu Arg Glu His Gln Ile Ser Pro Gly Asp
 340 345 350
 Phe Pro Ser Leu Arg Lys Met Gln Glu Leu Leu Gln Thr Gln Asp Phe
 355 360 365
 Ser Lys Phe Gln Ala Leu Lys Pro Lys Leu Leu Asp Thr Val Asp Asp
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 Phe Pro Phe Tyr Ser Cys Trp Arg Thr Gly Leu Leu Leu Leu Leu Leu
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 Lys Arg Leu Lys Pro Leu Phe Asn Lys Ser Phe Glu Ser Thr Val Gly
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 Gln Gly Ser Asp Thr Tyr Ile Tyr Ile Phe Arg Val Cys Arg Glu Ala
 70 75 80
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 Gly Asn His Thr Ser Gly Ala Gly Leu Val Gln Ile Asn Lys Ser Asn
 85 90 95
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 Gly Lys Glu Thr Val Val Gly Arg Leu Asn Glu Thr His Ile Phe Asn
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 Gly Ser Asn Trp Ile Met Leu Ile Tyr Lys Gly Gly Asp Glu Tyr Asp

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Ala Cys Ser Pro Glu Ile Ser His Leu Ser Val Gly Ser Ile Leu Leu			
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Val Thr Phe Ala Ser Leu Val Ala Val Tyr Val Val Gly Gly Phe Leu			
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Tyr Gln Arg Leu Val Val Gly Ala Lys Gly Met Glu Gln Phe Pro His			
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230	235	240	
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Ala Ala Gly			
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<211> 244

<212> PRT

<213> Homo sapiens

<400> 12

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 Val Lys Arg Leu Lys Pro Leu Phe Asn Lys Ser Phe Glu Ser Thr Val
 50 55 60
 Gly Gln Gly Ser Asp Thr Tyr Ile Tyr Ile Phe Arg Val Cys Arg Glu
 65 70 75 80
 Ala Gly Asn His Thr Ser Gly Ala Gly Leu Val Gln Ile Asn Lys Ser
 85 90 95
 Asn Gly Lys Glu Thr Val Val Gly Arg Leu Asn Glu Thr His Ile Phe
 100 105 110
 Asn Gly Ser Asn Trp Ile Met Leu Ile Tyr Lys Gly Gly Asp Glu Tyr
 115 120 125
 Asp Asn His Cys Gly Lys Glu Gln Arg Arg Ala Val Val Met Ile Ser

51/617

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 Cys Asn Arg His Thr Leu Ala Asp Asn Phe Asn Pro Val Ser Glu Glu
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 Arg Gly Lys Val Gln Asp Cys Phe Tyr Leu Phe Glu Met Asp Ser Ser
 165 170 175
 Leu Ala Cys Ser Pro Glu Ile Ser His Leu Ser Val Gly Ser Ile Leu
 180 185 190
 Leu Val Thr Phe Ala Ser Leu Val Ala Val Tyr Val Val Gly Gly Phe
 195 200 205
 Leu Tyr Gln Arg Leu Val Val Gly Ala Lys Gly Met Glu Gln Phe Pro
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<212> DNA

<213> Homo sapiens

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<222> (175).. (1005)

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 aagggtattc actggggatt ctgagctttg gctactccag tttcccacga cacg atg 177

Met

1

ttc cct ttc tac agc tgc tgg agg act gga ctg cta cta cta ctc ctg 225
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5 10 15

gct gtg gca gtg aga gaa tcc tgg cag aca gaa gaa aaa act tgc gac 273
Ala Val Ala Val Arg Glu Ser Trp Gln Thr Glu Glu Lys Thr Cys Asp

20 25 30

ttg gta gga gaa aag ggt aaa gag tca gag aaa gag ttg gct cta gtg 321
Leu Val Gly Glu Lys Gly Lys Glu Ser Glu Lys Glu Leu Ala Leu Val

35 40 45

aag agg ctg aaa cca ctg ttt aat aaa agc ttt gag agc act gtg ggc 369
Lys Arg Leu Lys Pro Leu Phe Asn Lys Ser Phe Glu Ser Thr Val Gly

50 55 60 65

cag ggt tca gac aca tac atc tac atc ttc agg gtg tgc cgg gaa gct 417
Gln Gly Ser Asp Thr Tyr Ile Tyr Ile Phe Arg Val Cys Arg Glu Ala

70 75 80

ggc aac cac act tct ggg gca ggc ctg gtg caa atc aac aaa agt aat 465
Gly Asn His Thr Ser Gly Ala Gly Leu Val Gln Ile Asn Lys Ser Asn

85 90 95

ggg aag gag aca gtg gta ggg aga ctc aac gag act cac atc ttc aac 513
Gly Lys Glu Thr Val Val Gly Arg Leu Asn Glu Thr His Ile Phe Asn

100 105 110

gga agt aat tgg atc atg ctg atc tat aaa ggg ggt gat gaa tat gac 561
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115 120 125

aac cac tgt ggc aag gag cag cgt cgt gca gtg gtg atg atc tcc tgc 609
Asn His Cys Gly Lys Glu Gln Arg Arg Ala Val Val Met Ile Ser Cys

130 135 140 145
 aat cga cac acc cta gcg gac aat ttt aac cct gtg tct gag gag cgt 657
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 150 155 160
 ggc aaa gtc caa gat tgt ttc tac ctc ttt gag atg gat agc agc ctg 705
 Gly Lys Val Gln Asp Cys Phe Tyr Leu Phe Glu Met Asp Ser Ser Leu
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 gcc tgt tca cca gag atc tcc cac ctc agt gtg ggt tcc atc tta ctt 753
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 180 185 190
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 Val Thr Phe Ala Ser Leu Val Ala Val Tyr Val Val Gly Gly Phe Leu
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 tac cag cga ctg gta gtg gga gcc aaa gga atg gag cag ttt ccc cac 849
 Tyr Gln Arg Leu Val Val Gly Ala Lys Gly Met Glu Gln Phe Pro His
 210 215 220 225
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 Leu Ala Phe Trp Gln Asp Leu Gly Asn Leu Val Ala Asp Gly Cys Asp
 230 235 240
 ttt gtc tgc cgt tct aaa cct cga aat gtg cct gca gca tat cgt ggt 945
 Phe Val Cys Arg Ser Lys Pro Arg Asn Val Pro Ala Ala Tyr Arg Gly
 245 250 255
 gtg ggg gat gac cag ctg ggg gag gag tca gaa gaa agg gat gac cat 993
 Val Gly Asp Asp Gln Leu Gly Glu Glu Ser Glu Glu Arg Asp Asp His
 260 265 270
 tta tta cca atg tagattgcac tttatatgtc cagcctcttc ctcagtcgcc 1045
 Leu Leu Pro Met

275

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<212> PRT

<213> Homo sapiens

<400> 14

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20 25 30

Asp Leu Val Gly Glu Lys Gly Lys Glu Ser Glu Lys Glu Leu Ala Leu

35 40 45

Val Lys Arg Leu Lys Pro Leu Phe Asn Lys Ser Phe Glu Ser Thr Val

50 55 60

Gly Gln Gly Ser Asp Thr Tyr Ile Tyr Ile Phe Arg Val Cys Arg Glu

65 70 75 80

Ala Gly Asn His Thr Ser Gly Ala Gly Leu Val Gln Ile Asn Lys Ser

85 90 95

Asn Gly Lys Glu Thr Val Val Gly Arg Leu Asn Glu Thr His Ile Phe

100 105 110

Asn Gly Ser Asn Trp Ile Met Leu Ile Tyr Lys Gly Gly Asp Glu Tyr

115 120 125

Asp Asn His Cys Gly Lys Glu Gln Arg Arg Ala Val Val Met Ile Ser

130 135 140

Cys Asn Arg His Thr Leu Ala Asp Asn Phe Asn Pro Val Ser Glu Glu

145 150 155 160

Arg Gly Lys Val Gln Asp Cys Phe Tyr Leu Phe Glu Met Asp Ser Ser

165 170 175

Leu Ala Cys Ser Pro Glu Ile Ser His Leu Ser Val Gly Ser Ile Leu

180 185 190
 Leu Val Thr Phe Ala Ser Leu Val Ala Val Tyr Val Val Gly Gly Phe
 195 200 205
 Leu Tyr Gln Arg Leu Val Val Gly Ala Lys Gly Met Glu Gln Phe Pro
 210 215 220
 His Leu Ala Phe Trp Gln Asp Leu Gly Asn Leu Val Ala Asp Gly Cys
 225 230 235 240
 Asp Phe Val Cys Arg Ser Lys Pro Arg Asn Val Pro Ala Ala Tyr Arg
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 Gly Val Gly Asp Asp Gln Leu Gly Glu Glu Ser Glu Glu Arg Asp Asp
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 His Leu Leu Pro Met
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<211> 2621

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<213> Mus musculus

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<222> (119).. (2128)

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 atg agc tca gcc aag agt gcc cgc tac gac cgc ttc tcc ggg gga cct 166
 Met Ser Ser Ala Lys Ser Ala Arg Tyr Asp Arg Phe Ser Gly Gly Pro

1

5

10

15


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gcc aac ctc ccc tcc tca gac agc agt ggg acc agg atg gaa aca acc 214
Ala Asn Leu Pro Ser Ser Asp Ser Ser Gly Thr Arg Met Glu Thr Thr
      20              25              30

ttt ggg cct acc ttt tcg acc gtc act acc atc acc aaa gca gct gat 262
Phe Gly Pro Thr Phe Ser Thr Val Thr Thr Ile Thr Lys Ala Ala Asp
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ggg act ggc aca tac aaa cag cat cgc agg aca cct tcc tcc tct agc 310
Gly Thr Gly Thr Tyr Lys Gln His Arg Arg Thr Pro Ser Ser Ser Ser
      50              55              60

acc ctt gcc tat tcg cca cgg gat gag gag gac ggc atg ccc ccc atc 358
Thr Leu Ala Tyr Ser Pro Arg Asp Glu Glu Asp Gly Met Pro Pro Ile
      65              70              75              80

aac act cct cgc cgc tct gac tca gcc atc tct gtc cgt tcc cta cac 406
Asn Thr Pro Arg Arg Ser Asp Ser Ala Ile Ser Val Arg Ser Leu His
      85              90              95

tcc gag tcc agc atg tcc ctg cgc tcc acg ttc tcg ctg cct gag gag 454
Ser Glu Ser Ser Met Ser Leu Arg Ser Thr Phe Ser Leu Pro Glu Glu
      100             105             110

gag gag gag ccg gag ccg ttg gta ttt gcc gag cag ccc tcg gta aag 502
Glu Glu Glu Pro Glu Pro Leu Val Phe Ala Glu Gln Pro Ser Val Lys
      115             120             125

ctg tgt tgc cag ctg tgc tgc agt gtg ttc aag gac cct gtg atc act 550
Leu Cys Cys Gln Leu Cys Cys Ser Val Phe Lys Asp Pro Val Ile Thr
      130             135             140

aca tgt ggg cac acc ttc tgc aga cga tgc gcc ttg aag tca gag aag 598
Thr Cys Gly His Thr Phe Cys Arg Arg Cys Ala Leu Lys Ser Glu Lys
      145             150             155             160

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 165 170 175
 gtc gct gag cag att gga gag ctc ttc ata cat tgt cgg cat ggc tgc 694
 Val Ala Glu Gln Ile Gly Glu Leu Phe Ile His Cys Arg His Gly Cys
 180 185 190
 cac gca gcg ggc act gga aag cct ggg gtc ttt gag gta gac ccg agg 742
 His Ala Ala Gly Thr Gly Lys Pro Gly Val Phe Glu Val Asp Pro Arg
 195 200 205
 ggc tgc ccc ttc acc atc aag ctt agt gcc cgg aag gac cac gag agt 790
 Gly Cys Pro Phe Thr Ile Lys Leu Ser Ala Arg Lys Asp His Glu Ser
 210 215 220
 agt tgt gac tac agg cct gtg cgc tgc ccc aac aac ccc agc tgc cca 838
 Ser Cys Asp Tyr Arg Pro Val Arg Cys Pro Asn Asn Pro Ser Cys Pro
 225 230 235 240
 ccc ctt ctc aag atg aat ctc gag gcc cac ctg aaa gaa tgc gag cac 886
 Pro Leu Leu Lys Met Asn Leu Glu Ala His Leu Lys Glu Cys Glu His
 245 250 255
 atc aag tgt ccc cac tct aag tac ggg tgc aca ttt att ggg aat cag 934
 Ile Lys Cys Pro His Ser Lys Tyr Gly Cys Thr Phe Ile Gly Asn Gln
 260 265 270
 gac acc tat gag aca cac tta gaa aca tgc cgc ttc gag ggc ctg aag 982
 Asp Thr Tyr Glu Thr His Leu Glu Thr Cys Arg Phe Glu Gly Leu Lys
 275 280 285
 gag ttc ctg cag cag acc gat gac cgc ttc cac gag atg cat gtg gca 1030
 Glu Phe Leu Gln Gln Thr Asp Asp Arg Phe His Glu Met His Val Ala
 290 295 300

ctg gcc caa aag gac cag gag att gcc ttc ccg cgt tcc atg ctg ggc 1078
 Leu Ala Gln Lys Asp Gln Glu Ile Ala Phe Pro Arg Ser Met Leu Gly
 305 310 315 320
 aaa ctc tca gag aag att gac cag cta gag aag agc ctt gag ctt aag 1126
 Lys Leu Ser Glu Lys Ile Asp Gln Leu Glu Lys Ser Leu Glu Leu Lys
 325 330 335
 ttt gac gta ctg gat gag aac cag agc aag ctc agc gag gac ctc atg 1174
 Phe Asp Val Leu Asp Glu Asn Gln Ser Lys Leu Ser Glu Asp Leu Met
 340 345 350
 gag ttc cgg agg gac gcg tcc atg ctg aat gat gag ctg tct cac atc 1222
 Glu Phe Arg Arg Asp Ala Ser Met Leu Asn Asp Glu Leu Ser His Ile
 355 360 365
 aat gca cgg ctg aac atg ggt atc ctt gga tcc tat gac cct cag cag 1270
 Asn Ala Arg Leu Asn Met Gly Ile Leu Gly Ser Tyr Asp Pro Gln Gln
 370 375 380
 atc ttc aag tgc aaa ggg acc ttt gtg gga cac cag ggc cct gtc tgg 1318
 Ile Phe Lys Cys Lys Gly Thr Phe Val Gly His Gln Gly Pro Val Trp
 385 390 395 400
 tgt ctc tgt gtc tat tcc atg ggt gac ctg ctc ttc agt ggc tct tct 1366
 Cys Leu Cys Val Tyr Ser Met Gly Asp Leu Leu Phe Ser Gly Ser Ser
 405 410 415
 gac aag aca atc aag gta tgg gac acg tgt acc act tac aag tgc caa 1414
 Asp Lys Thr Ile Lys Val Trp Asp Thr Cys Thr Thr Tyr Lys Cys Gln
 420 425 430
 aag aca ctg gaa ggt cat gat ggt att gtg ctg gcg ctc tgt atc cag 1462
 Lys Thr Leu Glu Gly His Asp Gly Ile Val Leu Ala Leu Cys Ile Gln
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 450 455 460
 gac atc cag aac cta cag aag gtg aat act atc cgg gcc cac gac aac 1558
 Asp Ile Gln Asn Leu Gln Lys Val Asn Thr Ile Arg Ala His Asp Asn
 465 470 475 480
 cct gta tgc acg ctg gtg tct tcc cac aac atg ctc ttc agt ggc tcc 1606
 Pro Val Cys Thr Leu Val Ser Ser His Asn Met Leu Phe Ser Gly Ser
 485 490 495
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 Leu Lys Ala Ile Lys Val Trp Asp Ile Val Gly Thr Glu Leu Lys Leu
 500 505 510
 aag aaa gaa ctc aca ggc ctc aac cac tgg gtg cgg gcc ctg gtg gca 1702
 Lys Lys Glu Leu Thr Gly Leu Asn His Trp Val Arg Ala Leu Val Ala
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 gca cgg agc tat ctg tac agt ggc tct tac cag aca atc aag atc tgg 1750
 Ala Arg Ser Tyr Leu Tyr Ser Gly Ser Tyr Gln Thr Ile Lys Ile Trp
 530 535 540
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 Asp Ile Arg Thr Leu Asp Cys Ile His Val Leu Gln Thr Ser Gly Gly
 545 550 555 560
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 Ser Val Tyr Ser Ile Ala Val Thr Asn His His Ile Val Cys Gly Thr
 565 570 575
 tat gag aac ctc att cat gtg tgg gac att gaa tcc aaa gag cag gtt 1894
 Tyr Glu Asn Leu Ile His Val Trp Asp Ile Glu Ser Lys Glu Gln Val
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cgg acc ctc aca ggt cac gtg ggc aca gtg tat gcc ctg gca gtc att 1942
 Arg Thr Leu Thr Gly His Val Gly Thr Val Tyr Ala Leu Ala Val Ile

595

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605

tca aca cca gac cag acc aaa gtc ttc agt gca tcc tat gac cgg tcc 1990
 Ser Thr Pro Asp Gln Thr Lys Val Phe Ser Ala Ser Tyr Asp Arg Ser

610

615

620

ctc agg gtc tgg agt atg gac aac atg atc tgc aca cag act ctg ctg 2038
 Leu Arg Val Trp Ser Met Asp Asn Met Ile Cys Thr Gln Thr Leu Leu

625

630

635

640

cgc cat cag ggc agt gta act gca ctg gct gtt tcc cgg ggc cgg ctc 2086
 Arg His Gln Gly Ser Val Thr Ala Leu Ala Val Ser Arg Gly Arg Leu

645

650

655

ttc tca ggg gct gtg gat agc acc gtg aag gtc tgg aca tgc 2128
 Phe Ser Gly Ala Val Asp Ser Thr Val Lys Val Trp Thr Cys

660

665

670

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<211> 670

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<213> Mus musculus

<400> 16

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 35 40 45
 Gly Thr Gly Thr Tyr Lys Gln His Arg Arg Thr Pro Ser Ser Ser Ser
 50 55 60
 Thr Leu Ala Tyr Ser Pro Arg Asp Glu Glu Asp Gly Met Pro Pro Ile
 65 70 75 80
 Asn Thr Pro Arg Arg Ser Asp Ser Ala Ile Ser Val Arg Ser Leu His
 85 90 95
 Ser Glu Ser Ser Met Ser Leu Arg Ser Thr Phe Ser Leu Pro Glu Glu
 100 105 110
 Glu Glu Glu Pro Glu Pro Leu Val Phe Ala Glu Gln Pro Ser Val Lys
 115 120 125
 Leu Cys Cys Gln Leu Cys Cys Ser Val Phe Lys Asp Pro Val Ile Thr
 130 135 140
 Thr Cys Gly His Thr Phe Cys Arg Arg Cys Ala Leu Lys Ser Glu Lys
 145 150 155 160
 Cys Pro Val Asp Asn Ala Lys Leu Thr Val Val Val Asn Asn Ile Ala
 165 170 175
 Val Ala Glu Gln Ile Gly Glu Leu Phe Ile His Cys Arg His Gly Cys
 180 185 190

63/617

His Ala Ala Gly Thr Gly Lys Pro Gly Val Phe Glu Val Asp Pro Arg
195 200 205
Gly Cys Pro Phe Thr Ile Lys Leu Ser Ala Arg Lys Asp His Glu Ser
210 215 220
Ser Cys Asp Tyr Arg Pro Val Arg Cys Pro Asn Asn Pro Ser Cys Pro
225 230 235 240
Pro Leu Leu Lys Met Asn Leu Glu Ala His Leu Lys Glu Cys Glu His
245 250 255
Ile Lys Cys Pro His Ser Lys Tyr Gly Cys Thr Phe Ile Gly Asn Gln
260 265 270
Asp Thr Tyr Glu Thr His Leu Glu Thr Cys Arg Phe Glu Gly Leu Lys
275 280 285
Glu Phe Leu Gln Gln Thr Asp Asp Arg Phe His Glu Met His Val Ala
290 295 300
Leu Ala Gln Lys Asp Gln Glu Ile Ala Phe Pro Arg Ser Met Leu Gly
305 310 315 320
Lys Leu Ser Glu Lys Ile Asp Gln Leu Glu Lys Ser Leu Glu Leu Lys
325 330 335
Phe Asp Val Leu Asp Glu Asn Gln Ser Lys Leu Ser Glu Asp Leu Met
340 345 350
Glu Phe Arg Arg Asp Ala Ser Met Leu Asn Asp Glu Leu Ser His Ile
355 360 365
Asn Ala Arg Leu Asn Met Gly Ile Leu Gly Ser Tyr Asp Pro Gln Gln
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Ile Phe Lys Cys Lys Gly Thr Phe Val Gly His Gln Gly Pro Val Trp
385 390 395 400
Cys Leu Cys Val Tyr Ser Met Gly Asp Leu Leu Phe Ser Gly Ser Ser

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Asp Lys Thr Ile Lys Val Trp Asp Thr Cys Thr Thr Tyr Lys Cys Gln		
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Lys Thr Leu Glu Gly His Asp Gly Ile Val Leu Ala Leu Cys Ile Gln		
435	440	445
Gly Cys Lys Leu Tyr Ser Gly Ser Ala Asp Cys Thr Ile Ile Val Trp		
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Asp Ile Gln Asn Leu Gln Lys Val Asn Thr Ile Arg Ala His Asp Asn		
465	470	475
Pro Val Cys Thr Leu Val Ser Ser His Asn Met Leu Phe Ser Gly Ser		
485	490	495
Leu Lys Ala Ile Lys Val Trp Asp Ile Val Gly Thr Glu Leu Lys Leu		
500	505	510
Lys Lys Glu Leu Thr Gly Leu Asn His Trp Val Arg Ala Leu Val Ala		
515	520	525
Ala Arg Ser Tyr Leu Tyr Ser Gly Ser Tyr Gln Thr Ile Lys Ile Trp		
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Asp Ile Arg Thr Leu Asp Cys Ile His Val Leu Gln Thr Ser Gly Gly		
545	550	555
Ser Val Tyr Ser Ile Ala Val Thr Asn His His Ile Val Cys Gly Thr		
565	570	575
Tyr Glu Asn Leu Ile His Val Trp Asp Ile Glu Ser Lys Glu Gln Val		
580	585	590
Arg Thr Leu Thr Gly His Val Gly Thr Val Tyr Ala Leu Ala Val Ile		
595	600	605
Ser Thr Pro Asp Gln Thr Lys Val Phe Ser Ala Ser Tyr Asp Arg Ser		
610	615	620

Leu Arg Val Trp Ser Met Asp Asn Met Ile Cys Thr Gln Thr Leu Leu

625 630 635 640

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645 650 655

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<210> 17

<211> 2636

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (239).. (2143)

<400> 17

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tacgaccgct tctccggggg acctgccaac ctccccctct cagacagcag tgggaccagg 180

atggaacaaa cctttgggcc taccttttgc accgtcacta ccatcaccaa agcagctg 238

atg gga ctg gca cat aca aac agc atc gca gga cac ctt cct cct cta 286

Met Gly Leu Ala His Thr Asn Ser Ile Ala Gly His Leu Pro Pro Leu

1 5 10 15

gca ccc ttg cct att cgc cac ggg atg agg agg acg gca tgg gct caa 334

Ala Pro Leu Pro Ile Arg His Gly Met Arg Arg Thr Ala Trp Ala Gln

20 25 30

gcc cct gaa agg ctg cct cca tct gtg cag ccc ccc atc aac act cct 382

Ala Pro Glu Arg Leu Pro Pro Ser Val Gln Pro Pro Ile Asn Thr Pro

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50	55	60	
agc atg tcc ctg cgc tcc acg ttc tcg ctg cct gag gag gag gag gag	478		
Ser Met Ser Leu Arg Ser Thr Phe Ser Leu Pro Glu Glu Glu Glu Glu			
65	70	75	80
ccg gag ccg ttg gta ttt gcc gag cag ccc tcg gta aag ctg tgt tgc	526		
Pro Glu Pro Leu Val Phe Ala Glu Gln Pro Ser Val Lys Leu Cys Cys			
85	90	95	
cag ctg tgc tgc agt gtg ttc aag gac cct gtg atc act aca tgt ggg	574		
Gln Leu Cys Cys Ser Val Phe Lys Asp Pro Val Ile Thr Thr Cys Gly			
100	105	110	
cac acc ttc tgc aga cga tgc gcc ttg aag tca gag aag tgt cct gtg	622		
His Thr Phe Cys Arg Arg Cys Ala Leu Lys Ser Glu Lys Cys Pro Val			
115	120	125	
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Asp Asn Ala Lys Leu Thr Val Val Val Asn Asn Ile Ala Val Ala Glu			
130	135	140	
cag att gga gag ctc ttc ata cat tgt cgg cat ggc tgc cac gca gcg	718		
Gln Ile Gly Glu Leu Phe Ile His Cys Arg His Gly Cys His Ala Ala			
145	150	155	160
ggc act gga aag cct ggg gtc ttt gag gta gac ccg agg ggc tgc ccc	766		
Gly Thr Gly Lys Pro Gly Val Phe Glu Val Asp Pro Arg Gly Cys Pro			
165	170	175	
ttc acc atc aag ctt agt gcc cgg aag gac cac gag agt agt tgt gac	814		
Phe Thr Ile Lys Leu Ser Ala Arg Lys Asp His Glu Ser Ser Cys Asp			

180	185	190	
tac agg cct gtg cgc tgc ccc aac aac ccc agc tgc cca ccc ctt ctc	862		
Tyr Arg Pro Val Arg Cys Pro Asn Asn Pro Ser Cys Pro Pro Leu Leu			
195	200	205	
aag atg aat ctc gag gcc cac ctg aaa gaa tgc gag cac atc aag tgt	910		
Lys Met Asn Leu Glu Ala His Leu Lys Glu Cys Glu His Ile Lys Cys			
210	215	220	
ccc cac tct aag tac ggg tgc aca ttt att ggg aat cag gac acc tat	958		
Pro His Ser Lys Tyr Gly Cys Thr Phe Ile Gly Asn Gln Asp Thr Tyr			
225	230	235	240
gag aca cac tta gaa aca tgc cgc ttc gag ggc ctg aag gag ttc ctg	1006		
Glu Thr His Leu Glu Thr Cys Arg Phe Glu Gly Leu Lys Glu Phe Leu			
245	250	255	
cag cag acc gat gac cgc ttc cac gag atg cat gtg gca ctg gcc caa	1054		
Gln Gln Thr Asp Asp Arg Phe His Glu Met His Val Ala Leu Ala Gln			
260	265	270	
aag gac cag gag att gcc ttc ctg cgt tcc atg ctg ggc aaa ctc tca	1102		
Lys Asp Gln Glu Ile Ala Phe Leu Arg Ser Met Leu Gly Lys Leu Ser			
275	280	285	
gag aag att gac cag cta gag aag agc ctt gag ctt aag ttt gac gta	1150		
Glu Lys Ile Asp Gln Leu Glu Lys Ser Leu Glu Leu Lys Phe Asp Val			
290	295	300	
ctg gat gag aac cag agc aag ctc agc gag gac ctc atg gag ttc cgg	1198		
Leu Asp Glu Asn Gln Ser Lys Leu Ser Glu Asp Leu Met Glu Phe Arg			
305	310	315	320
agg gac gcg tcc atg ctg aat gat gag ctg tct cac atc aat gca cgg	1246		
Arg Asp Ala Ser Met Leu Asn Asp Glu Leu Ser His Ile Asn Ala Arg			

325	330	335	
ctg aac atg ggt atc ctt gga tcc tat gac cct cag cag atc ttc aag			1294
Leu Asn Met Gly Ile Leu Gly Ser Tyr Asp Pro Gln Gln Ile Phe Lys			
340	345	350	
tgc aaa ggg acc ttt gtg gga cac cag ggc cct gtc tgg tgt ctc tgt			1342
Cys Lys Gly Thr Phe Val Gly His Gln Gly Pro Val Trp Cys Leu Cys			
355	360	365	
gtc tat tcc atg ggt gac ctg ctc ttc agt ggc tct tct gac aag aca			1390
Val Tyr Ser Met Gly Asp Leu Leu Phe Ser Gly Ser Ser Asp Lys Thr			
370	375	380	
atc aag gta tgg gac acg tgt acc act tac aag tgc caa aag aca ctg			1438
Ile Lys Val Trp Asp Thr Cys Thr Thr Tyr Lys Cys Gln Lys Thr Leu			
385	390	395	400
gaa ggt cat gat ggt att gtg ctg ggc ctc tgt atc cag ggg tgc aaa			1486
Glu Gly His Asp Gly Ile Val Leu Ala Leu Cys Ile Gln Gly Cys Lys			
405	410	415	
ctg tac agt ggg tct gca gac tgc acc atc att gtg tgg gac atc cag			1534
Leu Tyr Ser Gly Ser Ala Asp Cys Thr Ile Ile Val Trp Asp Ile Gln			
420	425	430	
aac cta cag aag gtg aat act atc cgg gcc cac gac aac cct gta tgc			1582
Asn Leu Gln Lys Val Asn Thr Ile Arg Ala His Asp Asn Pro Val Cys			
435	440	445	
acg ctg gtg tct tcc cac aac atg ctc ttc agt ggc tcc ctg aaa gcc			1630
Thr Leu Val Ser Ser His Asn Met Leu Phe Ser Gly Ser Leu Lys Ala			
450	455	460	
atc aag gtt tgg gac atc gtg ggc act gag cta aag ttg aag aaa gaa			1678
Ile Lys Val Trp Asp Ile Val Gly Thr Glu Leu Lys Leu Lys Lys Glu			

465	470	475	480	
ctc aca ggc ctc aac cac tgg gtg cgg gcc ctg gtg gca gca cag agc	1726			
Leu Thr Gly Leu Asn His Trp Val Arg Ala Leu Val Ala Ala Gln Ser				
485	490	495		
tat ctg tac agt ggc tct tac cag aca atc aag atc tgg gac att cgg	1774			
Tyr Leu Tyr Ser Gly Ser Tyr Gln Thr Ile Lys Ile Trp Asp Ile Arg				
500	505	510		
acc ctt gac tgc atc cat gtc ctg cag aca tct ggt ggc agt gtg tat	1822			
Thr Leu Asp Cys Ile His Val Leu Gln Thr Ser Gly Gly Ser Val Tyr				
515	520	525		
tcc att gct gtg acg aat cac cac att gtc tgt ggc acc tat gag aac	1870			
Ser Ile Ala Val Thr Asn His His Ile Val Cys Gly Thr Tyr Glu Asn				
530	535	540		
ctc att cat gtg tgg gac att gaa tcc aaa gag cag gtt cgg acc ctc	1918			
Leu Ile His Val Trp Asp Ile Glu Ser Lys Glu Gln Val Arg Thr Leu				
545	550	555	560	
aca ggt cac gtg ggc aca gtg tat gcc ctg gca gtc att tca aca cca	1966			
Thr Gly His Val Gly Thr Val Tyr Ala Leu Ala Val Ile Ser Thr Pro				
565	570	575		
gac cag acc aaa gtc ttc agt gca tcc tat gac cgg tcc ctc agg gtc	2014			
Asp Gln Thr Lys Val Phe Ser Ala Ser Tyr Asp Arg Ser Leu Arg Val				
580	585	590		
tgg agt atg gac aac atg atc tgc aca cag act ctg ctg cgc cat cag	2062			
Trp Ser Met Asp Asn Met Ile Cys Thr Gln Thr Leu Leu Arg His Gln				
595	600	605		
ggc agt gta act gca ctg gct gtt tcc cgg ggc cgg ctc ttc tca ggg	2110			
Gly Ser Val Thr Ala Leu Ala Val Ser Arg Gly Arg Leu Phe Ser Gly				

610 615 620
 gct gtg gat agc acc gtg aag gtc tgg aca tgc taacagaatc caggccaggc 2163
 Ala Val Asp Ser Thr Val Lys Val Trp Thr Cys
 625 630 635
 ttggctccct ctgggtctgt aagtcaggct ggacctccat tggaatgtct gcctgtctgt 2223
 ggagacaggt agacaggctc agctaggcag tgcctctctt gcctatactt ggcgagggat 2283
 ctttccaaag gccccgctgt tacttgtacc agagaaacac ccaggccctc ctctgggcac 2343
 caggtctgat gcttgcccag cccaccgtt catatcactc catagactct tgttctgaga 2403
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 ccaactcaca gatctgcctg cctccacctc ccaagtgtg ggagtaaagg cccgcaccgc 2523
 cgctcctggc aggaccggga tgaccagggt gtccttttta ctacactttt ctactggttt 2583
 tagactgtat atagatttta ttactttcca gttgaaataa aagctgcaca gac 2636

<210> 18

<211> 635

<212> PRT

<213> Mus musculus

<400> 18

Met Gly Leu Ala His Thr Asn Ser Ile Ala Gly His Leu Pro Pro Leu
 1 5 10 15
 Ala Pro Leu Pro Ile Arg His Gly Met Arg Arg Thr Ala Trp Ala Gln
 20 25 30
 Ala Pro Glu Arg Leu Pro Pro Ser Val Gln Pro Pro Ile Asn Thr Pro
 35 40 45
 Arg Arg Ser Asp Ser Ala Ile Ser Val Arg Ser Leu His Ser Glu Ser
 50 55 60
 Ser Met Ser Leu Arg Ser Thr Phe Ser Leu Pro Glu Glu Glu Glu

71/617

65	70	75	80
Pro Glu Pro Leu Val Phe Ala Glu Gln Pro Ser Val Lys Leu Cys Cys			
	85	90	95
Gln Leu Cys Cys Ser Val Phe Lys Asp Pro Val Ile Thr Thr Cys Gly			
	100	105	110
His Thr Phe Cys Arg Arg Cys Ala Leu Lys Ser Glu Lys Cys Pro Val			
	115	120	125
Asp Asn Ala Lys Leu Thr Val Val Val Asn Asn Ile Ala Val Ala Glu			
	130	135	140
Gln Ile Gly Glu Leu Phe Ile His Cys Arg His Gly Cys His Ala Ala			
145	150	155	160
Gly Thr Gly Lys Pro Gly Val Phe Glu Val Asp Pro Arg Gly Cys Pro			
	165	170	175
Phe Thr Ile Lys Leu Ser Ala Arg Lys Asp His Glu Ser Ser Cys Asp			
	180	185	190
Tyr Arg Pro Val Arg Cys Pro Asn Asn Pro Ser Cys Pro Pro Leu Leu			
	195	200	205
Lys Met Asn Leu Glu Ala His Leu Lys Glu Cys Glu His Ile Lys Cys			
	210	215	220
Pro His Ser Lys Tyr Gly Cys Thr Phe Ile Gly Asn Gln Asp Thr Tyr			
225	230	235	240
Glu Thr His Leu Glu Thr Cys Arg Phe Glu Gly Leu Lys Glu Phe Leu			
	245	250	255
Gln Gln Thr Asp Asp Arg Phe His Glu Met His Val Ala Leu Ala Gln			
	260	265	270
Lys Asp Gln Glu Ile Ala Phe Leu Arg Ser Met Leu Gly Lys Leu Ser			
	275	280	285

Glu Lys Ile Asp Gln Leu Glu Lys Ser Leu Glu Leu Lys Phe Asp Val
290 295 300
Leu Asp Glu Asn Gln Ser Lys Leu Ser Glu Asp Leu Met Glu Phe Arg
305 310 315 320
Arg Asp Ala Ser Met Leu Asn Asp Glu Leu Ser His Ile Asn Ala Arg
325 330 335
Leu Asn Met Gly Ile Leu Gly Ser Tyr Asp Pro Gln Gln Ile Phe Lys
340 345 350
Cys Lys Gly Thr Phe Val Gly His Gln Gly Pro Val Trp Cys Leu Cys
355 360 365
Val Tyr Ser Met Gly Asp Leu Leu Phe Ser Gly Ser Ser Asp Lys Thr
370 375 380
Ile Lys Val Trp Asp Thr Cys Thr Thr Tyr Lys Cys Gln Lys Thr Leu
385 390 395 400
Glu Gly His Asp Gly Ile Val Leu Ala Leu Cys Ile Gln Gly Cys Lys
405 410 415
Leu Tyr Ser Gly Ser Ala Asp Cys Thr Ile Ile Val Trp Asp Ile Gln
420 425 430
Asn Leu Gln Lys Val Asn Thr Ile Arg Ala His Asp Asn Pro Val Cys
435 440 445
Thr Leu Val Ser Ser His Asn Met Leu Phe Ser Gly Ser Leu Lys Ala
450 455 460
Ile Lys Val Trp Asp Ile Val Gly Thr Glu Leu Lys Leu Lys Lys Glu
465 470 475 480
Leu Thr Gly Leu Asn His Trp Val Arg Ala Leu Val Ala Ala Gln Ser
485 490 495
Tyr Leu Tyr Ser Gly Ser Tyr Gln Thr Ile Lys Ile Trp Asp Ile Arg

500 505 510
Thr Leu Asp Cys Ile His Val Leu Gln Thr Ser Gly Gly Ser Val Tyr
515 520 525
Ser Ile Ala Val Thr Asn His His Ile Val Cys Gly Thr Tyr Glu Asn
530 535 540
Leu Ile His Val Trp Asp Ile Glu Ser Lys Glu Gln Val Arg Thr Leu
545 550 555 560
Thr Gly His Val Gly Thr Val Tyr Ala Leu Ala Val Ile Ser Thr Pro
565 570 575
Asp Gln Thr Lys Val Phe Ser Ala Ser Tyr Asp Arg Ser Leu Arg Val
580 585 590
Trp Ser Met Asp Asn Met Ile Cys Thr Gln Thr Leu Leu Arg His Gln
595 600 605
Gly Ser Val Thr Ala Leu Ala Val Ser Arg Gly Arg Leu Phe Ser Gly
610 615 620
Ala Val Asp Ser Thr Val Lys Val Trp Thr Cys
625 630 635

<210> 19

<211> 3864

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (297).. (2306)

<400> 19

ggtagactggc tgtgactcag gacccagagg agtagaggga gccaggcagg ggtccctcca 60

cctcggggaa gagctggatg ggctcttcgg gagctcagaa aggctaagcc ttgaggacg 120
 gtgacgcaga gccgcctgcc tgcccgggcc tctgcatacc tgggatcggg gtgaaggacc 180
 ttgacctcct agaggcctgc ctgagccggg gctggtggtg gaaggctgct gcggcggccc 240
 cacggtgccc cacagcagga ggtgcttccc aaggaccgta gatgcctctc tagagc atg 299

Met

1

agc tca ggc aag agt gcc cgc tac aac cgc ttc tcc ggg ggg ccc agc 347
 Ser Ser Gly Lys Ser Ala Arg Tyr Asn Arg Phe Ser Gly Gly Pro Ser

5

10

15

aat ctt ccc acc cca gac gtc acc aca ggg acc aga atg gaa acg acc 395
 Asn Leu Pro Thr Pro Asp Val Thr Thr Gly Thr Arg Met Glu Thr Thr

20

25

30

ttc gga ccc gcc ttt tca gcc gtc acc acc atc aca aaa gct gac ggg 443
 Phe Gly Pro Ala Phe Ser Ala Val Thr Thr Ile Thr Lys Ala Asp Gly

35

40

45

acc agc acc tac aag cag cac tgc agg aca ccc tcc tcc tcc agc acc 491
 Thr Ser Thr Tyr Lys Gln His Cys Arg Thr Pro Ser Ser Ser Ser Thr

50

55

60

65

ctt gcc tac tcc ccg cgg gac gag gag gac agc atg ccc ccc atc agc 539
 Leu Ala Tyr Ser Pro Arg Asp Glu Glu Asp Ser Met Pro Pro Ile Ser

70

75

80

act ccc cgc cgc tcc gac tcc gcc atc tct gtc cgc tcc ctg cac tca 587
 Thr Pro Arg Arg Ser Asp Ser Ala Ile Ser Val Arg Ser Leu His Ser

85

90

95

gag tcc agc atg tct ctg cgc tcc aca ttc tca ctg ccc gag gag gag 635
 Glu Ser Ser Met Ser Leu Arg Ser Thr Phe Ser Leu Pro Glu Glu Glu

100

105

110

75/617

gag gag ccg gag cca ctg gtg ttt gcg gag cag ccc tcg gtg aag ctg 683
 Glu Glu Pro Glu Pro Leu Val Phe Ala Glu Gln Pro Ser Val Lys Leu
 115 120 125
 tgc tgt cag ctc tgc tgc agc gtc ttc aaa gac ccc gtg atc acc acg 731
 Cys Cys Gln Leu Cys Cys Ser Val Phe Lys Asp Pro Val Ile Thr Thr
 130 135 140 145
 tgt ggg cac acg ttc tgt agg aga tgc gcc ttg aag tca gag aag tgt 779
 Cys Gly His Thr Phe Cys Arg Arg Cys Ala Leu Lys Ser Glu Lys Cys
 150 155 160
 ccc gtg gac aac gtc aaa ctg acc gtg gtg gtg aac aac atc gcg gtg 827
 Pro Val Asp Asn Val Lys Leu Thr Val Val Val Asn Asn Ile Ala Val
 165 170 175
 gcc gag cag atc ggg gag ctc ttc atc cac tgc cgg cac ggc tgc cgg 875
 Ala Glu Gln Ile Gly Glu Leu Phe Ile His Cys Arg His Gly Cys Arg
 180 185 190
 gta gcg ggc agc ggg aag ccc ccc atc ttt gag gtg gac ccc cga ggg 923
 Val Ala Gly Ser Gly Lys Pro Pro Ile Phe Glu Val Asp Pro Arg Gly
 195 200 205
 tgc ccc ttc acc atc aag ctc agc gcc cgg aag gac cac gag ggc agc 971
 Cys Pro Phe Thr Ile Lys Leu Ser Ala Arg Lys Asp His Glu Gly Ser
 210 215 220 225
 tgt gac tac agg cct gtg cgg tgt ccc aac aac ccc agc tgc ccc ccg 1019
 Cys Asp Tyr Arg Pro Val Arg Cys Pro Asn Asn Pro Ser Cys Pro Pro
 230 235 240
 ctg ctc agg atg aac ctg gag gcc cac ctc aag gag tgc gag cac atc 1067
 Leu Leu Arg Met Asn Leu Glu Ala His Leu Lys Glu Cys Glu His Ile
 245 250 255

aaa tgc ccc cac tcc aag tac ggg tgc acg ttc atc ggg aac cag gac 1115
 Lys Cys Pro His Ser Lys Tyr Gly Cys Thr Phe Ile Gly Asn Gln Asp
 260 265 270
 act tac gag acc cac ctg gag act tgc cgc ttc gag ggc ctg aag gag 1163
 Thr Tyr Glu Thr His Leu Glu Thr Cys Arg Phe Glu Gly Leu Lys Glu
 275 280 285
 ttt ctg cag cag acg gat gac cgc ttc cac gag atg cac gtg gct ctg 1211
 Phe Leu Gln Gln Thr Asp Asp Arg Phe His Glu Met His Val Ala Leu
 290 295 300 305
 gcc cag aag gac cag gag atc gcc ttc ctg cgc tcc atg ctg gga aag 1259
 Ala Gln Lys Asp Gln Glu Ile Ala Phe Leu Arg Ser Met Leu Gly Lys
 310 315 320
 ctc tcg gag aag atc gac cag cta gag aag agc ctg gag ctc aag ttt 1307
 Leu Ser Glu Lys Ile Asp Gln Leu Glu Lys Ser Leu Glu Leu Lys Phe
 325 330 335
 gac gtc ctg gac gaa aac cag agc aag ctc agc gag gac ctc atg gag 1355
 Asp Val Leu Asp Glu Asn Gln Ser Lys Leu Ser Glu Asp Leu Met Glu
 340 345 350
 ttc cgg cgg gac gca tcc atg tta aat gac gag ctg tcc cac atc aac 1403
 Phe Arg Arg Asp Ala Ser Met Leu Asn Asp Glu Leu Ser His Ile Asn
 355 360 365
 gcg cgg ctg aac atg ggc atc cta ggc tcc tac gac cct cag cag atc 1451
 Ala Arg Leu Asn Met Gly Ile Leu Gly Ser Tyr Asp Pro Gln Gln Ile
 370 375 380 385
 ttc aag tgc aaa ggg acc ttt gtg ggc cac cag ggc cct gtg tgg tgt 1499
 Phe Lys Cys Lys Gly Thr Phe Val Gly His Gln Gly Pro Val Trp Cys
 390 395 400

ctc tgc gtc tac tcc atg ggt gac ctg ctc ttc agt ggc tcc tct gac 1547
 Leu Cys Val Tyr Ser Met Gly Asp Leu Leu Phe Ser Gly Ser Ser Asp
 405 410 415
 aag acc atc aag gtg tgg gac aca tgt acc acc tac aag tgt cag aag 1595
 Lys Thr Ile Lys Val Trp Asp Thr Cys Thr Thr Tyr Lys Cys Gln Lys
 420 425 430
 aca ctg gag ggc cat gat ggc atc gtg ctg gct ctc tgc atc cag ggg 1643
 Thr Leu Glu Gly His Asp Gly Ile Val Leu Ala Leu Cys Ile Gln Gly
 435 440 445
 tgc aaa ctc tac agc ggc tct gca gac tgc acc atc att gtg tgg gac 1691
 Cys Lys Leu Tyr Ser Gly Ser Ala Asp Cys Thr Ile Ile Val Trp Asp
 450 455 460 465
 atc cag aac ctg cag aag gtg aac acc atc cgg gcc cat gac aac ccg 1739
 Ile Gln Asn Leu Gln Lys Val Asn Thr Ile Arg Ala His Asp Asn Pro
 470 475 480
 gtg tgc acg ctg gtc tcc tca cac aac gtg ctc ttc agc ggc tcc ctg 1787
 Val Cys Thr Leu Val Ser Ser His Asn Val Leu Phe Ser Gly Ser Leu
 485 490 495
 aag gcc atc aag gtc tgg gac atc gtg ggc act gag ctg aag ttg aag 1835
 Lys Ala Ile Lys Val Trp Asp Ile Val Gly Thr Glu Leu Lys Leu Lys
 500 505 510
 aag gag ctc aca ggc ctc aac cac tgg gtg cgg gcc ctg gtg gct gcc 1883
 Lys Glu Leu Thr Gly Leu Asn His Trp Val Arg Ala Leu Val Ala Ala
 515 520 525
 cag agc tac ctg tac agc ggc tcc tac cag aca atc aag atc tgg gac 1931
 Gln Ser Tyr Leu Tyr Ser Gly Ser Tyr Gln Thr Ile Lys Ile Trp Asp
 530 535 540 545

atc cga acc ctt gac tgc atc cac gtc ctg cag acg tct ggt ggc agc 1979
 Ile Arg Thr Leu Asp Cys Ile His Val Leu Gln Thr Ser Gly Gly Ser
 550 555 560
 gtc tac tcc att gct gtg aca aat cac cac att gtc tgt ggc acc tac 2027
 Val Tyr Ser Ile Ala Val Thr Asn His His Ile Val Cys Gly Thr Tyr
 565 570 575
 gag aac ctc atc cac gtg tgg gac att gag tcc aag gag cag gtg cgg 2075
 Glu Asn Leu Ile His Val Trp Asp Ile Glu Ser Lys Glu Gln Val Arg
 580 585 590
 acc ctc acg ggc cac gtg ggc acc gtg tat gcc ctg gcg gtc atc tcg 2123
 Thr Leu Thr Gly His Val Gly Thr Val Tyr Ala Leu Ala Val Ile Ser
 595 600 605
 acg cca gac cag acc aaa gtc ttc agt gca tcc tac gac cgg tcc ctc 2171
 Thr Pro Asp Gln Thr Lys Val Phe Ser Ala Ser Tyr Asp Arg Ser Leu
 610 615 620 625
 agg gtc tgg agt atg gac aac atg atc tgc acg cag acc ctg ctg cgt 2219
 Arg Val Trp Ser Met Asp Asn Met Ile Cys Thr Gln Thr Leu Leu Arg
 630 635 640
 cac cag ggc agt gtc acc gcg ctg gct gtg tcc cgg ggc cga ctc ttc 2267
 His Gln Gly Ser Val Thr Ala Leu Ala Val Ser Arg Gly Arg Leu Phe
 645 650 655
 tca ggg gct gtg gat agc act gtg aag gtt tgg act tgc taacaggatc 2316
 Ser Gly Ala Val Asp Ser Thr Val Lys Val Trp Thr Cys
 660 665 670
 caggccaggc tgtggtttcc cctgaaccag ccctggacct ttctgagcca ggctggccac 2376
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cgccgagagc aaggcacaac ctcgagttct tggggcgag agaacttagg agagaagcac 3576
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ctggggcctc cactctggcc ggaggaagga ccgcaggcag acagcctggg cctctaacag 3696
cttttgtccg gagctagact tcgtgtcctt tcagttggta aatggttttc tatagaatca 3756
ataatatttc tttctttaa tatatattg ttaaagttat acctttttgt ttctctgggg 3816
aatccgcct cagctcattc ccaataaatt aatactcttg atagctta 3864

<210> 20

<211> 670

<212> PRT

<213> Homo sapiens

<400> 20

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 20 25 30
 Thr Phe Gly Pro Ala Phe Ser Ala Val Thr Thr Ile Thr Lys Ala Asp
 35 40 45
 Gly Thr Ser Thr Tyr Lys Gln His Cys Arg Thr Pro Ser Ser Ser Ser
 50 55 60
 Thr Leu Ala Tyr Ser Pro Arg Asp Glu Glu Asp Ser Met Pro Pro Ile
 65 70 75 80
 Ser Thr Pro Arg Arg Ser Asp Ser Ala Ile Ser Val Arg Ser Leu His
 85 90 95
 Ser Glu Ser Ser Met Ser Leu Arg Ser Thr Phe Ser Leu Pro Glu Glu
 100 105 110
 Glu Glu Glu Pro Glu Pro Leu Val Phe Ala Glu Gln Pro Ser Val Lys
 115 120 125
 Leu Cys Cys Gln Leu Cys Cys Ser Val Phe Lys Asp Pro Val Ile Thr
 130 135 140
 Thr Cys Gly His Thr Phe Cys Arg Arg Cys Ala Leu Lys Ser Glu Lys
 145 150 155 160
 Cys Pro Val Asp Asn Val Lys Leu Thr Val Val Val Asn Asn Ile Ala
 165 170 175
 Val Ala Glu Gln Ile Gly Glu Leu Phe Ile His Cys Arg His Gly Cys
 180 185 190
 Arg Val Ala Gly Ser Gly Lys Pro Pro Ile Phe Glu Val Asp Pro Arg

81/617

195 200 205
Gly Cys Pro Phe Thr Ile Lys Leu Ser Ala Arg Lys Asp His Glu Gly
210 215 220
Ser Cys Asp Tyr Arg Pro Val Arg Cys Pro Asn Asn Pro Ser Cys Pro
225 230 235 240
Pro Leu Leu Arg Met Asn Leu Glu Ala His Leu Lys Glu Cys Glu His
245 250 255
Ile Lys Cys Pro His Ser Lys Tyr Gly Cys Thr Phe Ile Gly Asn Gln
260 265 270
Asp Thr Tyr Glu Thr His Leu Glu Thr Cys Arg Phe Glu Gly Leu Lys
275 280 285
Glu Phe Leu Gln Gln Thr Asp Asp Arg Phe His Glu Met His Val Ala
290 295 300
Leu Ala Gln Lys Asp Gln Glu Ile Ala Phe Leu Arg Ser Met Leu Gly
305 310 315 320
Lys Leu Ser Glu Lys Ile Asp Gln Leu Glu Lys Ser Leu Glu Leu Lys
325 330 335
Phe Asp Val Leu Asp Glu Asn Gln Ser Lys Leu Ser Glu Asp Leu Met
340 345 350
Glu Phe Arg Arg Asp Ala Ser Met Leu Asn Asp Glu Leu Ser His Ile
355 360 365
Asn Ala Arg Leu Asn Met Gly Ile Leu Gly Ser Tyr Asp Pro Gln Gln
370 375 380
Ile Phe Lys Cys Lys Gly Thr Phe Val Gly His Gln Gly Pro Val Trp
385 390 395 400
Cys Leu Cys Val Tyr Ser Met Gly Asp Leu Leu Phe Ser Gly Ser Ser
405 410 415

Asp Lys Thr Ile Lys Val Trp Asp Thr Cys Thr Thr Tyr Lys Cys Gln
420 425 430

Lys Thr Leu Glu Gly His Asp Gly Ile Val Leu Ala Leu Cys Ile Gln
435 440 445

Gly Cys Lys Leu Tyr Ser Gly Ser Ala Asp Cys Thr Ile Ile Val Trp
450 455 460

Asp Ile Gln Asn Leu Gln Lys Val Asn Thr Ile Arg Ala His Asp Asn
465 470 475 480

Pro Val Cys Thr Leu Val Ser Ser His Asn Val Leu Phe Ser Gly Ser
485 490 495

Leu Lys Ala Ile Lys Val Trp Asp Ile Val Gly Thr Glu Leu Lys Leu
500 505 510

Lys Lys Glu Leu Thr Gly Leu Asn His Trp Val Arg Ala Leu Val Ala
515 520 525

Ala Gln Ser Tyr Leu Tyr Ser Gly Ser Tyr Gln Thr Ile Lys Ile Trp
530 535 540

Asp Ile Arg Thr Leu Asp Cys Ile His Val Leu Gln Thr Ser Gly Gly
545 550 555 560

Ser Val Tyr Ser Ile Ala Val Thr Asn His His Ile Val Cys Gly Thr
565 570 575

Tyr Glu Asn Leu Ile His Val Trp Asp Ile Glu Ser Lys Glu Gln Val
580 585 590

Arg Thr Leu Thr Gly His Val Gly Thr Val Tyr Ala Leu Ala Val Ile
595 600 605

Ser Thr Pro Asp Gln Thr Lys Val Phe Ser Ala Ser Tyr Asp Arg Ser
610 615 620

Leu Arg Val Trp Ser Met Asp Asn Met Ile Cys Thr Gln Thr Leu Leu

625 630 635 640
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 645 650 655
 Phe Ser Gly Ala Val Asp Ser Thr Val Lys Val Trp Thr Cys
 660 665 670

<210> 21

<211> 3169

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (73).. (1503)

<400> 21

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 agcgcggacg gg atg ttt cgt ctt aac acc ctt tct gcg ttg gca gaa cta 111

Met Phe Arg Leu Asn Thr Leu Ser Ala Leu Ala Glu Leu

1	5	10	
gct gtg ggc tct cgc tgg tac cat ggg gca tca cag ccc aca cag acc			159
Ala Val Gly Ser Arg Trp Tyr His Gly Ala Ser Gln Pro Thr Gln Thr			
15	20	25	
aaa cga aga ttg atg ctg gtg gcg ttc ctg gga gca tct gca gtg act			207
Lys Arg Arg Leu Met Leu Val Ala Phe Leu Gly Ala Ser Ala Val Thr			
30	35	40	45
gca agt acc ggt ctc ctg tgg aag aag gct cac gca gaa tct cca cca			255
Ala Ser Thr Gly Leu Leu Trp Lys Lys Ala His Ala Glu Ser Pro Pro			
50	55	60	

tgc gtt aac agc aag aag cct gac aca gaa gat aaa gag aga aac aaa	303
Cys Val Asn Ser Lys Lys Pro Asp Thr Glu Asp Lys Glu Arg Asn Lys	
65 70 75	
gac agc ggg gaa gtg tcc agc cgt gaa gga agg gct gca gat gct gcg	351
Asp Ser Gly Glu Val Ser Ser Arg Glu Gly Arg Ala Ala Asp Ala Ala	
80 85 90	
gca gag cct tat cct gag gac aag aag aag aag cgc tct gga ttc aga	399
Ala Glu Pro Tyr Pro Glu Asp Lys Lys Lys Lys Arg Ser Gly Phe Arg	
95 100 105	
gac aga aaa gtg atg gag tat gag aat cga atc cga gcc tac tcc aca	447
Asp Arg Lys Val Met Glu Tyr Glu Asn Arg Ile Arg Ala Tyr Ser Thr	
110 115 120 125	
cca gac aaa att ttc cga tat ttt gcc acc ttg aaa gta atc aac gaa	495
Pro Asp Lys Ile Phe Arg Tyr Phe Ala Thr Leu Lys Val Ile Asn Glu	
130 135 140	
cct ggt gaa acc gaa gtg ttc atg act ccg cag gac ttt gtg cgc tcc	543
Pro Gly Glu Thr Glu Val Phe Met Thr Pro Gln Asp Phe Val Arg Ser	
145 150 155	
ata acg ccc aat gag aag cag cca gaa cac ttg ggc ctg gat cag tat	591
Ile Thr Pro Asn Glu Lys Gln Pro Glu His Leu Gly Leu Asp Gln Tyr	
160 165 170	
ata ata aag cgc ttt gat gga aag aaa att gcc cag gaa cga gaa aaa	639
Ile Ile Lys Arg Phe Asp Gly Lys Lys Ile Ala Gln Glu Arg Glu Lys	
175 180 185	
ttt gct gat gaa ggc agc atc ttc tac agc ctt gga gag tgt ggg ctc	687
Phe Ala Asp Glu Gly Ser Ile Phe Tyr Ser Leu Gly Glu Cys Gly Leu	
190 195 200 205	

atc tcc ttc tct gac tac atc ttc ctc aca aca gtc ctc tcc act cct 735
 Ile Ser Phe Ser Asp Tyr Ile Phe Leu Thr Thr Val Leu Ser Thr Pro
 210 215 220
 cag aga aac ttt gaa att gct ttc aag atg ttt gac ttg aat gga gac 783
 Gln Arg Asn Phe Glu Ile Ala Phe Lys Met Phe Asp Leu Asn Gly Asp
 225 230 235
 gga gag gta gac atg gag gag ttt gag cag gtt cag agc atc att cgc 831
 Gly Glu Val Asp Met Glu Glu Phe Glu Gln Val Gln Ser Ile Ile Arg
 240 245 250
 tcc cag acc agc atg ggc atg cgt cac aga gac cgt cca acc act ggg 879
 Ser Gln Thr Ser Met Gly Met Arg His Arg Asp Arg Pro Thr Thr Gly
 255 260 265
 aac acc ctc aag tct ggc tta tgt tgc gcc ctc acg acc tac ttt ttt 927
 Asn Thr Leu Lys Ser Gly Leu Cys Ser Ala Leu Thr Thr Tyr Phe Phe
 270 275 280 285
 gga gct gat ctc aaa ggg aaa ctg acc atc aaa aac ttc ctg gaa ttt 975
 Gly Ala Asp Leu Lys Gly Lys Leu Thr Ile Lys Asn Phe Leu Glu Phe
 290 295 300
 cag cgc aaa ctt cag cat gac gtt cta aag ctg gag ttt gaa cgc cat 1023
 Gln Arg Lys Leu Gln His Asp Val Leu Lys Leu Glu Phe Glu Arg His
 305 310 315
 gac ccg gta gat ggg aga atc tct gag agg cag ttc ggg ggc atg ctg 1071
 Asp Pro Val Asp Gly Arg Ile Ser Glu Arg Gln Phe Gly Gly Met Leu
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 ctg gcc tac agt gga gtg cag tcc aag aag ctg acc gcc atg cag aga 1119
 Leu Ala Tyr Ser Gly Val Gln Ser Lys Lys Leu Thr Ala Met Gln Arg
 335 340 345

cag ctg aag aag cac ttc aaa gat ggg aag ggc ctg act ttc cag gag 1167
 Gln Leu Lys Lys His Phe Lys Asp Gly Lys Gly Leu Thr Phe Gln Glu
 350 355 360 365
 gta gag aac ttc ttc act ttc ctg aag aac att aat gac gtg gac act 1215
 Val Glu Asn Phe Phe Thr Phe Leu Lys Asn Ile Asn Asp Val Asp Thr
 370 375 380
 gca cta agc ttt tac cac atg gct gga gca tct ctt gat aaa gtg acc 1263
 Ala Leu Ser Phe Tyr His Met Ala Gly Ala Ser Leu Asp Lys Val Thr
 385 390 395
 atg cag caa gtg gcc agg aca gtg gcg aag gtc gaa ctc tcg gac cat 1311
 Met Gln Gln Val Ala Arg Thr Val Ala Lys Val Glu Leu Ser Asp His
 400 405 410
 gtg tgt gac gtg gtg ttc gcg ctc ttt gac tgt gat ggc aat ggg gag 1359
 Val Cys Asp Val Val Phe Ala Leu Phe Asp Cys Asp Gly Asn Gly Glu
 415 420 425
 ctg agc aac aag gag ttc gtt tcc atc atg aag cag cgg ctg atg aga 1407
 Leu Ser Asn Lys Glu Phe Val Ser Ile Met Lys Gln Arg Leu Met Arg
 430 435 440 445
 ggc ctg gag aag ccc aag gac atg ggc ttc acc cgc ctc atg cag gcc 1455
 Gly Leu Glu Lys Pro Lys Asp Met Gly Phe Thr Arg Leu Met Gln Ala
 450 455 460
 atg tgg aaa tgt gcc caa gaa act gcc tgg gac ttt gct ctg ccc aaa 1503
 Met Trp Lys Cys Ala Gln Glu Thr Ala Trp Asp Phe Ala Leu Pro Lys
 465 470 475
 tagtattccc acctcctgca ccttagcacc ctgcaagccc tggagtggcc cttcatgctg 1563
 ctgatgcac gccagtggtg cccacctccc catctttctg ggagtaacct ctgggctcag 1623
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ggagcggtg ggcttcctta acccgaggtt cactgttate ctaggagacc agaagaggaa 3123
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<210> 22

<211> 477

<212> PRT

<213> Mus musculus

<400> 22

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 20 25 30
 Leu Met Leu Val Ala Phe Leu Gly Ala Ser Ala Val Thr Ala Ser Thr
 35 40 45
 Gly Leu Leu Trp Lys Lys Ala His Ala Glu Ser Pro Pro Cys Val Asn
 50 55 60
 Ser Lys Lys Pro Asp Thr Glu Asp Lys Glu Arg Asn Lys Asp Ser Gly
 65 70 75 80
 Glu Val Ser Ser Arg Glu Gly Arg Ala Ala Asp Ala Ala Ala Glu Pro
 85 90 95
 Tyr Pro Glu Asp Lys Lys Lys Lys Arg Ser Gly Phe Arg Asp Arg Lys
 100 105 110
 Val Met Glu Tyr Glu Asn Arg Ile Arg Ala Tyr Ser Thr Pro Asp Lys
 115 120 125
 Ile Phe Arg Tyr Phe Ala Thr Leu Lys Val Ile Asn Glu Pro Gly Glu
 130 135 140
 Thr Glu Val Phe Met Thr Pro Gln Asp Phe Val Arg Ser Ile Thr Pro
 145 150 155 160
 Asn Glu Lys Gln Pro Glu His Leu Gly Leu Asp Gln Tyr Ile Ile Lys
 165 170 175
 Arg Phe Asp Gly Lys Lys Ile Ala Gln Glu Arg Glu Lys Phe Ala Asp

180 185 190
Glu Gly Ser Ile Phe Tyr Ser Leu Gly Glu Cys Gly Leu Ile Ser Phe
195 200 205
Ser Asp Tyr Ile Phe Leu Thr Thr Val Leu Ser Thr Pro Gln Arg Asn
210 215 220
Phe Glu Ile Ala Phe Lys Met Phe Asp Leu Asn Gly Asp Gly Glu Val
225 230 235 240
Asp Met Glu Glu Phe Glu Gln Val Gln Ser Ile Ile Arg Ser Gln Thr
245 250 255
Ser Met Gly Met Arg His Arg Asp Arg Pro Thr Thr Gly Asn Thr Leu
260 265 270
Lys Ser Gly Leu Cys Ser Ala Leu Thr Thr Tyr Phe Phe Gly Ala Asp
275 280 285
Leu Lys Gly Lys Leu Thr Ile Lys Asn Phe Leu Glu Phe Gln Arg Lys
290 295 300
Leu Gln His Asp Val Leu Lys Leu Glu Phe Glu Arg His Asp Pro Val
305 310 315 320
Asp Gly Arg Ile Ser Glu Arg Gln Phe Gly Gly Met Leu Leu Ala Tyr
325 330 335
Ser Gly Val Gln Ser Lys Lys Leu Thr Ala Met Gln Arg Gln Leu Lys
340 345 350
Lys His Phe Lys Asp Gly Lys Gly Leu Thr Phe Gln Glu Val Glu Asn
355 360 365
Phe Phe Thr Phe Leu Lys Asn Ile Asn Asp Val Asp Thr Ala Leu Ser
370 375 380
Phe Tyr His Met Ala Gly Ala Ser Leu Asp Lys Val Thr Met Gln Gln
385 390 395 400

Val Ala Arg Thr Val Ala Lys Val Glu Leu Ser Asp His Val Cys Asp

405

410

415

Val Val Phe Ala Leu Phe Asp Cys Asp Gly Asn Gly Glu Leu Ser Asn

420

425

430

Lys Glu Phe Val Ser Ile Met Lys Gln Arg Leu Met Arg Gly Leu Glu

435

440

445

Lys Pro Lys Asp Met Gly Phe Thr Arg Leu Met Gln Ala Met Trp Lys

450

455

460

Cys Ala Gln Glu Thr Ala Trp Asp Phe Ala Leu Pro Lys

465

470

475

<210> 23

<211> 2344

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (59).. (1486)

<400> 23

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atg ttt cgt ctg aac tca ctt tct gct ttg gca gaa ctg gct gtg ggt 106

Met Phe Arg Leu Asn Ser Leu Ser Ala Leu Ala Glu Leu Ala Val Gly

1

5

10

15

tct cga tgg tac cat gga gga tca cag ccc atc cag atc cgg cga aga 154

Ser Arg Trp Tyr His Gly Gly Ser Gln Pro Ile Gln Ile Arg Arg Arg

20

25

30

cta atg atg gtg gct ttc ctg gga gca tct gca gta act gca agt act 202

Leu Met Met Val Ala Phe Leu Gly Ala Ser Ala Val Thr Ala Ser Thr
 35 40 45
 ggt ctt ttg tgg aag agg gcc cat gca gaa tct cca cca tgt gta gac 250
 Gly Leu Leu Trp Lys Arg Ala His Ala Glu Ser Pro Pro Cys Val Asp
 50 55 60
 aac cta aaa agt gac atc ggt gat aaa ggg aag aat aaa gat gaa ggg 298
 Asn Leu Lys Ser Asp Ile Gly Asp Lys Gly Lys Asn Lys Asp Glu Gly
 65 70 75 80
 gat gtt tgt aac cat gag aaa aag act gca gat ctt gcc cct cac cca 346
 Asp Val Cys Asn His Glu Lys Lys Thr Ala Asp Leu Ala Pro His Pro
 85 90 95
 gaa gag aaa aag aag aaa cgt tct gga ttc aga gac aga aaa gtg atg 394
 Glu Glu Lys Lys Lys Lys Arg Ser Gly Phe Arg Asp Arg Lys Val Met
 100 105 110
 gaa tat gag aat agg att cga gcc tac tcc acg cca gac aaa atc ttc 442
 Glu Tyr Glu Asn Arg Ile Arg Ala Tyr Ser Thr Pro Asp Lys Ile Phe
 115 120 125
 cga tat ttt gcc acc ttg aaa gtc atc agt gag cct ggt gaa gca gaa 490
 Arg Tyr Phe Ala Thr Leu Lys Val Ile Ser Glu Pro Gly Glu Ala Glu
 130 135 140
 gtg ttt atg aca cca gaa gat ttt gtg cga tcc ata aca ccc aat gaa 538
 Val Phe Met Thr Pro Glu Asp Phe Val Arg Ser Ile Thr Pro Asn Glu
 145 150 155 160
 aaa caa cca gaa cac ttg ggt ctg gat caa tat ata ata aaa cgc ttt 586
 Lys Gln Pro Glu His Leu Gly Leu Asp Gln Tyr Ile Ile Lys Arg Phe
 165 170 175
 gat gga aag aaa att tcc cag gaa cga gaa aaa ttt gct gat gaa ggc 634

Asp Gly Lys Lys Ile Ser Gln Glu Arg Glu Lys Phe Ala Asp Glu Gly
 180 185 190
 agt ata ttt tac acc ctt gga gaa tgt ggg ctc ata tcc ttt tca gac 682
 Ser Ile Phe Tyr Thr Leu Gly Glu Cys Gly Leu Ile Ser Phe Ser Asp
 195 200 205
 tac att ttc ctc aca act gtt ctt tcc act cct cag aga aat ttt gaa 730
 Tyr Ile Phe Leu Thr Thr Val Leu Ser Thr Pro Gln Arg Asn Phe Glu
 210 215 220
 att gcc ttc aag atg ttt gat ttg aat gga gat gga gaa gta gat atg 778
 Ile Ala Phe Lys Met Phe Asp Leu Asn Gly Asp Gly Glu Val Asp Met
 225 230 235 240
 gaa gaa ttt gaa cag gtt cag agc atc att cgc tcc caa acc agt atg 826
 Glu Glu Phe Glu Gln Val Gln Ser Ile Ile Arg Ser Gln Thr Ser Met
 245 250 255
 ggt atg cgc cac aga gat cgt cca act act ggc aac acc ctc aag tct 874
 Gly Met Arg His Arg Asp Arg Pro Thr Thr Gly Asn Thr Leu Lys Ser
 260 265 270
 ggc ttg tgt tca gcc ctc aca acc tac ttt ttt gga gct gat ctg aag 922
 Gly Leu Cys Ser Ala Leu Thr Thr Tyr Phe Phe Gly Ala Asp Leu Lys
 275 280 285
 gga aag ctg aca atc aaa aac ttc ctc gaa ttt cag cgt aaa ctg cag 970
 Gly Lys Leu Thr Ile Lys Asn Phe Leu Glu Phe Gln Arg Lys Leu Gln
 290 295 300
 cat gat gtt ctg aag ctt gag ttt gaa cgc cat gac cct gtg gat ggg 1018
 His Asp Val Leu Lys Leu Glu Phe Glu Arg His Asp Pro Val Asp Gly
 305 310 315 320
 aga att act gag agg cag ttt ggt ggc atg cta ctt gcc tac agt ggg 1066

Arg Ile Thr Glu Arg Gln Phe Gly Gly Met Leu Leu Ala Tyr Ser Gly

325

330

335

gtg cag tcc aag aag ctg acc gcc atg cag agg cag ctc aag aag cac 1114

Val Gln Ser Lys Lys Leu Thr Ala Met Gln Arg Gln Leu Lys Lys His

340

345

350

ttc aaa gaa gga aag ggt ctg aca ttt cag gag gtg gag aac ttc ttt 1162

Phe Lys Glu Gly Lys Gly Leu Thr Phe Gln Glu Val Glu Asn Phe Phe

355

360

365

act ttc cta aag aac att aat gat gtg gac act gca ttg agt ttt tac 1210

Thr Phe Leu Lys Asn Ile Asn Asp Val Asp Thr Ala Leu Ser Phe Tyr

370

375

380

cat atg gct gga gca tct ctt gat aaa gtg acc atg cag cag gtg gcc 1258

His Met Ala Gly Ala Ser Leu Asp Lys Val Thr Met Gln Gln Val Ala

385

390

395

400

agg aca gtg gct aaa gtg gag ctc tca gac cac gtg tgt gat gtg gtg 1306

Arg Thr Val Ala Lys Val Glu Leu Ser Asp His Val Cys Asp Val Val

405

410

415

ttt gca ctc ttt gac tgt gat ggc aat ggc gaa ctg agc aat aag gaa 1354

Phe Ala Leu Phe Asp Cys Asp Gly Asn Gly Glu Leu Ser Asn Lys Glu

420

425

430

ttt gtt tcc atc atg aag caa cgg ctg atg aga ggc ctg gaa aag ccc 1402

Phe Val Ser Ile Met Lys Gln Arg Leu Met Arg Gly Leu Glu Lys Pro

435

440

445

aaa gac atg ggt ttc act cgc ctc atg cag gcc atg tgg aaa tgt gca 1450

Lys Asp Met Gly Phe Thr Arg Leu Met Gln Ala Met Trp Lys Cys Ala

450

455

460

cag gaa act gcc tgg gac ttc gct tta ccc aaa cag taacccca 1496

Gln Glu Thr Ala Trp Asp Phe Ala Leu Pro Lys Gln

465

470

475

ctgcaagagg ggacccctcc acccccagta ccttgaccc cctccgcaga gtctcggcag 1556
 agccctttgt gctgctgctt ctggaagtag tctcccttcc tcccgggatg acctcaggac 1616
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 tgtcagcctc aacagcacca ccattcaag catcctgtgg ataaagaatt cagggaacca 1796
 tccacacacc tgccaaccct gggaagcatc cagtctcaa atcgtttttg ctatggattt 1856
 atactaacia gaacattcct tgacttcctt cctgctgggt ttttaaagcc acaagtaggg 1916
 aagatatctg gcaggcagaa agaagtctgt gatgataaac aatgatgagg atgacctagg 1976
 caccctacgc tagtgtgaga agcctgcgcc ccaggaagga tctgtgttag tccctgggat 2036
 ggctccaagg cctgctctag gaaggcagca tgctcagtgg gaacacagca agattcagaa 2096
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 agtgccattt cctctccagg atgggcctct aaagctgagg cctggctcag agcctgtttg 2276
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 ccaaagtt 2344

<210> 24

<211> 476

<212> PRT

<213> Homo sapiens

<400> 24

Met Phe Arg Leu Asn Ser Leu Ser Ala Leu Ala Glu Leu Ala Val Gly

1

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10

15

Ser Arg Trp Tyr His Gly Gly Ser Gln Pro Ile Gln Ile Arg Arg Arg

20

25

30

95/617

Leu Met Met Val Ala Phe Leu Gly Ala Ser Ala Val Thr Ala Ser Thr
 35 40 45
 Gly Leu Leu Trp Lys Arg Ala His Ala Glu Ser Pro Pro Cys Val Asp
 50 55 60
 Asn Leu Lys Ser Asp Ile Gly Asp Lys Gly Lys Asn Lys Asp Glu Gly
 65 70 75 80
 Asp Val Cys Asn His Glu Lys Lys Thr Ala Asp Leu Ala Pro His Pro
 85 90 95
 Glu Glu Lys Lys Lys Lys Arg Ser Gly Phe Arg Asp Arg Lys Val Met
 100 105 110
 Glu Tyr Glu Asn Arg Ile Arg Ala Tyr Ser Thr Pro Asp Lys Ile Phe
 115 120 125
 Arg Tyr Phe Ala Thr Leu Lys Val Ile Ser Glu Pro Gly Glu Ala Glu
 130 135 140
 Val Phe Met Thr Pro Glu Asp Phe Val Arg Ser Ile Thr Pro Asn Glu
 145 150 155 160
 Lys Gln Pro Glu His Leu Gly Leu Asp Gln Tyr Ile Ile Lys Arg Phe
 165 170 175
 Asp Gly Lys Lys Ile Ser Gln Glu Arg Glu Lys Phe Ala Asp Glu Gly
 180 185 190
 Ser Ile Phe Tyr Thr Leu Gly Glu Cys Gly Leu Ile Ser Phe Ser Asp
 195 200 205
 Tyr Ile Phe Leu Thr Thr Val Leu Ser Thr Pro Gln Arg Asn Phe Glu
 210 215 220
 Ile Ala Phe Lys Met Phe Asp Leu Asn Gly Asp Gly Glu Val Asp Met
 225 230 235 240
 Glu Glu Phe Glu Gln Val Gln Ser Ile Ile Arg Ser Gln Thr Ser Met

245	250	255
Gly Met Arg His Arg Asp Arg Pro Thr Thr Gly Asn Thr Leu Lys Ser		
260	265	270
Gly Leu Cys Ser Ala Leu Thr Thr Tyr Phe Phe Gly Ala Asp Leu Lys		
275	280	285
Gly Lys Leu Thr Ile Lys Asn Phe Leu Glu Phe Gln Arg Lys Leu Gln		
290	295	300
His Asp Val Leu Lys Leu Glu Phe Glu Arg His Asp Pro Val Asp Gly		
305	310	315
Arg Ile Thr Glu Arg Gln Phe Gly Gly Met Leu Leu Ala Tyr Ser Gly		
325	330	335
Val Gln Ser Lys Lys Leu Thr Ala Met Gln Arg Gln Leu Lys Lys His		
340	345	350
Phe Lys Glu Gly Lys Gly Leu Thr Phe Gln Glu Val Glu Asn Phe Phe		
355	360	365
Thr Phe Leu Lys Asn Ile Asn Asp Val Asp Thr Ala Leu Ser Phe Tyr		
370	375	380
His Met Ala Gly Ala Ser Leu Asp Lys Val Thr Met Gln Gln Val Ala		
385	390	395
Arg Thr Val Ala Lys Val Glu Leu Ser Asp His Val Cys Asp Val Val		
405	410	415
Phe Ala Leu Phe Asp Cys Asp Gly Asn Gly Glu Leu Ser Asn Lys Glu		
420	425	430
Phe Val Ser Ile Met Lys Gln Arg Leu Met Arg Gly Leu Glu Lys Pro		
435	440	445
Lys Asp Met Gly Phe Thr Arg Leu Met Gln Ala Met Trp Lys Cys Ala		
450	455	460

Gln Glu Thr Ala Trp Asp Phe Ala Leu Pro Lys Gln

465

470

475

<210> 25

<211> 1354

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (4).. (1020)

<400> 25

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Met Leu Arg Ser Phe Leu Thr Lys Leu Glu Trp Phe Ser Thr Leu

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5

10

15

ttt cca aga att cca gtt cca gtc cag aag aac att gat cag cag att 96

Phe Pro Arg Ile Pro Val Pro Val Gln Lys Asn Ile Asp Gln Gln Ile

20

25

30

aaa act cga cct agg aaa atc aag aaa gac gga aag gaa ggc att gag 144

Lys Thr Arg Pro Arg Lys Ile Lys Lys Asp Gly Lys Glu Gly Ile Glu

35

40

45

gag ata gac aga cat gtt gag aga cgg cga tcc aga tct cca aga aga 192

Glu Ile Asp Arg His Val Glu Arg Arg Arg Ser Arg Ser Pro Arg Arg

50

55

60

tca ctg agc cca cgg agg tct cca aga aga tca aga agc aga agt cat 240

Ser Leu Ser Pro Arg Arg Ser Pro Arg Arg Ser Arg Ser Arg Ser His

65

70

75

cac cgg gag ggc cat gga tct tct agt ttt gac aga gaa tta gag aga 288

98/617

His Arg Glu Gly His Gly Ser Ser Ser Phe Asp Arg Glu Leu Glu Arg
 80 85 90 95
 gag aaa gaa cgc caa cga cta gag cgg gaa gcc aaa gag aga gag aaa 336
 Glu Lys Glu Arg Gln Arg Leu Glu Arg Glu Ala Lys Glu Arg Glu Lys
 100 105 110
 gaa agg cga aga tcc cga agc att gat cgg ggc tta gat cgc agg cga 384
 Glu Arg Arg Arg Ser Arg Ser Ile Asp Arg Gly Leu Asp Arg Arg Arg
 115 120 125
 agc cgc agt cgg gag agg cac aga agt cgc agt cgc agt cgt gat agg 432
 Ser Arg Ser Arg Glu Arg His Arg Ser Arg Ser Arg Ser Arg Asp Arg
 130 135 140
 aaa ggg gat aga aga gac agg gat cgg gaa aga gag aaa gaa aat gag 480
 Lys Gly Asp Arg Arg Asp Arg Asp Arg Glu Arg Glu Lys Glu Asn Glu
 145 150 155
 agg ggt cga aga cga gac cga gat tat gac aag gag aga ggc agt gac 528
 Arg Gly Arg Arg Arg Asp Arg Asp Tyr Asp Lys Glu Arg Gly Ser Asp
 160 165 170 175
 cga gaa agg gac aga gag aga tca aga gag cgc tcc aag gag cag aga 576
 Arg Glu Arg Asp Arg Glu Arg Ser Arg Glu Arg Ser Lys Glu Gln Arg
 180 185 190
 agt agg ggt gat gga gaa gag aag aag cac aaa gaa gac aag gag gac 624
 Ser Arg Gly Asp Gly Glu Glu Lys Lys His Lys Glu Asp Lys Glu Asp
 195 200 205
 aga cga cac aga gat gac aaa aaa gag tcc aag aaa aaa cac agc aga 672
 Arg Arg His Arg Asp Asp Lys Lys Glu Ser Lys Lys Lys His Ser Arg
 210 215 220
 agc agg agc aga gag agg aaa cac agg agc agg agc aga aac gca ggg 720

Ser Arg Ser Arg Glu Arg Lys His Arg Ser Arg Ser Arg Asn Ala Gly
 225 230 235
 aag cgg agc agg agc agg agc aag gac aag tca agc aga cat aaa aac 768
 Lys Arg Ser Arg Ser Arg Ser Lys Asp Lys Ser Ser Arg His Lys Asn
 240 245 250 255
 gaa agc aag gag aag gca aat aaa aga agc aga agt ggc agt caa gga 816
 Glu Ser Lys Glu Lys Ala Asn Lys Arg Ser Arg Ser Gly Ser Gln Gly
 260 265 270
 aga act ggc agt gtt gaa aag aga aaa cga gaa cac agc cct agc aga 864
 Arg Thr Gly Ser Val Glu Lys Arg Lys Arg Glu His Ser Pro Ser Arg
 275 280 285
 gag aag tct aga aag cgc agc agg agc caa gac cgt tcc cac aag aga 912
 Glu Lys Ser Arg Lys Arg Ser Arg Ser Gln Asp Arg Ser His Lys Arg
 290 295 300
 gag cat aat gat atc aag gac cag tca gac aga cag gat cat cag agc 960
 Glu His Asn Asp Ile Lys Asp Gln Ser Asp Arg Gln Asp His Gln Ser
 305 310 315
 agc cag agt gga gag cca gag agc caa gaa aag gaa cac aaa agc aaa 1008
 Ser Gln Ser Gly Glu Pro Glu Ser Gln Glu Lys Glu His Lys Ser Lys
 320 325 330 335
 gat gag act gtg tgaagattgt gtaaacttgg atcacattga atcctataaa 1060
 Asp Glu Thr Val
 tgttgattaa attctgcttt ttttcccccc aagttgagat tgtgcagtag ttatgcactc 1120
 tgagctcccc gtagctgtg ttttcttttg ttaggggaag tgccttttgta atcccattac 1180
 gcattgatgt tttcacctg ttgagttgac acatgatgca cagaatgttc ttgcattttt 1240
 gtttgttttt aaaatgtaca gtctgtacat acgtcctgga aaatgtttta attccttttg 1300
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<210> 26

<211> 339

<212> PRT

<213> Mus musculus

<400> 26

Met Leu Arg Ser Phe Leu Thr Lys Leu Glu Trp Phe Ser Thr Leu Phe
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 Thr Arg Pro Arg Lys Ile Lys Lys Asp Gly Lys Glu Gly Ile Glu Glu
 35 40 45
 Ile Asp Arg His Val Glu Arg Arg Arg Ser Arg Ser Pro Arg Arg Ser
 50 55 60
 Leu Ser Pro Arg Arg Ser Pro Arg Arg Ser Arg Ser Arg Ser His His
 65 70 75 80
 Arg Glu Gly His Gly Ser Ser Ser Phe Asp Arg Glu Leu Glu Arg Glu
 85 90 95
 Lys Glu Arg Gln Arg Leu Glu Arg Glu Ala Lys Glu Arg Glu Lys Glu
 100 105 110
 Arg Arg Arg Ser Arg Ser Ile Asp Arg Gly Leu Asp Arg Arg Arg Ser
 115 120 125
 Arg Ser Arg Glu Arg His Arg Ser Arg Ser Arg Ser Arg Asp Arg Lys
 130 135 140
 Gly Asp Arg Arg Asp Arg Asp Arg Glu Arg Glu Lys Glu Asn Glu Arg
 145 150 155 160
 Gly Arg Arg Arg Asp Arg Asp Tyr Asp Lys Glu Arg Gly Ser Asp Arg

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	165	170	175
Glu Arg Asp Arg Glu Arg Ser Arg	Glu Arg Ser Lys Glu Gln Arg Ser		
180	185	190	
Arg Gly Asp Gly Glu Glu Lys Lys His Lys Glu Asp Lys Glu Asp Arg			
195	200	205	
Arg His Arg Asp Asp Lys Lys Glu Ser Lys Lys Lys His Ser Arg Ser			
210	215	220	
Arg Ser Arg Glu Arg Lys His Arg Ser Arg Ser Arg Asn Ala Gly Lys			
225	230	235	240
Arg Ser Arg Ser Arg Ser Lys Asp Lys Ser Ser Arg His Lys Asn Glu			
245	250	255	
Ser Lys Glu Lys Ala Asn Lys Arg Ser Arg Ser Gly Ser Gln Gly Arg			
260	265	270	
Thr Gly Ser Val Glu Lys Arg Lys Arg Glu His Ser Pro Ser Arg Glu			
275	280	285	
Lys Ser Arg Lys Arg Ser Arg Ser Gln Asp Arg Ser His Lys Arg Glu			
290	295	300	
His Asn Asp Ile Lys Asp Gln Ser Asp Arg Gln Asp His Gln Ser Ser			
305	310	315	320
Gln Ser Gly Glu Pro Glu Ser Gln Glu Lys Glu His Lys Ser Lys Asp			
325	330	335	
Glu Thr Val			

<210> 27

<211> 1354

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (4).. (1020)

<400> 27

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      1              5              10              15
ttt cca aga att cca gtt cca gtc cag aag aac att gat cag cag att      96
Phe Pro Arg Ile Pro Val Pro Val Gln Lys Asn Ile Asp Gln Gln Ile
      20              25              30
aaa act cga cct agg aaa atc aag aaa gac gga aag gaa ggc att gag      144
Lys Thr Arg Pro Arg Lys Ile Lys Lys Asp Gly Lys Glu Gly Ile Glu
      35              40              45
gag ata gac aga cat gtt gag aga cgg cga tcc aga tct cca aga aga      192
Glu Ile Asp Arg His Val Glu Arg Arg Arg Ser Arg Ser Pro Arg Arg
      50              55              60
tca ctg agc cca cgg agg tct cca aga aga tca aga agc aga agt cat      240
Ser Leu Ser Pro Arg Arg Ser Pro Arg Arg Ser Arg Ser Arg Ser His
      65              70              75
cac cgg gag ggc cat gga tct tct agt ttt gac aga gaa tta gag aga      288
His Arg Glu Gly His Gly Ser Ser Ser Phe Asp Arg Glu Leu Glu Arg
      80              85              90              95
gag aaa gaa cgc caa cga cta gag cgg gaa gcc aaa gag aga gag aaa      336
Glu Lys Glu Arg Gln Arg Leu Glu Arg Glu Ala Lys Glu Arg Glu Lys
      100             105             110
gaa agg cga aga tcc cga agc att gat cgg ggc tta gat cgc agg cga      384
Glu Arg Arg Arg Ser Arg Ser Ile Asp Arg Gly Leu Asp Arg Arg Arg

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115	120	125	
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Ser Arg Ser Arg Glu Arg His Arg Ser Arg Ser Arg Ser Arg Asp Arg			
130	135	140	
aaa ggg gat aga aga gac agg gat cgg gaa aga gag aaa gaa aat gag	480		
Lys Gly Asp Arg Arg Asp Arg Asp Arg Glu Arg Glu Lys Glu Asn Glu			
145	150	155	
agg ggt cga aga cga gac cga gat tat gac aag gag aga ggc agt gac	528		
Arg Gly Arg Arg Arg Asp Arg Asp Tyr Asp Lys Glu Arg Gly Ser Asp			
160	165	170	175
cga gaa agg gac aga gag aga tca aga gag cgc tcc aag gag cag aga	576		
Arg Glu Arg Asp Arg Glu Arg Ser Arg Glu Arg Ser Lys Glu Gln Arg			
180	185	190	
agt agg ggt gat gga gaa gag aag aag cac aaa gaa gac aag gag gac	624		
Ser Arg Gly Asp Gly Glu Glu Lys Lys His Lys Glu Asp Lys Glu Asp			
195	200	205	
aga cga cac aga gat gac aaa aaa gag tcc aag aaa aaa cac agc aga	672		
Arg Arg His Arg Asp Asp Lys Lys Glu Ser Lys Lys Lys His Ser Arg			
210	215	220	
agc agg agc aga gag agg aaa cac agg agc agg agc aga aac gca ggg	720		
Ser Arg Ser Arg Glu Arg Lys His Arg Ser Arg Ser Arg Asn Ala Gly			
225	230	235	
aag cgg agc agg agc agg agc aag gac aag tca agc aga cat aaa aac	768		
Lys Arg Ser Arg Ser Arg Ser Lys Asp Lys Ser Ser Arg His Lys Asn			
240	245	250	255
gaa agc aag gag aag gca aat aaa aga agc aga agt ggc agt caa gga	816		
Glu Ser Lys Glu Lys Ala Asn Lys Arg Ser Arg Ser Gly Ser Gln Gly			

260	265	270	
aga act ggc agt gtt gaa aag aga aaa cga gaa cac agc cct agc aga			864
Arg Thr Gly Ser Val Glu Lys Arg Lys Arg Glu His Ser Pro Ser Arg			
275	280	285	
gag aag tct aga aag cgc agc agg agc caa gac cgt tcc cac aag aga			912
Glu Lys Ser Arg Lys Arg Ser Arg Ser Gln Asp Arg Ser His Lys Arg			
290	295	300	
gag cat aat gat agc aag gac cag tca gac aga cag gat cat cag agc			960
Glu His Asn Asp Ser Lys Asp Gln Ser Asp Arg Gln Asp His Gln Ser			
305	310	315	
agc cag agt gga gag cca gag agc caa gaa aag gaa cac aaa agc aaa			1008
Ser Gln Ser Gly Glu Pro Glu Ser Gln Glu Lys Glu His Lys Ser Lys			
320	325	330	335
gat gag act gtg tgaagattgt gtaaacttgg atcacattga atcctataaa			1060
Asp Glu Thr Val			
tgttgattaa attctgcttt ttttcccccc aagttgagat tgtgcagtag ttatgcactc			1120
tgagctcccc gtaggctgtg ttttcttttg ttagggaag tgcctttgta atcccattac			1180
gcattgatgt tttcaccctg ttgagttgac acatgatgca cagaatgttc ttgcattttt			1240
gtttgttttt aaaatgtaca gtctgtacat acgtcctgga aaatgtttta attcctttgg			1300
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<210> 28

<211> 339

<212> PRT

<213> Mus musculus

<400> 28

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Thr Arg Pro Arg Lys Ile Lys Lys Asp Gly Lys Glu Gly Ile Glu Glu
35 40 45
Ile Asp Arg His Val Glu Arg Arg Arg Ser Arg Ser Pro Arg Arg Ser
50 55 60
Leu Ser Pro Arg Arg Ser Pro Arg Arg Ser Arg Ser Arg Ser His His
65 70 75 80
Arg Glu Gly His Gly Ser Ser Ser Phe Asp Arg Glu Leu Glu Arg Glu
85 90 95
Lys Glu Arg Gln Arg Leu Glu Arg Glu Ala Lys Glu Arg Glu Lys Glu
100 105 110
Arg Arg Arg Ser Arg Ser Ile Asp Arg Gly Leu Asp Arg Arg Arg Ser
115 120 125
Arg Ser Arg Glu Arg His Arg Ser Arg Ser Arg Ser Arg Asp Arg Lys
130 135 140
Gly Asp Arg Arg Asp Arg Asp Arg Glu Arg Glu Lys Glu Asn Glu Arg
145 150 155 160
Gly Arg Arg Arg Asp Arg Asp Tyr Asp Lys Glu Arg Gly Ser Asp Arg
165 170 175
Glu Arg Asp Arg Glu Arg Ser Arg Glu Arg Ser Lys Glu Gln Arg Ser
180 185 190
Arg Gly Asp Gly Glu Glu Lys Lys His Lys Glu Asp Lys Glu Asp Arg
195 200 205
Arg His Arg Asp Asp Lys Lys Glu Ser Lys Lys Lys His Ser Arg Ser
210 215 220

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Met Ala Asn Asn Ser Pro Ala Leu Thr

1

5

ggc aac tcg cag ccg cag cac cag gcg gct gca gct gcg gct cag caa 342

Gly Asn Ser Gln Pro Gln His Gln Ala Ala Ala Ala Ala Ala Gln Gln

10

15

20

25

cag cag cag tgc ggc ggc ggc ggc gct acc aag ccg gcg gtc tcc ggc 390

Gln Gln Gln Cys Gly Gly Gly Gly Ala Thr Lys Pro Ala Val Ser Gly

30

35

40

aag cag ggc aat gtg ctc ccg ctc tgg ggc agc gag aag acc atg aac 438

Lys Gln Gly Asn Val Leu Pro Leu Trp Gly Ser Glu Lys Thr Met Asn

45

50

55

ctc aac ccc atg atc ctg acc aac atc ctg tcg tcg cct tac ttc aaa 486

Leu Asn Pro Met Ile Leu Thr Asn Ile Leu Ser Ser Pro Tyr Phe Lys

60

65

70

gta cag ctc tac gag ctc aag acc tac cac gag gtg gtg gac gag atc 534

Val Gln Leu Tyr Glu Leu Lys Thr Tyr His Glu Val Val Asp Glu Ile

75

80

85

tac ttt aag gtc acg cac gtt gaa cca tgg gag aaa gga agc agg aaa 582

Tyr Phe Lys Val Thr His Val Glu Pro Trp Glu Lys Gly Ser Arg Lys

90

95

100

105

aca gcg ggc cag aca ggg atg tgc gga ggg gtt cga ggt gtt gga aca 630

Thr Ala Gly Gln Thr Gly Met Cys Gly Gly Val Arg Gly Val Gly Thr

110

115

120

gga gga att gtt tct aca gca ttt tgc ctg tta tac aaa tta ttt acc 678

Gly Gly Ile Val Ser Thr Ala Phe Cys Leu Leu Tyr Lys Leu Phe Thr

125	130	135	
ctg aag tta act cga aag caa gtg atg ggt ctt ata aca cac aca gac			726
Leu Lys Leu Thr Arg Lys Gln Val Met Gly Leu Ile Thr His Thr Asp			
140	145	150	
tct cca tat att aga gcg ctt gga ttt atg tat ata aga tat aca cag			774
Ser Pro Tyr Ile Arg Ala Leu Gly Phe Met Tyr Ile Arg Tyr Thr Gln			
155	160	165	
ccc cct aca gat ctg tgg gac tgg ttt gaa tcc ttc ctt gat gat gaa			822
Pro Pro Thr Asp Leu Trp Asp Trp Phe Glu Ser Phe Leu Asp Asp Glu			
170	175	180	185
gag gac cta gat gtg aag gct ggt gga ggc tgt gta atg acc att gga			870
Glu Asp Leu Asp Val Lys Ala Gly Gly Gly Cys Val Met Thr Ile Gly			
190	195	200	
gaa atg cta cga tct ttt ctc aca aaa ctg gag tgg ttt tct acc ttg			918
Glu Met Leu Arg Ser Phe Leu Thr Lys Leu Glu Trp Phe Ser Thr Leu			
205	210	215	
ttt cca aga att cca gtt cca gtt caa aag aat att gat caa cag att			966
Phe Pro Arg Ile Pro Val Pro Val Gln Lys Asn Ile Asp Gln Gln Ile			
220	225	230	
aaa acc cga cct aga aaa atc aag aaa gat ggg aag gaa ggt gct gag			1014
Lys Thr Arg Pro Arg Lys Ile Lys Lys Asp Gly Lys Glu Gly Ala Glu			
235	240	245	
gaa ata gac aga cat gtt gaa cgc aga cgt tca agg tct cca agg aga			1062
Glu Ile Asp Arg His Val Glu Arg Arg Arg Ser Arg Ser Pro Arg Arg			
250	255	260	265
tct ctg agt cca cgg agg tcc cca aga agg tca aga agt aga agt cat			1110
Ser Leu Ser Pro Arg Arg Ser Pro Arg Arg Ser Arg Ser Arg Ser His			

270	275	280	
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His Arg Glu Gly His Gly Ser Ser Ser Phe Asp Arg Glu Leu Glu Arg			
285	290	295	
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Glu Lys Glu Arg Gln Arg Leu Glu Arg Glu Ala Lys Glu Arg Glu Lys			
300	305	310	
gaa cgg cga aga tcc cga agt att gac cgg ggg tta gaa cgc agg cgc			1254
Glu Arg Arg Arg Ser Arg Ser Ile Asp Arg Gly Leu Glu Arg Arg Arg			
315	320	325	
agc aga agt agg gaa agg cat aga agt cgc agt cga agt cgt gat agg			1302
Ser Arg Ser Arg Glu Arg His Arg Ser Arg Ser Arg Ser Arg Asp Arg			
330	335	340	345
aaa ggg gat aga agg gac agg gat cga gaa aga gag aaa gaa aat gag			1350
Lys Gly Asp Arg Arg Asp Arg Asp Arg Glu Arg Glu Lys Glu Asn Glu			
350	355	360	
aga ggt aga aga cga gat cgt gac tat gat aag gaa aga gga aat gaa			1398
Arg Gly Arg Arg Arg Asp Arg Asp Tyr Asp Lys Glu Arg Gly Asn Glu			
365	370	375	
cga gaa aaa gag aga gag cga tca aga gaa agg tcc aag gaa cag aga			1446
Arg Glu Lys Glu Arg Glu Arg Ser Arg Glu Arg Ser Lys Glu Gln Arg			
380	385	390	
agt agg gga gag gta gaa gag aag aaa cat aaa gaa gac aaa gat gat			1494
Ser Arg Gly Glu Val Glu Glu Lys Lys His Lys Glu Asp Lys Asp Asp			
395	400	405	
agg cgg cac aga gat gac aaa aga gat tcc aag aaa gag aaa aaa cac			1542
Arg Arg His Arg Asp Asp Lys Arg Asp Ser Lys Lys Glu Lys Lys His			

410 415 420 425
 agt aga agc aga agc aga gaa agg aaa cac aga agt agg agt cga agt 1590
 Ser Arg Ser Arg Ser Arg Glu Arg Lys His Arg Ser Arg Ser Arg Ser
 430 435 440
 aga aat gca ggg aaa cga agt aga agt aga agc aaa gag aaa tca agt 1638
 Arg Asn Ala Gly Lys Arg Ser Arg Ser Arg Ser Lys Glu Lys Ser Ser
 445 450 455
 aaa cat aaa aat gaa agt aaa gaa aaa tca aat aaa cga agt cga agt 1686
 Lys His Lys Asn Glu Ser Lys Glu Lys Ser Asn Lys Arg Ser Arg Ser
 460 465 470
 ggc agt caa gga aga act gac agt gtt gaa aaa tca aaa aaa cgg gaa 1734
 Gly Ser Gln Gly Arg Thr Asp Ser Val Glu Lys Ser Lys Lys Arg Glu
 475 480 485
 cat agt ccc agc aaa gaa aaa tct aga aag cgt agt aga agc aaa gaa 1782
 His Ser Pro Ser Lys Glu Lys Ser Arg Lys Arg Ser Arg Ser Lys Glu
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 Arg Ser His Lys Arg Asp His Ser Asp Ser Lys Asp Gln Ser Asp Lys
 510 515 520
 cat gat cgt cga agg agc caa agt ata gaa caa gag agc caa gaa aaa 1878
 His Asp Arg Arg Arg Ser Gln Ser Ile Glu Gln Glu Ser Gln Glu Lys
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 Gln His Lys Asn Lys Asp Glu Thr Val
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<211> 546

<212> PRT

<213> Homo sapiens

<400> 30

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 Leu Trp Gly Ser Glu Lys Thr Met Asn Leu Asn Pro Met Ile Leu Thr
 50 55 60
 Asn Ile Leu Ser Ser Pro Tyr Phe Lys Val Gln Leu Tyr Glu Leu Lys
 65 70 75 80
 Thr Tyr His Glu Val Val Asp Glu Ile Tyr Phe Lys Val Thr His Val
 85 90 95
 Glu Pro Trp Glu Lys Gly Ser Arg Lys Thr Ala Gly Gln Thr Gly Met
 100 105 110
 Cys Gly Gly Val Arg Gly Val Gly Thr Gly Gly Ile Val Ser Thr Ala
 115 120 125
 Phe Cys Leu Leu Tyr Lys Leu Phe Thr Leu Lys Leu Thr Arg Lys Gln
 130 135 140
 Val Met Gly Leu Ile Thr His Thr Asp Ser Pro Tyr Ile Arg Ala Leu
 145 150 155 160
 Gly Phe Met Tyr Ile Arg Tyr Thr Gln Pro Pro Thr Asp Leu Trp Asp
 165 170 175
 Trp Phe Glu Ser Phe Leu Asp Asp Glu Glu Asp Leu Asp Val Lys Ala
 180 185 190

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Gly Gly Gly Cys Val Met Thr Ile Gly Glu Met Leu Arg Ser Phe Leu
195 200 205
Thr Lys Leu Glu Trp Phe Ser Thr Leu Phe Pro Arg Ile Pro Val Pro
210 215 220
Val Gln Lys Asn Ile Asp Gln Gln Ile Lys Thr Arg Pro Arg Lys Ile
225 230 235 240
Lys Lys Asp Gly Lys Glu Gly Ala Glu Glu Ile Asp Arg His Val Glu
245 250 255
Arg Arg Arg Ser Arg Ser Pro Arg Arg Ser Leu Ser Pro Arg Arg Ser
260 265 270
Pro Arg Arg Ser Arg Ser Arg Ser His His Arg Glu Gly His Gly Ser
275 280 285
Ser Ser Phe Asp Arg Glu Leu Glu Arg Glu Lys Glu Arg Gln Arg Leu
290 295 300
Glu Arg Glu Ala Lys Glu Arg Glu Lys Glu Arg Arg Arg Ser Arg Ser
305 310 315 320
Ile Asp Arg Gly Leu Glu Arg Arg Arg Ser Arg Ser Arg Glu Arg His
325 330 335
Arg Ser Arg Ser Arg Ser Arg Asp Arg Lys Gly Asp Arg Arg Asp Arg
340 345 350
Asp Arg Glu Arg Glu Lys Glu Asn Glu Arg Gly Arg Arg Arg Asp Arg
355 360 365
Asp Tyr Asp Lys Glu Arg Gly Asn Glu Arg Glu Lys Glu Arg Glu Arg
370 375 380
Ser Arg Glu Arg Ser Lys Glu Gln Arg Ser Arg Gly Glu Val Glu Glu
385 390 395 400
Lys Lys His Lys Glu Asp Lys Asp Asp Arg Arg His Arg Asp Asp Lys

405 410 415
 Arg Asp Ser Lys Lys Glu Lys Lys His Ser Arg Ser Arg Ser Arg Glu
 420 425 430
 Arg Lys His Arg Ser Arg Ser Arg Ser Arg Asn Ala Gly Lys Arg Ser
 435 440 445
 Arg Ser Arg Ser Lys Glu Lys Ser Ser Lys His Lys Asn Glu Ser Lys
 450 455 460
 Glu Lys Ser Asn Lys Arg Ser Arg Ser Gly Ser Gln Gly Arg Thr Asp
 465 470 475 480
 Ser Val Glu Lys Ser Lys Lys Arg Glu His Ser Pro Ser Lys Glu Lys
 485 490 495
 Ser Arg Lys Arg Ser Arg Ser Lys Glu Arg Ser His Lys Arg Asp His
 500 505 510
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 515 520 525
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<210> 31

<211> 2290

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (82).. (1167)

<400> 31

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aaa aaa aaa acg gaa ctg gct cag aag gca agg aag gag att gct gac 207
Lys Lys Lys Thr Glu Leu Ala Gln Lys Ala Arg Lys Glu Ile Ala Asp
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Tyr Leu Ala Ala Gly Lys Asp Glu Arg Ala Arg Ile Arg Val Glu His
              45              50              55
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Ile Ile Arg Glu Asp Tyr Leu Val Glu Ala Met Glu Ile Leu Glu Leu
              60              65              70
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Tyr Cys Asp Leu Leu Leu Ala Arg Phe Gly Leu Ile Gln Ser Met Lys
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gag cta gat tct ggt cta gct gaa tcc gtg tct aca ctg atc tgg gct 399
Glu Leu Asp Ser Gly Leu Ala Glu Ser Val Ser Thr Leu Ile Trp Ala
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gcg cct cgg ctt cag tca gaa gtg gct gag ttg aaa ata gtt gcc gat 447
Ala Pro Arg Leu Gln Ser Glu Val Ala Glu Leu Lys Ile Val Ala Asp
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cag ctc tgt gcc aaa tac agc aag gaa tat ggc aag ttg tgc agg acc 495

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 140 145 150
 gaa gcc cca ccc aaa atc cta gtg gag aga tac ctg att gaa att gcc 591
 Glu Ala Pro Pro Lys Ile Leu Val Glu Arg Tyr Leu Ile Glu Ile Ala
 155 160 165 170
 aag aat tac aat gta ccc tac gaa cct gac tct gtg gtc atg gca gaa 639
 Lys Asn Tyr Asn Val Pro Tyr Glu Pro Asp Ser Val Val Met Ala Glu
 175 180 185
 gct cct gtt ggg gtg gag aca gat ctt att gat gtt gga ttt acg gac 687
 Ala Pro Val Gly Val Glu Thr Asp Leu Ile Asp Val Gly Phe Thr Asp
 190 195 200
 gat gtg aag aaa ggt ggt cct gga aga gga gga ggg ggc ggg ttc aca 735
 Asp Val Lys Lys Gly Gly Pro Gly Arg Gly Gly Gly Gly Gly Phe Thr
 205 210 215
 gcc ccc gtt ggg gga cct gat ggg att gtg ccc atg ccc atg cct atg 783
 Ala Pro Val Gly Gly Pro Asp Gly Ile Val Pro Met Pro Met Pro Met
 220 225 230
 ccc atg cca tct cca aat gct ccc ttc gca tac cca ctg cca aag gga 831
 Pro Met Pro Ser Pro Asn Ala Pro Phe Ala Tyr Pro Leu Pro Lys Gly
 235 240 245 250
 cca tcg gat ttc agt gga ttg cca gtg ggg act tac cag gcc ttt cct 879
 Pro Ser Asp Phe Ser Gly Leu Pro Val Gly Thr Tyr Gln Ala Phe Pro
 255 260 265
 aac att cac cca cct cag ata cca gca act ccc cca tcc tat gaa tct 927

Asn Ile His Pro Pro Gln Ile Pro Ala Thr Pro Pro Ser Tyr Glu Ser
 270 275 280
 gtt gat gac att aat ggt gat aaa act gtt tct tct gca cag att gtt 975
 Val Asp Asp Ile Asn Gly Asp Lys Thr Val Ser Ser Ala Gln Ile Val
 285 290 295
 gga ccc aag cca gaa gct cct gca aag ccc cct tcc aga cct gtg gat 1023
 Gly Pro Lys Pro Glu Ala Pro Ala Lys Pro Pro Ser Arg Pro Val Asp
 300 305 310
 aat tac aac acc ttt gta ctg cca gag ttg cca tcg gtg cca gac aca 1071
 Asn Tyr Asn Thr Phe Val Leu Pro Glu Leu Pro Ser Val Pro Asp Thr
 315 320 325 330
 ctt cca act gca tct gct gga gcc agc acc tca gca tca gaa gac ata 1119
 Leu Pro Thr Ala Ser Ala Gly Ala Ser Thr Ser Ala Ser Glu Asp Ile
 335 340 345
 gac ttt gat gat ctt tcc cgg aga ttt gag gaa ctg aaa aag aaa aca 1167
 Asp Phe Asp Asp Leu Ser Arg Arg Phe Glu Glu Leu Lys Lys Lys Thr
 350 355 360
 taggtctctt aaaccaggca gcatccacat tctggaagtt gatagtgaac agttctccgt 1227
 gtaacagtga ctctccatga aattccgttt cctctgttaa ccgtcactga gcaactctcc 1287
 tcggggctct ctgctgctct accaattgtg ttgctttcca cttcttcagt gattcttcag 1347
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 gcactgttcc acctggatcc agttgcaaag tttggaaaag ttctcttagt tttactggat 1767

tctcaggag ccctctgtgg ccttttcctt tttttgagt gctgtttcct ttttaggaaa 1827
 gaacagcact gtggaaattt gcttttcccc atagcatgtt aggaaggaag tacaggctgt 1887
 tacctaagct agcgtgggct tccagttgcc ttaatagaag tactcaagtc tcttgggtag 1947
 agatctggaa gcctgcagga gaggaggggt acttgttttc attggaaaac ttttatgatt 2007
 aagggactct ttacaaactg gcattcttaag ttttagtgcc atgtcgtgt agtctgctgc 2067
 tttcctgggt ggatgaacct ctttattatg gtaacttctg tgctgcttg cccctagcca 2127
 aggctctcct tccccaagag gttagctttg gcattggaag atgagatttt tgcttaccg 2187
 tagtatttct gtacatacct gttccagca acttcagtgt caatgttttt gatttatttg 2247
 tgtcttatag ctctagctgc taataaagat cccatgtcct gct 2290

<210> 32

<211> 362

<212> PRT

<213> Mus musculus

<400> 32

Met Leu Gly Ser Gly Phe Lys Ala Glu Arg Leu Arg Val Asn Leu Arg
 1 5 10 15
 Leu Val Ile Asn Arg Leu Lys Leu Leu Glu Lys Lys Lys Thr Glu Leu
 20 25 30
 Ala Gln Lys Ala Arg Lys Glu Ile Ala Asp Tyr Leu Ala Ala Gly Lys
 35 40 45
 Asp Glu Arg Ala Arg Ile Arg Val Glu His Ile Ile Arg Glu Asp Tyr
 50 55 60
 Leu Val Glu Ala Met Glu Ile Leu Glu Leu Tyr Cys Asp Leu Leu Leu
 65 70 75 80
 Ala Arg Phe Gly Leu Ile Gln Ser Met Lys Glu Leu Asp Ser Gly Leu
 85 90 95

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Ala Glu Ser Val Ser Thr Leu Ile Trp Ala Ala Pro Arg Leu Gln Ser
100 105 110
Glu Val Ala Glu Leu Lys Ile Val Ala Asp Gln Leu Cys Ala Lys Tyr
115 120 125
Ser Lys Glu Tyr Gly Lys Leu Cys Arg Thr Asn Gln Ile Gly Thr Val
130 135 140
Asn Asp Arg Leu Met His Lys Leu Ser Val Glu Ala Pro Pro Lys Ile
145 150 155 160
Leu Val Glu Arg Tyr Leu Ile Glu Ile Ala Lys Asn Tyr Asn Val Pro
165 170 175
Tyr Glu Pro Asp Ser Val Val Met Ala Glu Ala Pro Val Gly Val Glu
180 185 190
Thr Asp Leu Ile Asp Val Gly Phe Thr Asp Asp Val Lys Lys Gly Gly
195 200 205
Pro Gly Arg Gly Gly Gly Gly Gly Phe Thr Ala Pro Val Gly Gly Pro
210 215 220
Asp Gly Ile Val Pro Met Pro Met Pro Met Pro Met Pro Ser Pro Asn
225 230 235 240
Ala Pro Phe Ala Tyr Pro Leu Pro Lys Gly Pro Ser Asp Phe Ser Gly
245 250 255
Leu Pro Val Gly Thr Tyr Gln Ala Phe Pro Asn Ile His Pro Pro Gln
260 265 270
Ile Pro Ala Thr Pro Pro Ser Tyr Glu Ser Val Asp Asp Ile Asn Gly
275 280 285
Asp Lys Thr Val Ser Ser Ala Gln Ile Val Gly Pro Lys Pro Glu Ala
290 295 300
Pro Ala Lys Pro Pro Ser Arg Pro Val Asp Asn Tyr Asn Thr Phe Val

305 310 315 320
 Leu Pro Glu Leu Pro Ser Val Pro Asp Thr Leu Pro Thr Ala Ser Ala
 325 330 335
 Gly Ala Ser Thr Ser Ala Ser Glu Asp Ile Asp Phe Asp Asp Leu Ser
 340 345 350
 Arg Arg Phe Glu Glu Leu Lys Lys Lys Thr
 355 360

<210> 33

<211> 2366

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (76).. (1173)

<400> 33

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 gaggaacagc acagc atg ctg ggc tct gga ttt aaa gct gag cgc tta aga 111

Met Leu Gly Ser Gly Phe Lys Ala Glu Arg Leu Arg

1 5 10

gtg aat ttg aga tta gtc ata aat cgc ctt aaa cta ttg gag aaa aag 159
 Val Asn Leu Arg Leu Val Ile Asn Arg Leu Lys Leu Leu Glu Lys Lys

15 20 25

aaa acg gaa ctg gcc cag aaa gca agg aag gag att gct gac tat ctg 207
 Lys Thr Glu Leu Ala Gln Lys Ala Arg Lys Glu Ile Ala Asp Tyr Leu

30 35 40

gct gct ggg aaa gat gaa cga gct cgg atc cgt gtg gag cac att atc 255

121/617

Ala Ala Gly Lys Asp Glu Arg Ala Arg Ile Arg Val Glu His Ile Ile
 45 50 55 60
 cgg gaa gac tac ctc gtg gag gcc atg gag atc ctg gag ctg tac tgt 303
 Arg Glu Asp Tyr Leu Val Glu Ala Met Glu Ile Leu Glu Leu Tyr Cys
 65 70 75
 gac ctg ctg ctg gct cgg ttt ggc ctt atc cag tct atg aag gaa cta 351
 Asp Leu Leu Leu Ala Arg Phe Gly Leu Ile Gln Ser Met Lys Glu Leu
 80 85 90
 gat tct ggt ctg gct gaa tct gtg tct aca ttg atc tgg gct gct cct 399
 Asp Ser Gly Leu Ala Glu Ser Val Ser Thr Leu Ile Trp Ala Ala Pro
 95 100 105
 cga ctc cag tca gaa gtg gct gag ttg aaa ata gtt gct gat cag ctc 447
 Arg Leu Gln Ser Glu Val Ala Glu Leu Lys Ile Val Ala Asp Gln Leu
 110 115 120
 tgt gcc aag tat agc aag gaa tat ggc aag cta tgt agg acc aac cag 495
 Cys Ala Lys Tyr Ser Lys Glu Tyr Gly Lys Leu Cys Arg Thr Asn Gln
 125 130 135 140
 att gga act gtg aat gac agg cta atg cac aag ctg agt gtg gaa gcc 543
 Ile Gly Thr Val Asn Asp Arg Leu Met His Lys Leu Ser Val Glu Ala
 145 150 155
 cca ccc aaa atc ctg gtg gag aga tac ctg att gaa att gca aag aat 591
 Pro Pro Lys Ile Leu Val Glu Arg Tyr Leu Ile Glu Ile Ala Lys Asn
 160 165 170
 tac aac gta ccc tat gaa cct gac tct gtg gtc atg gca gaa gct cct 639
 Tyr Asn Val Pro Tyr Glu Pro Asp Ser Val Val Met Ala Glu Ala Pro
 175 180 185
 cct ggg gta gag aca gat ctt att gat gtt gga ttc aca gat gat gtg 687

Pro Gly Val Glu Thr Asp Leu Ile Asp Val Gly Phe Thr Asp Asp Val
 190 195 200

aag aaa gga ggc cct gga aga gga ggg agt ggt ggc ttc aca gca cca 735
 Lys Lys Gly Gly Pro Gly Arg Gly Gly Ser Gly Gly Phe Thr Ala Pro
 205 210 215 220

gtt ggt gga cct gat gga acg gtg cca atg ccc atg ccc atg ccc atg 783
 Val Gly Gly Pro Asp Gly Thr Val Pro Met Pro Met Pro Met Pro Met
 225 230 235

cct atg cca tct gca aat acg cct ttc tca tat cca ctg cca aag gga 831
 Pro Met Pro Ser Ala Asn Thr Pro Phe Ser Tyr Pro Leu Pro Lys Gly
 240 245 250

cca tca gat ttc aat gga ctg cca atg ggg act tat cag gcc ttt ccc 879
 Pro Ser Asp Phe Asn Gly Leu Pro Met Gly Thr Tyr Gln Ala Phe Pro
 255 260 265

aat att cat cca cct cag ata cca gca act ccc cca tcg tat gaa tct 927
 Asn Ile His Pro Pro Gln Ile Pro Ala Thr Pro Pro Ser Tyr Glu Ser
 270 275 280

gta gat gac att aat gct gat aag aat atc tct tct gca cag att gtt 975
 Val Asp Asp Ile Asn Ala Asp Lys Asn Ile Ser Ser Ala Gln Ile Val
 285 290 295 300

ggt cct gga ccc aag cca gaa gcc tct gca aag ctt cct tcc aga cct 1023
 Gly Pro Gly Pro Lys Pro Glu Ala Ser Ala Lys Leu Pro Ser Arg Pro
 305 310 315

gca gat aac tat gac aac ttt gtc cta cca gag ttg cca tct gtg cca 1071
 Ala Asp Asn Tyr Asp Asn Phe Val Leu Pro Glu Leu Pro Ser Val Pro
 320 325 330

gac aca cta cca act gca tct gct ggt gcc agc acc tca gca tct gaa 1119

Asp Thr Leu Pro Thr Ala Ser Ala Gly Ala Ser Thr Ser Ala Ser Glu

335

340

345

gac att gac ttt gat gat ctt tcc cgg agg ttt gaa gag ctg aaa aag 1167

Asp Ile Asp Phe Asp Asp Leu Ser Arg Arg Phe Glu Glu Leu Lys Lys

350

355

360

aaa aca taggtctctt aaaccaggca actttcacgt tttgggagtt gagactgagc 1223

Lys Thr

365

aatttctcct tgtaacaaag aatctccatg aaattctgtt tcattctgtta accgtcactc 1283

agcacaacac tccctctggg ctctcttctt gctcctccag attctgctgc tttccagttc 1343

tctgttgatc ctgagactaa caattggaga ctgaggccag agcaactggc tcctggcagc 1403

tgtgcttgtc cgtttcctgt cagagtgtc ccaggtttcc tcctggcccg tcccatggtc 1463

cctccacagg agtgtgagag gatgggggaa gcaactgtggg aagaccacca aagatggctg 1523

gacagtggga gagagcacgt tgtgaagcat ccagcctcg tgttgagggt ccagacttag 1583

aaacagaccc ctctgtacag ggggattgtg gtgagtgaga atcaaggcca cttgtgtgt 1643

tttctcactc tcgaatgcaa gtgggagagg gaaaatgact cgggacgcca ttgtaacggt 1703

tcctggaagc tgggccctct cattggcata tacagtactc ctgctgcag ggcactgtcc 1763

caccgggatc cagttgcaaa gtttgtcttg acagttgaag gcctcgctta gttgtactgg 1823

attctcaggg agccctctgt ggccttttgc tttgcgtgct gtttcccttg taccagaggg 1883

cggcaccgtg gaaattctgt tttccctgta gcatattgtg ttggattgca ttactggcag 1943

agaaaggaca aggtgccatt caagtcctag ggtgggcttc cagctgcctt aatagaagta 2003

ctcaagtctt ttgggtagtg agctggaaag cctacaggaa aagaggggta cctgttttca 2063

tttgaaaact ttgattcatg gaacctttaa aactaatctc agaaaaattt ttggtgcccc 2123

tgcagctgta gttgttcaact gctttcctgg atgggtggga ctcttatgtc ataacttctg 2183

ttactccttt ggcccatagc taaggtcatc cttccccaca ggggtggctt tgggattgga 2243

tgatacagct tttgcttctg tgtagtatac ctgtacatac ttgtttcagg cagcctttct 2303

ttaatgtttt cagttggttt gtattctgta gctcagtagc tgctaataaa gttaaagatc 2363

ctg

2366

<210> 34

<211> 366

<212> PRT

<213> Homo sapiens

<400> 34

Met Leu Gly Ser Gly Phe Lys Ala Glu Arg Leu Arg Val Asn Leu Arg
1 5 10 15
Leu Val Ile Asn Arg Leu Lys Leu Leu Glu Lys Lys Lys Thr Glu Leu
20 25 30
Ala Gln Lys Ala Arg Lys Glu Ile Ala Asp Tyr Leu Ala Ala Gly Lys
35 40 45
Asp Glu Arg Ala Arg Ile Arg Val Glu His Ile Ile Arg Glu Asp Tyr
50 55 60
Leu Val Glu Ala Met Glu Ile Leu Glu Leu Tyr Cys Asp Leu Leu Leu
65 70 75 80
Ala Arg Phe Gly Leu Ile Gln Ser Met Lys Glu Leu Asp Ser Gly Leu
85 90 95
Ala Glu Ser Val Ser Thr Leu Ile Trp Ala Ala Pro Arg Leu Gln Ser
100 105 110
Glu Val Ala Glu Leu Lys Ile Val Ala Asp Gln Leu Cys Ala Lys Tyr
115 120 125
Ser Lys Glu Tyr Gly Lys Leu Cys Arg Thr Asn Gln Ile Gly Thr Val
130 135 140
Asn Asp Arg Leu Met His Lys Leu Ser Val Glu Ala Pro Pro Lys Ile
145 150 155 160

125/617

Leu Val Glu Arg Tyr Leu Ile Glu Ile Ala Lys Asn Tyr Asn Val Pro
165 170 175

Tyr Glu Pro Asp Ser Val Val Met Ala Glu Ala Pro Pro Gly Val Glu
180 185 190

Thr Asp Leu Ile Asp Val Gly Phe Thr Asp Asp Val Lys Lys Gly Gly
195 200 205

Pro Gly Arg Gly Gly Ser Gly Gly Phe Thr Ala Pro Val Gly Gly Pro
210 215 220

Asp Gly Thr Val Pro Met Pro Met Pro Met Pro Met Pro Met Pro Ser
225 230 235 240

Ala Asn Thr Pro Phe Ser Tyr Pro Leu Pro Lys Gly Pro Ser Asp Phe
245 250 255

Asn Gly Leu Pro Met Gly Thr Tyr Gln Ala Phe Pro Asn Ile His Pro
260 265 270

Pro Gln Ile Pro Ala Thr Pro Pro Ser Tyr Glu Ser Val Asp Asp Ile
275 280 285

Asn Ala Asp Lys Asn Ile Ser Ser Ala Gln Ile Val Gly Pro Gly Pro
290 295 300

Lys Pro Glu Ala Ser Ala Lys Leu Pro Ser Arg Pro Ala Asp Asn Tyr
305 310 315 320

Asp Asn Phe Val Leu Pro Glu Leu Pro Ser Val Pro Asp Thr Leu Pro
325 330 335

Thr Ala Ser Ala Gly Ala Ser Thr Ser Ala Ser Glu Asp Ile Asp Phe
340 345 350

Asp Asp Leu Ser Arg Arg Phe Glu Glu Leu Lys Lys Lys Thr
355 360 365

<210> 35

<211> 2349

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (63).. (1142)

<400> 35

gaaccctgaa gtcggtgtct gctgcgttca cggcaggatt cggttaggag gaacagcaca 60
gc atg ctg ggc tct gga ttt aaa gct gag cgc tta aga gtg aat ttg 107
Met Leu Gly Ser Gly Phe Lys Ala Glu Arg Leu Arg Val Asn Leu
1 5 10 15
aga tta gtc ata aat cgc ctt aaa cta ttg gag aaa aag aaa acg gaa 155
Arg Leu Val Ile Asn Arg Leu Lys Leu Leu Glu Lys Lys Lys Thr Glu
20 25 30
ctg gcc cag aaa gca agg aag gag att gct gac tat ctg gct gct ggg 203
Leu Ala Gln Lys Ala Arg Lys Glu Ile Ala Asp Tyr Leu Ala Ala Gly
35 40 45
aaa gat gaa cga gct cgg atc cgt gtg gag cac att atc cgg gaa gac 251
Lys Asp Glu Arg Ala Arg Ile Arg Val Glu His Ile Ile Arg Glu Asp
50 55 60
tac ctc gtg gag gcc atg gag atc ctg gag ctg tac tgt gac ctg ctg 299
Tyr Leu Val Glu Ala Met Glu Ile Leu Glu Leu Tyr Cys Asp Leu Leu
65 70 75
ctg gct cgg ttt ggc ctt atc cag tct atg aag gaa cta gat tct ggt 347
Leu Ala Arg Phe Gly Leu Ile Gln Ser Met Lys Glu Leu Asp Ser Gly
80 85 90 95

ctg gct gaa tct gtg tct aca ttg atc tgg gct gct cct cga ctc cag 395
 Leu Ala Glu Ser Val Ser Thr Leu Ile Trp Ala Ala Pro Arg Leu Gln
 100 105 110
 tca gaa gtg gct gag ttg aaa ata gtt gct gat cag ctc tgt gcc aag 443
 Ser Glu Val Ala Glu Leu Lys Ile Val Ala Asp Gln Leu Cys Ala Lys
 115 120 125
 tat agc aag gaa tat ggc aag cta tgt agg acc aac cag att gga act 491
 Tyr Ser Lys Glu Tyr Gly Lys Leu Cys Arg Thr Asn Gln Ile Gly Thr
 130 135 140
 gtg aat gac agg cta atg cac aag ctg agt gtg gaa gcc cca ccc aaa 539
 Val Asn Asp Arg Leu Met His Lys Leu Ser Val Glu Ala Pro Pro Lys
 145 150 155
 atc ctg gtg gag aga tac ctg att gaa att gca aag aat tac aac gta 587
 Ile Leu Val Glu Arg Tyr Leu Ile Glu Ile Ala Lys Asn Tyr Asn Val
 160 165 170 175
 ccc tat gaa cct gac tct gtg gtc atg gca gaa gct cct cct ggg gta 635
 Pro Tyr Glu Pro Asp Ser Val Val Met Ala Glu Ala Pro Pro Gly Val
 180 185 190
 gag aca gat ctt att gat gtt gga ttc aca gat gat gtg aag aaa gga 683
 Glu Thr Asp Leu Ile Asp Val Gly Phe Thr Asp Asp Val Lys Lys Gly
 195 200 205
 ggc cct gga aga gga ggg agt ggt ggc ttc aca gca cca gtt ggt gga 731
 Gly Pro Gly Arg Gly Gly Ser Gly Gly Phe Thr Ala Pro Val Gly Gly
 210 215 220
 cct gat gga acg gtg cca atg ccc atg ccc atg ccc atg cct atg cca 779
 Pro Asp Gly Thr Val Pro Met Pro Met Pro Met Pro Met Pro Met Pro
 225 230 235

tct gca aat acg cct ttc tca tat cca ctg cca aag gga cca tca gat 827
 Ser Ala Asn Thr Pro Phe Ser Tyr Pro Leu Pro Lys Gly Pro Ser Asp
 240 245 250 255
 ttc aat gga ctg cca atg ggg act tat cag gcc ttt ccc aat att cat 875
 Phe Asn Gly Leu Pro Met Gly Thr Tyr Gln Ala Phe Pro Asn Ile His
 260 265 270
 cca cct cag ata cca gca act ccc cca tcg tat gaa tct atg aca tta 923
 Pro Pro Gln Ile Pro Ala Thr Pro Pro Ser Tyr Glu Ser Met Thr Leu
 275 280 285
 atg ctg ata aga ata tct ctt ctg cac aga ttg ttg gtc ctg gac cca 971
 Met Leu Ile Arg Ile Ser Leu Leu His Arg Leu Leu Val Leu Asp Pro
 290 295 300
 agc cag aag cct ctg caa agc ttc ctt cca gac ctg cag ata act atg 1019
 Ser Gln Lys Pro Leu Gln Ser Phe Leu Pro Asp Leu Gln Ile Thr Met
 305 310 315
 aca act ttg tcc tac cag agt tgc cat ctg tgc cag aca cac tac caa 1067
 Thr Thr Leu Ser Tyr Gln Ser Cys His Leu Cys Gln Thr His Tyr Gln
 320 325 330 335
 ctg cat ctg ctg gtg cca gca cct cag cat ctg aag aca ttg act ttg 1115
 Leu His Leu Leu Val Pro Ala Pro Gln His Leu Lys Thr Leu Thr Leu
 340 345 350
 atg atc ttt ccc gga ggt ttg aag agc tgaaaaagaa aacataggtc 1162
 Met Ile Phe Pro Gly Gly Leu Lys Ser
 355 360
 tcttaaacca ggcaactttc acgttttggg agttgagact gagcaatttc tccttgtaac 1222
 aaagaatctc catgaaattc tgtttcatct gttaaccgtc actcagcaca acactccctc 1282
 tgggctctct tcctgctcct ccagattctg ctgctttcca gttctctgtt gatcctgaga 1342

ctaacaattg gagactgagg ccagagcaac tggctcctgg cagctgtgct tgtccgtttc 1402
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 ctgttttccc tgtagcatat tgtgttgat tgcattactg gcagagaaag gacaaggtgc 1942
 cattcaagtc ctaggggtggg cttccagctg ccttaataga agtactcaag tcttttgggt 2002
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 tctgtgtagt atacctgtac atacttgttt caggcagcct ttctttaatg ttttcagttg 2302
 gtttgtattc tgtagctcag tagctgctaa taaagttaaa gatcctg 2349

<210> 36

<211> 360

<212> PRT

<213> Homo sapiens

<400> 36

Met Leu Gly Ser Gly Phe Lys Ala Glu Arg Leu Arg Val Asn Leu Arg

1

5

10

15

Leu Val Ile Asn Arg Leu Lys Leu Leu Glu Lys Lys Lys Thr Glu Leu

20

25

30

Ala Gln Lys Ala Arg Lys Glu Ile Ala Asp Tyr Leu Ala Ala Gly Lys
 35 40 45
 Asp Glu Arg Ala Arg Ile Arg Val Glu His Ile Ile Arg Glu Asp Tyr
 50 55 60
 Leu Val Glu Ala Met Glu Ile Leu Glu Leu Tyr Cys Asp Leu Leu Leu
 65 70 75 80
 Ala Arg Phe Gly Leu Ile Gln Ser Met Lys Glu Leu Asp Ser Gly Leu
 85 90 95
 Ala Glu Ser Val Ser Thr Leu Ile Trp Ala Ala Pro Arg Leu Gln Ser
 100 105 110
 Glu Val Ala Glu Leu Lys Ile Val Ala Asp Gln Leu Cys Ala Lys Tyr
 115 120 125
 Ser Lys Glu Tyr Gly Lys Leu Cys Arg Thr Asn Gln Ile Gly Thr Val
 130 135 140
 Asn Asp Arg Leu Met His Lys Leu Ser Val Glu Ala Pro Pro Lys Ile
 145 150 155 160
 Leu Val Glu Arg Tyr Leu Ile Glu Ile Ala Lys Asn Tyr Asn Val Pro
 165 170 175
 Tyr Glu Pro Asp Ser Val Val Met Ala Glu Ala Pro Pro Gly Val Glu
 180 185 190
 Thr Asp Leu Ile Asp Val Gly Phe Thr Asp Asp Val Lys Lys Gly Gly
 195 200 205
 Pro Gly Arg Gly Gly Ser Gly Gly Phe Thr Ala Pro Val Gly Gly Pro
 210 215 220
 Asp Gly Thr Val Pro Met Pro Met Pro Met Pro Met Pro Met Pro Ser
 225 230 235 240
 Ala Asn Thr Pro Phe Ser Tyr Pro Leu Pro Lys Gly Pro Ser Asp Phe

245 250 255
 Asn Gly Leu Pro Met Gly Thr Tyr Gln Ala Phe Pro Asn Ile His Pro
 260 265 270
 Pro Gln Ile Pro Ala Thr Pro Pro Ser Tyr Glu Ser Met Thr Leu Met
 275 280 285
 Leu Ile Arg Ile Ser Leu Leu His Arg Leu Leu Val Leu Asp Pro Ser
 290 295 300
 Gln Lys Pro Leu Gln Ser Phe Leu Pro Asp Leu Gln Ile Thr Met Thr
 305 310 315 320
 Thr Leu Ser Tyr Gln Ser Cys His Leu Cys Gln Thr His Tyr Gln Leu
 325 330 335
 His Leu Leu Val Pro Ala Pro Gln His Leu Lys Thr Leu Thr Leu Met
 340 345 350
 Ile Phe Pro Gly Gly Leu Lys Ser
 355 360

<210> 37

<211> 1188

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (124).. (720)

<400> 37

ctcgaaaccc gctacaaccg ccaccctccg cgcgcccaag cgaccacaaa ctgcggggtc 60
 cagccctgt cccgcgtgtt acctgccct cccctcctc ccgcccgtg aactcgagag 120
 atc atg tcg aac atg gag aaa cac tta ttt aac ttg aag ttt gct gca 168

Met Ser Asn Met Glu Lys His Leu Phe Asn Leu Lys Phe Ala Ala
1 5 10 15
aaa gaa ctt aat agg aat gcc aag aag tgt gat aaa gaa gaa aaa gct 216
Lys Glu Leu Asn Arg Asn Ala Lys Lys Cys Asp Lys Glu Glu Lys Ala
20 25 30
gaa aag gcc aag ata aaa aag gcc att cag aag ggc aat aca gaa gtt 264
Glu Lys Ala Lys Ile Lys Lys Ala Ile Gln Lys Gly Asn Thr Glu Val
35 40 45
gca aga ata cat gct gaa aat gca atc cgt cag aaa aac caa gca atc 312
Ala Arg Ile His Ala Glu Asn Ala Ile Arg Gln Lys Asn Gln Ala Ile
50 55 60
aat ttc ttg aga atg agt gct agg gtt gat gct gtg gca gcc aga gtt 360
Asn Phe Leu Arg Met Ser Ala Arg Val Asp Ala Val Ala Ala Arg Val
65 70 75
caa act gca gta aca atg ggc aag gtg aca aaa tcc atg gca ggt gta 408
Gln Thr Ala Val Thr Met Gly Lys Val Thr Lys Ser Met Ala Gly Val
80 85 90 95
gtt aaa tct atg gat gct aca ttg agg agt atg aac ctt gag aag att 456
Val Lys Ser Met Asp Ala Thr Leu Arg Ser Met Asn Leu Glu Lys Ile
100 105 110
tct gcc tta atg gac aaa ttt gaa cat cag ttt gaa aca ttg gat gtt 504
Ser Ala Leu Met Asp Lys Phe Glu His Gln Phe Glu Thr Leu Asp Val
115 120 125
cag aca cag caa atg gaa gat aca atg agt agc act act acc ctt acg 552
Gln Thr Gln Gln Met Glu Asp Thr Met Ser Ser Thr Thr Thr Leu Thr
130 135 140
aca cca cag aac caa gtg gat atg ctg ctc cag gaa atg gca gat gaa 600

Thr Pro Gln Asn Gln Val Asp Met Leu Leu Gln Glu Met Ala Asp Glu

145

150

155

gct ggc ctc gat ctc aat atg gaa cta cca cag ggt cag aca ggg tct 648

Ala Gly Leu Asp Leu Asn Met Glu Leu Pro Gln Gly Gln Thr Gly Ser

160

165

170

175

gtt ggt gca agt gtt gct tct aca gag cag gat gaa ctg tca cag agg 696

Val Gly Ala Ser Val Ala Ser Thr Glu Gln Asp Glu Leu Ser Gln Arg

180

185

190

ctt gct cgt ctt cgt gat caa gtg taacttaaata aactggtgct tctgttcctc 750

Leu Ala Arg Leu Arg Asp Gln Val

195

cacatatttc tgagccatca ttgtgtgtg tgtctataga taaggtgtat tccagttaca 810

aaaacatcat acatgacagg atgtttggac atcatttcta taagatgctt tcttttgctt 870

tgtgtatttc acagtgcatt gcgaaattcc aaggaatttc cacattggca gattttatag 930

ttctatatat tgtgtgtaaa agtgtgaggg acatattttt ctagatgtct ttggcaaagc 990

tagcattagt tttctgtata ttatacatct tccgcaaata ttagagcaaa catctagcac 1050

caaagtaatg ctaagtaaag taattttgtc agaataatgt ataaaggctt tgtttttact 1110

tattgaaagt aactttcaat tattgtctgt gatgaatttt gattttgtaa aaataaaaaac 1170

aggaaagcat gttcattt 1188

<210> 38

<211> 199

<212> PRT

<213> Mus musculus

<400> 38

Met Ser Asn Met Glu Lys His Leu Phe Asn Leu Lys Phe Ala Ala Lys

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Lys Ala Lys Ile Lys Lys Ala Ile Gln Lys Gly Asn Thr Glu Val Ala
35 40 45
Arg Ile His Ala Glu Asn Ala Ile Arg Gln Lys Asn Gln Ala Ile Asn
50 55 60
Phe Leu Arg Met Ser Ala Arg Val Asp Ala Val Ala Ala Arg Val Gln
65 70 75 80
Thr Ala Val Thr Met Gly Lys Val Thr Lys Ser Met Ala Gly Val Val
85 90 95
Lys Ser Met Asp Ala Thr Leu Arg Ser Met Asn Leu Glu Lys Ile Ser
100 105 110
Ala Leu Met Asp Lys Phe Glu His Gln Phe Glu Thr Leu Asp Val Gln
115 120 125
Thr Gln Gln Met Glu Asp Thr Met Ser Ser Thr Thr Thr Leu Thr Thr
130 135 140
Pro Gln Asn Gln Val Asp Met Leu Leu Gln Glu Met Ala Asp Glu Ala
145 150 155 160
Gly Leu Asp Leu Asn Met Glu Leu Pro Gln Gly Gln Thr Gly Ser Val
165 170 175
Gly Ala Ser Val Ala Ser Thr Glu Gln Asp Glu Leu Ser Gln Arg Leu
180 185 190
Ala Arg Leu Arg Asp Gln Val
195

<210> 39

<211> 1253

135/617

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (64).. (660)

<400> 39

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act atg tct aac atg gag aaa cac ctg ttc aac ctg aag ttc gcg gcc 108
    Met Ser Asn Met Glu Lys His Leu Phe Asn Leu Lys Phe Ala Ala
        1             5             10             15
aaa gaa ctg agt agg agt gcc aaa aaa tgc gat aag gag gaa aag gcc 156
Lys Glu Leu Ser Arg Ser Ala Lys Lys Cys Asp Lys Glu Glu Lys Ala
        20             25             30
gaa aag gcc aaa att aaa aag gcc att cag aag ggc aac atg gaa gtt 204
Glu Lys Ala Lys Ile Lys Lys Ala Ile Gln Lys Gly Asn Met Glu Val
        35             40             45
gcg agg ata cac gcc gaa aat gcc atc cgc cag aag aac cag gcg gtg 252
Ala Arg Ile His Ala Glu Asn Ala Ile Arg Gln Lys Asn Gln Ala Val
        50             55             60
aat ttc ttg aga atg agt gcg cga gtc gat gca gtg gct gcc agg gtc 300
Asn Phe Leu Arg Met Ser Ala Arg Val Asp Ala Val Ala Ala Arg Val
        65             70             75
cag acg gcg gtg acg atg ggc aag gtg acc aag tcg atg gct ggt gtg 348
Gln Thr Ala Val Thr Met Gly Lys Val Thr Lys Ser Met Ala Gly Val
        80             85             90             95
gtt aag tcg atg gat gcg aca ttg aag acc atg aat ctg gag aag att 396
Val Lys Ser Met Asp Ala Thr Leu Lys Thr Met Asn Leu Glu Lys Ile

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100	105	110	
tct gct ttg atg gac aaa ttc gag cac cag ttt gag act ctg gac gtc			444
Ser Ala Leu Met Asp Lys Phe Glu His Gln Phe Glu Thr Leu Asp Val			
115	120	125	
cag acg cag caa atg gaa gac acg atg agc agc acg acg acg ctc acc			492
Gln Thr Gln Gln Met Glu Asp Thr Met Ser Ser Thr Thr Thr Leu Thr			
130	135	140	
act ccc cag aac caa gtg gat atg ctg ctc cag gaa atg gca gat gag			540
Thr Pro Gln Asn Gln Val Asp Met Leu Leu Gln Glu Met Ala Asp Glu			
145	150	155	
gcg ggc ctc gac ctc aac atg gag ctg ccg cag ggc cag acc ggc tcc			588
Ala Gly Leu Asp Leu Asn Met Glu Leu Pro Gln Gly Gln Thr Gly Ser			
160	165	170	175
gtg ggc acg agc gtg gct tcg gcg gag cag gat gaa ctg tct cag aga			636
Val Gly Thr Ser Val Ala Ser Ala Glu Gln Asp Glu Leu Ser Gln Arg			
180	185	190	
ctg gcc cgc ctt cgg gat caa gtg tgacggcaga acccgctctg aggtttcctg			690
Leu Ala Arg Leu Arg Asp Gln Val			
195			
gccatagcca ccctttgaaa tgctctctgt gtgtagaga gatactatac cctagaaact			750
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aaattaagaa attcagtatt tctgcactct tagctggatt ctaaagtict gtatagctcg			870
taatgatggt atttttatag cagcctttta acagaactag ttaatttcgt gtatatgaat			930
ctttctcgaa gatctggtca aaactgtatt cagtttctg cccagaatga tcagattgaa			990
ggtggttggt ttttattatt atttagtgtg attgatagta tctagaatgg caggtggtgc			1050
ataaaaagta aagagagggg aaagattact tagtttggtt atacagttat aaacaccatg			1110
cagtgtattc ggtggactgt gctatttctg tttatccttt gggttttggt ttttgttttt			1170

137/617

tttttttgcc ttacacagtga gactgcaaatt gattgttctc ataacgtata ttattaataa 1230
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<210> 40

<211> 199

<212> PRT

<213> Homo sapiens

<400> 40

Met Ser Asn Met Glu Lys His Leu Phe Asn Leu Lys Phe Ala Ala Lys

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Glu Leu Ser Arg Ser Ala Lys Lys Cys Asp Lys Glu Glu Lys Ala Glu

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Lys Ala Lys Ile Lys Lys Ala Ile Gln Lys Gly Asn Met Glu Val Ala

35 40 45

Arg Ile His Ala Glu Asn Ala Ile Arg Gln Lys Asn Gln Ala Val Asn

50 55 60

Phe Leu Arg Met Ser Ala Arg Val Asp Ala Val Ala Ala Arg Val Gln

65 70 75 80

Thr Ala Val Thr Met Gly Lys Val Thr Lys Ser Met Ala Gly Val Val

85 90 95

Lys Ser Met Asp Ala Thr Leu Lys Thr Met Asn Leu Glu Lys Ile Ser

100 105 110

Ala Leu Met Asp Lys Phe Glu His Gln Phe Glu Thr Leu Asp Val Gln

115 120 125

Thr Gln Gln Met Glu Asp Thr Met Ser Ser Thr Thr Thr Leu Thr Thr

130 135 140

Pro Gln Asn Gln Val Asp Met Leu Leu Gln Glu Met Ala Asp Glu Ala

138/617

145 150 155 160
 Gly Leu Asp Leu Asn Met Glu Leu Pro Gln Gly Gln Thr Gly Ser Val
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 Gly Thr Ser Val Ala Ser Ala Glu Gln Asp Glu Leu Ser Gln Arg Leu
 180 185 190
 Ala Arg Leu Arg Asp Gln Val
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<210> 41

<211> 2774

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (92).. (2098)

<400> 41

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 Met Lys Ile Phe Val Gly Asn

1

5

gtc gat ggg gcg gat acg aca ccg gag gag ttg gca gct ctc ttc gcg 160
 Val Asp Gly Ala Asp Thr Thr Pro Glu Glu Leu Ala Ala Leu Phe Ala

10

15

20

ccc tat ggc acg gtc atg agc tgc gcc gtc atg aaa cag ttt gcc ttc 208
 Pro Tyr Gly Thr Val Met Ser Cys Ala Val Met Lys Gln Phe Ala Phe

25

30

35

gtg cac atg cgc gag aac gct ggc gcg gtg cgc gcc atc gag gcc ctg 256

139/617

Val His Met Arg Glu Asn Ala Gly Ala Val Arg Ala Ile Glu Ala Leu
 40 45 50 55
 cat ggc cac gag ctg cgt cca ggt cgc gcg ctc gtg gtg gag atg tcg 304
 His Gly His Glu Leu Arg Pro Gly Arg Ala Leu Val Val Glu Met Ser
 60 65 70
 cgc ccg agg ccc ctg aac act tgg aag att ttc gtg ggc aat gta tcg 352
 Arg Pro Arg Pro Leu Asn Thr Trp Lys Ile Phe Val Gly Asn Val Ser
 75 80 85
 gct gca tgt aca agt cag gaa ttg cgc agc ctc ttc gag cgc cgt gga 400
 Ala Ala Cys Thr Ser Gln Glu Leu Arg Ser Leu Phe Glu Arg Arg Gly
 90 95 100
 cgc gtc atc gag tgt gac gtg gta aaa gac tac gcg ttt gtt cac atg 448
 Arg Val Ile Glu Cys Asp Val Val Lys Asp Tyr Ala Phe Val His Met
 105 110 115
 gag aag gaa gca gat gcc aaa gcc gcc atc gcg cag ctc aac ggc aaa 496
 Glu Lys Glu Ala Asp Ala Lys Ala Ala Ile Ala Gln Leu Asn Gly Lys
 120 125 130 135
 gaa gtg aag ggc aag cgc atc aac gtg gaa ctc tca acc aag ggg cag 544
 Glu Val Lys Gly Lys Arg Ile Asn Val Glu Leu Ser Thr Lys Gly Gln
 140 145 150
 aag aag ggg cct gcc ctg gct atc cag tct ggg gac aag acc aag aaa 592
 Lys Lys Gly Pro Ala Leu Ala Ile Gln Ser Gly Asp Lys Thr Lys Lys
 155 160 165
 cca ggg gct ggg gac aca gca ttc cct gga act ggt ggc ttc tct gcc 640
 Pro Gly Ala Gly Asp Thr Ala Phe Pro Gly Thr Gly Gly Phe Ser Ala
 170 175 180
 acc ttc gac tac cag cag gct ttt ggc aac agc act ggt ggc ttt gat 688

Thr Phe Asp Tyr Gln Gln Ala Phe Gly Asn Ser Thr Gly Gly Phe Asp
 185 190 195
 ggg caa gcc cgt cag ccc aca cca cca ttc ttt ggt cgc gac cgc agc 736
 Gly Gln Ala Arg Gln Pro Thr Pro Pro Phe Phe Gly Arg Asp Arg Ser
 200 205 210 215
 ccc ctg cgc cgt tca cct cct cga gcc tct tat gtg gcg cct ctg acg 784
 Pro Leu Arg Arg Ser Pro Pro Arg Ala Ser Tyr Val Ala Pro Leu Thr
 220 225 230
 gcc cag cca gcc acc tac cgg gcc caa ccc tca gtg tct ctg gga gct 832
 Ala Gln Pro Ala Thr Tyr Arg Ala Gln Pro Ser Val Ser Leu Gly Ala
 235 240 245
 gca tat agg gcc cag cct tcc gcc tct ttg ggt gtt ggc tat cgg act 880
 Ala Tyr Arg Ala Gln Pro Ser Ala Ser Leu Gly Val Gly Tyr Arg Thr
 250 255 260
 cag ccc atg gca gct cag gca gct tct tac cgt gct cag ccc tct gtc 928
 Gln Pro Met Ala Ala Gln Ala Ala Ser Tyr Arg Ala Gln Pro Ser Val
 265 270 275
 tcc ctt ggg gcc cca tac agg ggt cag ctg gct agc cct agt tcc cag 976
 Ser Leu Gly Ala Pro Tyr Arg Gly Gln Leu Ala Ser Pro Ser Ser Gln
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 tct gct gca gct tcc tcg ctt ggc cca tat ggt gga gtc cag ccc tca 1024
 Ser Ala Ala Ala Ser Ser Leu Gly Pro Tyr Gly Gly Val Gln Pro Ser
 300 305 310
 gcc tca gcc ctt tcc act tat ggg ggt cag gca gct gca gct tct tcg 1072
 Ala Ser Ala Leu Ser Thr Tyr Gly Gly Gln Ala Ala Ala Ala Ser Ser
 315 320 325
 ctt aat tcc tat ggg gct cag ggc tcc tcc ctt gct tcc tat ggt aac 1120

Leu Asn Ser Tyr Gly Ala Gln Gly Ser Ser Leu Ala Ser Tyr Gly Asn
 330 335 340
 cag cca tcc tct tat ggc gcc cag gct gcc tct tcg tat ggg gct cgt 1168
 Gln Pro Ser Ser Tyr Gly Ala Gln Ala Ala Ser Ser Tyr Gly Ala Arg
 345 350 355
 gcg gct gct tct tcc tat aac aca caa gga gca gct tct tcc cta ggt 1216
 Ala Ala Ala Ser Ser Tyr Asn Thr Gln Gly Ala Ala Ser Ser Leu Gly
 360 365 370 375
 tcc tat ggg gct caa gca gcc tcc tat ggt gcc cag tct gca gcc tcc 1264
 Ser Tyr Gly Ala Gln Ala Ala Ser Tyr Gly Ala Gln Ser Ala Ala Ser
 380 385 390
 tca cta gct tat gga gcc cag gca gcg tct tac agt gcc cag ccc tca 1312
 Ser Leu Ala Tyr Gly Ala Gln Ala Ala Ser Tyr Ser Ala Gln Pro Ser
 395 400 405
 gcc tct tac agt gcc cag tct gcc cca tat gct gca caa cag gct gct 1360
 Ala Ser Tyr Ser Ala Gln Ser Ala Pro Tyr Ala Ala Gln Gln Ala Ala
 410 415 420
 tct tat tct tcc cag cct gct gct tat gtg gca caa cca gcc aca gct 1408
 Ser Tyr Ser Ser Gln Pro Ala Ala Tyr Val Ala Gln Pro Ala Thr Ala
 425 430 435
 gct gcc tat gct agc cag cca gct gcc tat gct gca caa gcc act acc 1456
 Ala Ala Tyr Ala Ser Gln Pro Ala Ala Tyr Ala Ala Gln Ala Thr Thr
 440 445 450 455
 cca atg gct ggt tcc tat ggg gct caa cca gtt gtt cag acc cag ctg 1504
 Pro Met Ala Gly Ser Tyr Gly Ala Gln Pro Val Val Gln Thr Gln Leu
 460 465 470
 aat agc tat ggg gct caa gca tct att ggc ctg tca gcc tca tat gga 1552

Asn Ser Tyr Gly Ala Gln Ala Ser Ile Gly Leu Ser Gly Ser Tyr Gly
 475 480 485
 gct cag tct gct gct gcg gcc act ggc tcc tat ggg gcg gca gct gct 1600
 Ala Gln Ser Ala Ala Ala Ala Thr Gly Ser Tyr Gly Ala Ala Ala Ala
 490 495 500
 tac ggg gct cag cct tct gcc acc ctg gca gct cct tac cgc act cag 1648
 Tyr Gly Ala Gln Pro Ser Ala Thr Leu Ala Ala Pro Tyr Arg Thr Gln
 505 510 515
 tca tca gcc tca ttg gct gct tcc tat gct gcc cag cag cat ccc cag 1696
 Ser Ser Ala Ser Leu Ala Ala Ser Tyr Ala Ala Gln Gln His Pro Gln
 520 525 530 535
 gct gct gcc tcc tac cgt ggc cag ccg ggc agt gcc tac gat ggg aca 1744
 Ala Ala Ala Ser Tyr Arg Gly Gln Pro Gly Ser Ala Tyr Asp Gly Thr
 540 545 550
 ggc cag cca tca gca gcc tac ctg tct atg tcc cag ggg gcc gtt gcc 1792
 Gly Gln Pro Ser Ala Ala Tyr Leu Ser Met Ser Gln Gly Ala Val Ala
 555 560 565
 aac gcc aac agc acc ccg ccg ccc tat gag cgt acc cgc ctc tcc cca 1840
 Asn Ala Asn Ser Thr Pro Pro Pro Tyr Glu Arg Thr Arg Leu Ser Pro
 570 575 580
 ccc cgg gcc agc tac gac gat ccc tac aaa aag gct gtc gcc atg tca 1888
 Pro Arg Ala Ser Tyr Asp Asp Pro Tyr Lys Lys Ala Val Ala Met Ser
 585 590 595
 aaa agg tat ggt tcc gac cgg cgt tta gcc gag ctc tct gat tac cgc 1936
 Lys Arg Tyr Gly Ser Asp Arg Arg Leu Ala Glu Leu Ser Asp Tyr Arg
 600 605 610 615
 cgt tta tca gag tcg cag ctt tcg ttc cgc cgc tcg ccg aca aag tcc 1984

Arg Leu Ser Glu Ser Gln Leu Ser Phe Arg Arg Ser Pro Thr Lys Ser

620

625

630

tcg ctg gat tac cgt cgc ctg ccc gat gcc cat tcc gat tac gca cgc 2032

Ser Leu Asp Tyr Arg Arg Leu Pro Asp Ala His Ser Asp Tyr Ala Arg

635

640

645

tat tcg ggc tcc tat aat gat tac ctg cgg gca gct cag atg cac tct 2080

Tyr Ser Gly Ser Tyr Asn Asp Tyr Leu Arg Ala Ala Gln Met His Ser

650

655

660

ggc tac cag cgc cgc atg tagggccatc ctggggatgg ggcaccacag 2128

Gly Tyr Gln Arg Arg Met

665

gaagggagag agaggaagag gtagggtagg gtgcagaccc aggttatcac caccctctct 2188

catactctc ccaatggtgg cttttcattc cctccctcta tcatgtgggc cttccccagg 2248

agaggaccct tttgtgtttg gcagtaacct gctttgtttc tttgcctcag cagcacatct 2308

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cttttgtatg gactacaaat aaaacttggg gcgattcgtg gtttgg 2774

<210> 42

<211> 669

<212> PRT

<213> Mus musculus

<400> 42

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Val Met Lys Gln Phe Ala Phe Val His Met Arg Glu Asn Ala Gly Ala
35 40 45
Val Arg Ala Ile Glu Ala Leu His Gly His Glu Leu Arg Pro Gly Arg
50 55 60
Ala Leu Val Val Glu Met Ser Arg Pro Arg Pro Leu Asn Thr Trp Lys
65 70 75 80
Ile Phe Val Gly Asn Val Ser Ala Ala Cys Thr Ser Gln Glu Leu Arg
85 90 95
Ser Leu Phe Glu Arg Arg Gly Arg Val Ile Glu Cys Asp Val Val Lys
100 105 110
Asp Tyr Ala Phe Val His Met Glu Lys Glu Ala Asp Ala Lys Ala Ala
115 120 125
Ile Ala Gln Leu Asn Gly Lys Glu Val Lys Gly Lys Arg Ile Asn Val
130 135 140
Glu Leu Ser Thr Lys Gly Gln Lys Lys Gly Pro Ala Leu Ala Ile Gln
145 150 155 160
Ser Gly Asp Lys Thr Lys Lys Pro Gly Ala Gly Asp Thr Ala Phe Pro
165 170 175
Gly Thr Gly Gly Phe Ser Ala Thr Phe Asp Tyr Gln Gln Ala Phe Gly
180 185 190
Asn Ser Thr Gly Gly Phe Asp Gly Gln Ala Arg Gln Pro Thr Pro Pro
195 200 205

145/617

Phe Phe Gly Arg Asp Arg Ser Pro Leu Arg Arg Ser Pro Pro Arg Ala
210 215 220
Ser Tyr Val Ala Pro Leu Thr Ala Gln Pro Ala Thr Tyr Arg Ala Gln
225 230 235 240
Pro Ser Val Ser Leu Gly Ala Ala Tyr Arg Ala Gln Pro Ser Ala Ser
245 250 255
Leu Gly Val Gly Tyr Arg Thr Gln Pro Met Ala Ala Gln Ala Ala Ser
260 265 270
Tyr Arg Ala Gln Pro Ser Val Ser Leu Gly Ala Pro Tyr Arg Gly Gln
275 280 285
Leu Ala Ser Pro Ser Ser Gln Ser Ala Ala Ala Ser Ser Leu Gly Pro
290 295 300
Tyr Gly Gly Val Gln Pro Ser Ala Ser Ala Leu Ser Thr Tyr Gly Gly
305 310 315 320
Gln Ala Ala Ala Ala Ser Ser Leu Asn Ser Tyr Gly Ala Gln Gly Ser
325 330 335
Ser Leu Ala Ser Tyr Gly Asn Gln Pro Ser Ser Tyr Gly Ala Gln Ala
340 345 350
Ala Ser Ser Tyr Gly Ala Arg Ala Ala Ala Ser Ser Tyr Asn Thr Gln
355 360 365
Gly Ala Ala Ser Ser Leu Gly Ser Tyr Gly Ala Gln Ala Ala Ser Tyr
370 375 380
Gly Ala Gln Ser Ala Ala Ser Ser Leu Ala Tyr Gly Ala Gln Ala Ala
385 390 395 400
Ser Tyr Ser Ala Gln Pro Ser Ala Ser Tyr Ser Ala Gln Ser Ala Pro
405 410 415
Tyr Ala Ala Gln Gln Ala Ala Ser Tyr Ser Ser Gln Pro Ala Ala Tyr

420	425	430
Val Ala Gln Pro Ala Thr Ala Ala Ala Tyr Ala Ser Gln Pro Ala Ala		
435	440	445
Tyr Ala Ala Gln Ala Thr Thr Pro Met Ala Gly Ser Tyr Gly Ala Gln		
450	455	460
Pro Val Val Gln Thr Gln Leu Asn Ser Tyr Gly Ala Gln Ala Ser Ile		
465	470	475
Gly Leu Ser Gly Ser Tyr Gly Ala Gln Ser Ala Ala Ala Ala Thr Gly		
485	490	495
Ser Tyr Gly Ala Ala Ala Ala Tyr Gly Ala Gln Pro Ser Ala Thr Leu		
500	505	510
Ala Ala Pro Tyr Arg Thr Gln Ser Ser Ala Ser Leu Ala Ala Ser Tyr		
515	520	525
Ala Ala Gln Gln His Pro Gln Ala Ala Ala Ser Tyr Arg Gly Gln Pro		
530	535	540
Gly Ser Ala Tyr Asp Gly Thr Gly Gln Pro Ser Ala Ala Tyr Leu Ser		
545	550	555
Met Ser Gln Gly Ala Val Ala Asn Ala Asn Ser Thr Pro Pro Pro Tyr		
565	570	575
Glu Arg Thr Arg Leu Ser Pro Pro Arg Ala Ser Tyr Asp Asp Pro Tyr		
580	585	590
Lys Lys Ala Val Ala Met Ser Lys Arg Tyr Gly Ser Asp Arg Arg Leu		
595	600	605
Ala Glu Leu Ser Asp Tyr Arg Arg Leu Ser Glu Ser Gln Leu Ser Phe		
610	615	620
Arg Arg Ser Pro Thr Lys Ser Ser Leu Asp Tyr Arg Arg Leu Pro Asp		
625	630	635
		640

147/617

Ala His Ser Asp Tyr Ala Arg Tyr Ser Gly Ser Tyr Asn Asp Tyr Leu

645

650

655

Arg Ala Ala Gln Met His Ser Gly Tyr Gln Arg Arg Met

660

665

<210> 43

<211> 2774

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (92).. (2098)

<400> 43

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Met Lys Ile Phe Val Gly Asn

1

5

gtc gat ggg gcg gat acg aca ccg gag gag ttg gca gct ctc ttc gcg 160
Val Asp Gly Ala Asp Thr Thr Pro Glu Glu Leu Ala Ala Leu Phe Ala

10

15

20

ccc tat ggc acg gtc atg agc tgc gcc gtc atg aaa cag ttt gcc ttc 208
Pro Tyr Gly Thr Val Met Ser Cys Ala Val Met Lys Gln Phe Ala Phe

25

30

35

gtg cac atg cgc gag aac gct ggc gcg gtg cgc gcc atc gag gcc ctg 256
Val His Met Arg Glu Asn Ala Gly Ala Val Arg Ala Ile Glu Ala Leu

40

45

50

55

cat ggc cac gag ctg cgt cca ggt cgc gcg ctc gtg gtg gag atg tcg 304

His Gly His Glu Leu Arg Pro Gly Arg Ala Leu Val Val Glu Met Ser
 60 65 70
 cgc ccg agg ccc ctg aac act tgg aag att ttc gtg ggc aat gta tcg 352
 Arg Pro Arg Pro Leu Asn Thr Trp Lys Ile Phe Val Gly Asn Val Ser
 75 80 85
 gct gca tgt aca agt cag gaa ttg cgc agc ctc ttc gag cgc cgt gga 400
 Ala Ala Cys Thr Ser Gln Glu Leu Arg Ser Leu Phe Glu Arg Arg Gly
 90 95 100
 cgc gtc atc gag tgt gac gtg gta aaa gac tac gcg ttt gtt cac atg 448
 Arg Val Ile Glu Cys Asp Val Val Lys Asp Tyr Ala Phe Val His Met
 105 110 115
 gag aag gaa gca gat gcc aaa gcc gcc atc gcg cag ctc aac ggc aaa 496
 Glu Lys Glu Ala Asp Ala Lys Ala Ala Ile Ala Gln Leu Asn Gly Lys
 120 125 130 135
 gaa gtg aag ggc aag cgc atc aac gtg gaa ctc tca acc aag ggg cag 544
 Glu Val Lys Gly Lys Arg Ile Asn Val Glu Leu Ser Thr Lys Gly Gln
 140 145 150
 aag aag ggg cct gcc ctg gct atc cag tct ggg gac aag acc aag aaa 592
 Lys Lys Gly Pro Ala Leu Ala Ile Gln Ser Gly Asp Lys Thr Lys Lys
 155 160 165
 cca ggg gct ggg gac aca gca ttc cct gga act ggt ggc ttc tct gcc 640
 Pro Gly Ala Gly Asp Thr Ala Phe Pro Gly Thr Gly Gly Phe Ser Ala
 170 175 180
 acc ttc gac tac cag cag gct ttt ggc aac agc act ggt ggc ttt gat 688
 Thr Phe Asp Tyr Gln Gln Ala Phe Gly Asn Ser Thr Gly Gly Phe Asp
 185 190 195
 ggg caa gcc cgt cag ccc aca cca cca ttc ttt ggt cgc gac cgc agc 736

Gly Gln Ala Arg Gln Pro Thr Pro Pro Phe Phe Gly Arg Asp Arg Ser
 200 205 210 215
 ccc ctg cgc cgt tca cct cct cga gcc tct tat gtg gcg cct ctg acg 784
 Pro Leu Arg Arg Ser Pro Pro Arg Ala Ser Tyr Val Ala Pro Leu Thr
 220 225 230
 gcc cag cca gcc acc tac cgg gcc caa ccc tca gtg tct ctg gga gct 832
 Ala Gln Pro Ala Thr Tyr Arg Ala Gln Pro Ser Val Ser Leu Gly Ala
 235 240 245
 gca tat agg gcc cag cct tcc gcc tct ttg ggt gtt ggc tat cgg act 880
 Ala Tyr Arg Ala Gln Pro Ser Ala Ser Leu Gly Val Gly Tyr Arg Thr
 250 255 260
 cag ccc atg gca gct cag gca gct tct tac cgt gct cag ccc tct gtc 928
 Gln Pro Met Ala Ala Gln Ala Ala Ser Tyr Arg Ala Gln Pro Ser Val
 265 270 275
 tcc ctt ggg gcc cca tac agg ggt cag ctg gct agc cct agt tcc cag 976
 Ser Leu Gly Ala Pro Tyr Arg Gly Gln Leu Ala Ser Pro Ser Ser Gln
 280 285 290 295
 tct gct gca gct tcc tcg ctt ggc cca tat ggt gga gtc cag ccc tca 1024
 Ser Ala Ala Ala Ser Ser Leu Gly Pro Tyr Gly Gly Val Gln Pro Ser
 300 305 310
 gcc tca gcc ctt tcc act tat ggg ggt cag gca gct gca gct tct tcg 1072
 Ala Ser Ala Leu Ser Thr Tyr Gly Gly Gln Ala Ala Ala Ala Ser Ser
 315 320 325
 ctt aat tcc tat ggg gct cag ggc tcc tcc ctt gct tcc tat ggt aac 1120
 Leu Asn Ser Tyr Gly Ala Gln Gly Ser Ser Leu Ala Ser Tyr Gly Asn
 330 335 340
 cag cca tcc tct tat ggc gcc cag gct gcc tct tcg tat ggg gtt cgt 1168

Gln Pro Ser Ser Tyr Gly Ala Gln Ala Ala Ser Ser Tyr Gly Val Arg
 345 350 355
 gcg gct gct tct tcc tat aac aca caa gga gca gct tct tcc cta ggt 1216
 Ala Ala Ala Ser Ser Tyr Asn Thr Gln Gly Ala Ala Ser Ser Leu Gly
 360 365 370 375
 tcc tat ggg gct caa gca gcc tcc tat ggt gcc cag tct gca gcc tcc 1264
 Ser Tyr Gly Ala Gln Ala Ala Ser Tyr Gly Ala Gln Ser Ala Ala Ser
 380 385 390
 tca cta gct tat gga gcc cag gca gcg tct tac agt gcc cag ccc tca 1312
 Ser Leu Ala Tyr Gly Ala Gln Ala Ala Ser Tyr Ser Ala Gln Pro Ser
 395 400 405
 gcc tct tac agt gcc cag tct gcc cca tat gct gca caa cag gct gct 1360
 Ala Ser Tyr Ser Ala Gln Ser Ala Pro Tyr Ala Ala Gln Gln Ala Ala
 410 415 420
 tct tat tct tcc cag cct gct gct tat gtg gca caa cca gcc aca gct 1408
 Ser Tyr Ser Ser Gln Pro Ala Ala Tyr Val Ala Gln Pro Ala Thr Ala
 425 430 435
 gct gcc tat gct agc cag cca gct gcc tat gct gca caa gcc act acc 1456
 Ala Ala Tyr Ala Ser Gln Pro Ala Ala Tyr Ala Ala Gln Ala Thr Thr
 440 445 450 455
 cca atg gct ggt tcc tat ggg gct caa cca gtt gtt cag acc cag ctg 1504
 Pro Met Ala Gly Ser Tyr Gly Ala Gln Pro Val Val Gln Thr Gln Leu
 460 465 470
 aat agc tat ggg gct caa gca tct att ggc ctg tca ggc tca tat gga 1552
 Asn Ser Tyr Gly Ala Gln Ala Ser Ile Gly Leu Ser Gly Ser Tyr Gly
 475 480 485
 gct cag tct gct gct gcg gcc act ggc tcc tat ggg gcg gca gct gct 1600

151/617

Ala Gln Ser Ala Ala Ala Ala Thr Gly Ser Tyr Gly Ala Ala Ala Ala
490 495 500
tac ggg gct cag cct tct gcc acc ctg gca gct cct tac cgc act cag 1648
Tyr Gly Ala Gln Pro Ser Ala Thr Leu Ala Ala Pro Tyr Arg Thr Gln
505 510 515
tca tca gcc tca ttg gct gct tcc tat gct gcc cag cag cat ccc cag 1696
Ser Ser Ala Ser Leu Ala Ala Ser Tyr Ala Ala Gln Gln His Pro Gln
520 525 530 535
gct gct gcc tcc tac cgt ggc cag ccg ggc agt gcc tac gat ggg aca 1744
Ala Ala Ala Ser Tyr Arg Gly Gln Pro Gly Ser Ala Tyr Asp Gly Thr
540 545 550
ggc cag cca tca gca gcc tac ctg tct atg tcc cag ggg gcc gtt gcc 1792
Gly Gln Pro Ser Ala Ala Tyr Leu Ser Met Ser Gln Gly Ala Val Ala
555 560 565
aac gcc aac agc acc ccg ccg ccc tat gag cgt acc cgc ctc tcc cca 1840
Asn Ala Asn Ser Thr Pro Pro Pro Tyr Glu Arg Thr Arg Leu Ser Pro
570 575 580
ccc cgg gcc agc tac gac gat ccc tac aaa aag gct gtc gcc atg tca 1888
Pro Arg Ala Ser Tyr Asp Asp Pro Tyr Lys Lys Ala Val Ala Met Ser
585 590 595
aaa agg tat ggt tcc gac cgg cgt tta gcc gag ctc tct gat tac cgc 1936
Lys Arg Tyr Gly Ser Asp Arg Arg Leu Ala Glu Leu Ser Asp Tyr Arg
600 605 610 615
cgt tta tca gag tcg cag ctt tcg ttc cgc cgc tcg ccg aca aag tcc 1984
Arg Leu Ser Glu Ser Gln Leu Ser Phe Arg Arg Ser Pro Thr Lys Ser
620 625 630
tcg ctg gat tac cgt cgc ctg ccc gat gcc cat tcc gat tac gca cgc 2032

Ser Leu Asp Tyr Arg Arg Leu Pro Asp Ala His Ser Asp Tyr Ala Arg
635 640 645
tat tcg ggc tcc tat aat gat tac ctg cgg gca gct cag atg cac tct 2080
Tyr Ser Gly Ser Tyr Asn Asp Tyr Leu Arg Ala Ala Gln Met His Ser
650 655 660
ggc tac cag cgc cgc atg tagggccatc ctggggatgg ggcaccacag 2128
Gly Tyr Gln Arg Arg Met
665
gaagggagag agaggaagag gtagggtagg gtgcagaccc aggttatcac caccctctct 2188
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agaggacct tttgtgttg gcagtaacct gctttgtttc tttgcctcag cagcacatct 2308
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tagtcccaat tccctatctc tccaagtagg tgggtgttaga aatcttaatt cttttccctt 2728
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<210> 44

<211> 669

<212> PRT

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<400> 44

Met Lys Ile Phe Val Gly Asn Val Asp Gly Ala Asp Thr Thr Pro Glu

1

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10

15

Glu Leu Ala Ala Leu Phe Ala Pro Tyr Gly Thr Val Met Ser Cys Ala
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 Val Met Lys Gln Phe Ala Phe Val His Met Arg Glu Asn Ala Gly Ala
 35 40 45
 Val Arg Ala Ile Glu Ala Leu His Gly His Glu Leu Arg Pro Gly Arg
 50 55 60
 Ala Leu Val Val Glu Met Ser Arg Pro Arg Pro Leu Asn Thr Trp Lys
 65 70 75 80
 Ile Phe Val Gly Asn Val Ser Ala Ala Cys Thr Ser Gln Glu Leu Arg
 85 90 95
 Ser Leu Phe Glu Arg Arg Gly Arg Val Ile Glu Cys Asp Val Val Lys
 100 105 110
 Asp Tyr Ala Phe Val His Met Glu Lys Glu Ala Asp Ala Lys Ala Ala
 115 120 125
 Ile Ala Gln Leu Asn Gly Lys Glu Val Lys Gly Lys Arg Ile Asn Val
 130 135 140
 Glu Leu Ser Thr Lys Gly Gln Lys Lys Gly Pro Ala Leu Ala Ile Gln
 145 150 155 160
 Ser Gly Asp Lys Thr Lys Lys Pro Gly Ala Gly Asp Thr Ala Phe Pro
 165 170 175
 Gly Thr Gly Gly Phe Ser Ala Thr Phe Asp Tyr Gln Gln Ala Phe Gly
 180 185 190
 Asn Ser Thr Gly Gly Phe Asp Gly Gln Ala Arg Gln Pro Thr Pro Pro
 195 200 205
 Phe Phe Gly Arg Asp Arg Ser Pro Leu Arg Arg Ser Pro Pro Arg Ala
 210 215 220
 Ser Tyr Val Ala Pro Leu Thr Ala Gln Pro Ala Thr Tyr Arg Ala Gln

225 230 235 240
Pro Ser Val Ser Leu Gly Ala Ala Tyr Arg Ala Gln Pro Ser Ala Ser
 245 250 255
Leu Gly Val Gly Tyr Arg Thr Gln Pro Met Ala Ala Gln Ala Ala Ser
 260 265 270
Tyr Arg Ala Gln Pro Ser Val Ser Leu Gly Ala Pro Tyr Arg Gly Gln
 275 280 285
Leu Ala Ser Pro Ser Ser Gln Ser Ala Ala Ala Ser Ser Leu Gly Pro
 290 295 300
Tyr Gly Gly Val Gln Pro Ser Ala Ser Ala Leu Ser Thr Tyr Gly Gly
305 310 315 320
Gln Ala Ala Ala Ala Ser Ser Leu Asn Ser Tyr Gly Ala Gln Gly Ser
 325 330 335
Ser Leu Ala Ser Tyr Gly Asn Gln Pro Ser Ser Tyr Gly Ala Gln Ala
 340 345 350
Ala Ser Ser Tyr Gly Val Arg Ala Ala Ala Ser Ser Tyr Asn Thr Gln
 355 360 365
Gly Ala Ala Ser Ser Leu Gly Ser Tyr Gly Ala Gln Ala Ala Ser Tyr
 370 375 380
Gly Ala Gln Ser Ala Ala Ser Ser Leu Ala Tyr Gly Ala Gln Ala Ala
385 390 395 400
Ser Tyr Ser Ala Gln Pro Ser Ala Ser Tyr Ser Ala Gln Ser Ala Pro
 405 410 415
Tyr Ala Ala Gln Gln Ala Ala Ser Tyr Ser Ser Gln Pro Ala Ala Tyr
 420 425 430
Val Ala Gln Pro Ala Thr Ala Ala Ala Tyr Ala Ser Gln Pro Ala Ala
 435 440 445

Tyr Ala Ala Gln Ala Thr Thr Pro Met Ala Gly Ser Tyr Gly Ala Gln
450 455 460
Pro Val Val Gln Thr Gln Leu Asn Ser Tyr Gly Ala Gln Ala Ser Ile
465 470 475 480
Gly Leu Ser Gly Ser Tyr Gly Ala Gln Ser Ala Ala Ala Thr Gly
485 490 495
Ser Tyr Gly Ala Ala Ala Tyr Gly Ala Gln Pro Ser Ala Thr Leu
500 505 510
Ala Ala Pro Tyr Arg Thr Gln Ser Ser Ala Ser Leu Ala Ala Ser Tyr
515 520 525
Ala Ala Gln Gln His Pro Gln Ala Ala Ala Ser Tyr Arg Gly Gln Pro
530 535 540
Gly Ser Ala Tyr Asp Gly Thr Gly Gln Pro Ser Ala Ala Tyr Leu Ser
545 550 555 560
Met Ser Gln Gly Ala Val Ala Asn Ala Asn Ser Thr Pro Pro Pro Tyr
565 570 575
Glu Arg Thr Arg Leu Ser Pro Pro Arg Ala Ser Tyr Asp Asp Pro Tyr
580 585 590
Lys Lys Ala Val Ala Met Ser Lys Arg Tyr Gly Ser Asp Arg Arg Leu
595 600 605
Ala Glu Leu Ser Asp Tyr Arg Arg Leu Ser Glu Ser Gln Leu Ser Phe
610 615 620
Arg Arg Ser Pro Thr Lys Ser Ser Leu Asp Tyr Arg Arg Leu Pro Asp
625 630 635 640
Ala His Ser Asp Tyr Ala Arg Tyr Ser Gly Ser Tyr Asn Asp Tyr Leu
645 650 655
Arg Ala Ala Gln Met His Ser Gly Tyr Gln Arg Arg Met

660

665

<210> 45

<211> 2807

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (126).. (2132)

<400> 45

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 cggacgtctt gcctgtcgct ggaggagagg tccgggctct ccaggaaggt ggctgcggcg 120
 acaaa atg aag ata ttc gtg ggc aac gtc gac ggg gcg gat acg act ccg 170

Met Lys Ile Phe Val Gly Asn Val Asp Gly Ala Asp Thr Thr Pro

1 5 10 15

gag gag ctg gca gcc ctc ttt gcg ccc tac ggc acg gtc atg agc tgc 218
 Glu Glu Leu Ala Ala Leu Phe Ala Pro Tyr Gly Thr Val Met Ser Cys

20 25 30

gcc gtc atg aaa cag ttc gcc ttc gtg cac atg cgc gag aac gcg ggc 266
 Ala Val Met Lys Gln Phe Ala Phe Val His Met Arg Glu Asn Ala Gly

35 40 45

gcg ctg cgc gcc atc gaa gcc ctg cac ggc cac gag ctg cgg ccg ggg 314
 Ala Leu Arg Ala Ile Glu Ala Leu His Gly His Glu Leu Arg Pro Gly

50 55 60

cgc gcg ctc gtg gtg gag atg tcg cgc cca agg cct ctt aat act tgg 362
 Arg Ala Leu Val Val Glu Met Ser Arg Pro Arg Pro Leu Asn Thr Trp

65 70 75

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aag att ttc gtg ggc aat gtg tcg gct gca tgc acg agc cag gaa ctg 410
Lys Ile Phe Val Gly Asn Val Ser Ala Ala Cys Thr Ser Gln Glu Leu
80 85 90 95
cgc agc ctc ttc gag cgc cgc gga cgc gtc atc gag tgt gac gtg gtg 458
Arg Ser Leu Phe Glu Arg Arg Gly Arg Val Ile Glu Cys Asp Val Val
100 105 110
aaa gac tac gcg ttt gtt cac atg gag aag gaa gca gat gcc aaa gcc 506
Lys Asp Tyr Ala Phe Val His Met Glu Lys Glu Ala Asp Ala Lys Ala
115 120 125
gca atc gcg cag ctc aac ggc aaa gaa gtg aag ggc aag cgc atc aac 554
Ala Ile Ala Gln Leu Asn Gly Lys Glu Val Lys Gly Lys Arg Ile Asn
130 135 140
gtg gaa ctc tcc acc aag ggt cag aag aag ggg cct gcc ctg gct gtc 602
Val Glu Leu Ser Thr Lys Gly Gln Lys Lys Gly Pro Gly Leu Ala Val
145 150 155
cag tct ggg gac aag acc aag aaa cca ggg gct ggg gat acg gcc ttc 650
Gln Ser Gly Asp Lys Thr Lys Lys Pro Gly Ala Gly Asp Thr Ala Phe
160 165 170 175
cct gga act ggt ggc ttc tct gcc acc ttc gac tac cag cag gct ttt 698
Pro Gly Thr Gly Gly Phe Ser Ala Thr Phe Asp Tyr Gln Gln Ala Phe
180 185 190
ggc aac agc act ggt ggc ttt gat ggg caa gcc cgt cag ccc aca cca 746
Gly Asn Ser Thr Gly Gly Phe Asp Gly Gln Ala Arg Gln Pro Thr Pro
195 200 205
ccc ttc ttt ggt cgc gac cgc agc cct ctg cgc cgt tca cct ccc cga 794
Pro Phe Phe Gly Arg Asp Arg Ser Pro Leu Arg Arg Ser Pro Pro Arg
210 215 220

gcc tct tat gtg gct cct ctg acg gcc cag cca gct acc tac cgg gcc 842
 Ala Ser Tyr Val Ala Pro Leu Thr Ala Gln Pro Ala Thr Tyr Arg Ala
 225 230 235
 cag ccg tcc gtg tca ctg gga gct gcc tac agg gcc cag cct tct gcc 890
 Gln Pro Ser Val Ser Leu Gly Ala Ala Tyr Arg Ala Gln Pro Ser Ala
 240 245 250 255
 tct ttg ggt gtt ggc tat cgg act cag ccc atg aca gcc cag gca gcc 938
 Ser Leu Gly Val Gly Tyr Arg Thr Gln Pro Met Thr Ala Gln Ala Ala
 260 265 270
 tct tac cgc gct cag ccc tct gtc tcc ctt ggg gca cca tac agg ggc 986
 Ser Tyr Arg Ala Gln Pro Ser Val Ser Leu Gly Ala Pro Tyr Arg Gly
 275 280 285
 cag ctg gct agt cct agc tcc cag tct gct gca gct tct tca ctc ggc 1034
 Gln Leu Ala Ser Pro Ser Ser Gln Ser Ala Ala Ala Ser Ser Leu Gly
 290 295 300
 cca tat ggt gga gcc cag ccc tca gcc tcg gcc ctt tcc tcc tat ggg 1082
 Pro Tyr Gly Gly Ala Gln Pro Ser Ala Ser Ala Leu Ser Ser Tyr Gly
 305 310 315
 ggt cag gca gct gca gct tct tcg ctc aac tcc tat ggg gct cag ggt 1130
 Gly Gln Ala Ala Ala Ala Ser Ser Leu Asn Ser Tyr Gly Ala Gln Gly
 320 325 330 335
 tcc tcc ctt gcc tcc tat ggt aac cag cca tcc tct tac ggc gcc cag 1178
 Ser Ser Leu Ala Ser Tyr Gly Asn Gln Pro Ser Ser Tyr Gly Ala Gln
 340 345 350
 gct gcc tct tcc tat ggg gtt cgt gca gct gct tct tcc tac aac acc 1226
 Ala Ala Ser Ser Tyr Gly Val Arg Ala Ala Ala Ser Ser Tyr Asn Thr
 355 360 365

cag gga gca gct tcc tcc tta ggc tcc tac ggg gct cag gca gcc tcc 1274
 Gln Gly Ala Ala Ser Ser Leu Gly Ser Tyr Gly Ala Gln Ala Ala Ser
 370 375 380
 tat ggg gcc cag tct gca gcc tcc tca cta gct tat gga gcc cag gca 1322
 Tyr Gly Ala Gln Ser Ala Ala Ser Ser Leu Ala Tyr Gly Ala Gln Ala
 385 390 395
 gct tca tat aat gcc cag ccc tcg gcc tct tac aat gcc cag tct gcc 1370
 Ala Ser Tyr Asn Ala Gln Pro Ser Ala Ser Tyr Asn Ala Gln Ser Ala
 400 405 410 415
 cca tat gct gca cag cag gct gct tcc tac tct tcc caa cct gct gcc 1418
 Pro Tyr Ala Ala Gln Gln Ala Ala Ser Tyr Ser Ser Gln Pro Ala Ala
 420 425 430
 tat gtg gca cag cca gcc aca gct gct gcc tat gcc agc cag cca gca 1466
 Tyr Val Ala Gln Pro Ala Thr Ala Ala Tyr Ala Ser Gln Pro Ala
 435 440 445
 gcc tac gcc gca caa gcc act acc cca atg gct ggc tcc tat ggg gcc 1514
 Ala Tyr Ala Ala Gln Ala Thr Thr Pro Met Ala Gly Ser Tyr Gly Ala
 450 455 460
 cag ccg gtt gtg cag acc cag ctg aat agt tac ggg gcc caa gca tca 1562
 Gln Pro Val Val Gln Thr Gln Leu Asn Ser Tyr Gly Ala Gln Ala Ser
 465 470 475
 atg ggc ctt tca ggc tcc tat ggg gct cag tcg gct gct gcg gcc act 1610
 Met Gly Leu Ser Gly Ser Tyr Gly Ala Gln Ser Ala Ala Ala Thr
 480 485 490 495
 ggc tcc tat ggt gcc gca gca gcc tac ggg gcc caa cct tct gcc acc 1658
 Gly Ser Tyr Gly Ala Ala Ala Tyr Gly Ala Gln Pro Ser Ala Thr
 500 505 510

ctg gca gct cct tac cgc act cag tca tca gcc tca ttg gct gct tcc 1706
 Leu Ala Ala Pro Tyr Arg Thr Gln Ser Ser Ala Ser Leu Ala Ala Ser
 515 520 525
 tat gct gcc cag cag cat ccc cag gct gct gcc tcc tac cgc ggc cag 1754
 Tyr Ala Ala Gln Gln His Pro Gln Ala Ala Ala Ser Tyr Arg Gly Gln
 530 535 540
 cca ggc aat gcc tac gat ggg gca ggt cag ccg tct gca gcc tac ctg 1802
 Pro Gly Asn Ala Tyr Asp Gly Ala Gly Gln Pro Ser Ala Ala Tyr Leu
 545 550 555
 tcc atg tcc cag ggg gcc gtt gcc aac gcc aac agc acc ccg ccg ccc 1850
 Ser Met Ser Gln Gly Ala Val Ala Asn Ala Asn Ser Thr Pro Pro Pro
 560 565 570 575
 tat gag cgt acc cgc ctc tcc cca ccc cgg gcc agc tac gac gat ccc 1898
 Tyr Glu Arg Thr Arg Leu Ser Pro Pro Arg Ala Ser Tyr Asp Asp Pro
 580 585 590
 tac aaa aag gct gtc gcc atg tcg aaa agg tat ggt tcc gac cgg cgt 1946
 Tyr Lys Lys Ala Val Ala Met Ser Lys Arg Tyr Gly Ser Asp Arg Arg
 595 600 605
 tta gcc gag ctc tct gat tac cgc cgt tta tca gag tcg cag ctt tcg 1994
 Leu Ala Glu Leu Ser Asp Tyr Arg Arg Leu Ser Glu Ser Gln Leu Ser
 610 615 620
 ttc cgc cgc tcg ccg aca aag tcc tcg ctg gat tac cgt cgc ctg ccc 2042
 Phe Arg Arg Ser Pro Thr Lys Ser Ser Leu Asp Tyr Arg Arg Leu Pro
 625 630 635
 gat gcc cat tcc gat tac gca cgc tat tcg ggc tcc tat aat gat tac 2090
 Asp Ala His Ser Asp Tyr Ala Arg Tyr Ser Gly Ser Tyr Asn Asp Tyr
 640 645 650 655

ctg cgg gcg gct cag atg cac tct ggc tac cag cgc cgc atg 2132

Leu Arg Ala Ala Gln Met His Ser Gly Tyr Gln Arg Arg Met

660

665

tagggccatc ctgggatggg gcaccacagg gagggaggga gaaaagaggt gggtagggtt 2192

acagatccag gttataacta ctctggccca tacctttcct gtttgtggtt tttcatgccc 2252

tctaccatgt ggcccttccc caggagatga tcctgttaag tgttcggcag taacctactt 2312

tgttccttcg cctcagcagc aaatcttgct actggctcta gatctgcggt tccccctcta 2372

ccctgcctcc cgtctcccca gaatgggaat ttcttttatg tttttatttt tttcctggct 2432

cccttttatt tttgtgcgcg atatttaagg tcgtctggat ggggaagcaa cctgcagctg 2492

aggctgcccg cgcctttttc tttttagatg ggaaggaggc caggaaaggg tcagcttaac 2552

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ctgttgagac tgagttcctg ttgggacagt cagttggtat gtatccaagt ccctgctgac 2672

cactaatgtt ctagctgatg gtgagcgga cagtccact tccccatctc cccaagtagg 2732

tggtgttaga aaaccttaat tttttttccc ttttgtatgg actacaaata aaacttgggg 2792

caatttgacg tttgg 2807

<210> 46

<211> 669

<212> PRT

<213> Homo sapiens

<400> 46

Met Lys Ile Phe Val Gly Asn Val Asp Gly Ala Asp Thr Thr Pro Glu

1

5

10

15

Glu Leu Ala Ala Leu Phe Ala Pro Tyr Gly Thr Val Met Ser Cys Ala

20

25

30

Val Met Lys Gln Phe Ala Phe Val His Met Arg Glu Asn Ala Gly Ala

35

40

45

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Leu Arg Ala Ile Glu Ala Leu His Gly His Glu Leu Arg Pro Gly Arg
 50 55 60
 Ala Leu Val Val Glu Met Ser Arg Pro Arg Pro Leu Asn Thr Trp Lys
 65 70 75 80
 Ile Phe Val Gly Asn Val Ser Ala Ala Cys Thr Ser Gln Glu Leu Arg
 85 90 95
 Ser Leu Phe Glu Arg Arg Gly Arg Val Ile Glu Cys Asp Val Val Lys
 100 105 110
 Asp Tyr Ala Phe Val His Met Glu Lys Glu Ala Asp Ala Lys Ala Ala
 115 120 125
 Ile Ala Gln Leu Asn Gly Lys Glu Val Lys Gly Lys Arg Ile Asn Val
 130 135 140
 Glu Leu Ser Thr Lys Gly Gln Lys Lys Gly Pro Gly Leu Ala Val Gln
 145 150 155 160
 Ser Gly Asp Lys Thr Lys Lys Pro Gly Ala Gly Asp Thr Ala Phe Pro
 165 170 175
 Gly Thr Gly Gly Phe Ser Ala Thr Phe Asp Tyr Gln Gln Ala Phe Gly
 180 185 190
 Asn Ser Thr Gly Gly Phe Asp Gly Gln Ala Arg Gln Pro Thr Pro Pro
 195 200 205
 Phe Phe Gly Arg Asp Arg Ser Pro Leu Arg Arg Ser Pro Pro Arg Ala
 210 215 220
 Ser Tyr Val Ala Pro Leu Thr Ala Gln Pro Ala Thr Tyr Arg Ala Gln
 225 230 235 240
 Pro Ser Val Ser Leu Gly Ala Ala Tyr Arg Ala Gln Pro Ser Ala Ser
 245 250 255
 Leu Gly Val Gly Tyr Arg Thr Gln Pro Met Thr Ala Gln Ala Ala Ser

260	265	270
Tyr Arg Ala Gln Pro Ser Val Ser Leu Gly Ala Pro Tyr Arg Gly Gln		
275	280	285
Leu Ala Ser Pro Ser Ser Gln Ser Ala Ala Ala Ser Ser Leu Gly Pro		
290	295	300
Tyr Gly Gly Ala Gln Pro Ser Ala Ser Ala Leu Ser Ser Tyr Gly Gly		
305	310	315
Gln Ala Ala Ala Ala Ser Ser Leu Asn Ser Tyr Gly Ala Gln Gly Ser		
325	330	335
Ser Leu Ala Ser Tyr Gly Asn Gln Pro Ser Ser Tyr Gly Ala Gln Ala		
340	345	350
Ala Ser Ser Tyr Gly Val Arg Ala Ala Ala Ser Ser Tyr Asn Thr Gln		
355	360	365
Gly Ala Ala Ser Ser Leu Gly Ser Tyr Gly Ala Gln Ala Ala Ser Tyr		
370	375	380
Gly Ala Gln Ser Ala Ala Ser Ser Leu Ala Tyr Gly Ala Gln Ala Ala		
385	390	395
Ser Tyr Asn Ala Gln Pro Ser Ala Ser Tyr Asn Ala Gln Ser Ala Pro		
405	410	415
Tyr Ala Ala Gln Gln Ala Ala Ser Tyr Ser Ser Gln Pro Ala Ala Tyr		
420	425	430
Val Ala Gln Pro Ala Thr Ala Ala Ala Tyr Ala Ser Gln Pro Ala Ala		
435	440	445
Tyr Ala Ala Gln Ala Thr Thr Pro Met Ala Gly Ser Tyr Gly Ala Gln		
450	455	460
Pro Val Val Gln Thr Gln Leu Asn Ser Tyr Gly Ala Gln Ala Ser Met		
465	470	475
		480

Gly Leu Ser Gly Ser Tyr Gly Ala Gln Ser Ala Ala Ala Ala Thr Gly

485

490

495

Ser Tyr Gly Ala Ala Ala Ala Tyr Gly Ala Gln Pro Ser Ala Thr Leu

500

505

510

Ala Ala Pro Tyr Arg Thr Gln Ser Ser Ala Ser Leu Ala Ala Ser Tyr

515

520

525

Ala Ala Gln Gln His Pro Gln Ala Ala Ala Ser Tyr Arg Gly Gln Pro

530

535

540

Gly Asn Ala Tyr Asp Gly Ala Gly Gln Pro Ser Ala Ala Tyr Leu Ser

545

550

555

560

Met Ser Gln Gly Ala Val Ala Asn Ala Asn Ser Thr Pro Pro Pro Tyr

565

570

575

Glu Arg Thr Arg Leu Ser Pro Pro Arg Ala Ser Tyr Asp Asp Pro Tyr

580

585

590

Lys Lys Ala Val Ala Met Ser Lys Arg Tyr Gly Ser Asp Arg Arg Leu

595

600

605

Ala Glu Leu Ser Asp Tyr Arg Arg Leu Ser Glu Ser Gln Leu Ser Phe

610

615

620

Arg Arg Ser Pro Thr Lys Ser Ser Leu Asp Tyr Arg Arg Leu Pro Asp

625

630

635

640

Ala His Ser Asp Tyr Ala Arg Tyr Ser Gly Ser Tyr Asn Asp Tyr Leu

645

650

655

Arg Ala Ala Gln Met His Ser Gly Tyr Gln Arg Arg Met

660

665

<210> 47

<211> 2665

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (116)..(1855)

<400> 47

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 tgccgcgggc cacagcgagc gcagcgcgga gaccgtcagc cccgcggcgt cgagc atg 118

Met

1

gac ttc gag gac gat tac gtg cac tct act tgc agg ggt gct tac cag 166
 Asp Phe Glu Asp Asp Tyr Val His Ser Thr Cys Arg Gly Ala Tyr Gln

5

10

15

gac ttt aac gga atg gat cgt gat tat ggc cct gga tct tac gga ggg 214
 Asp Phe Asn Gly Met Asp Arg Asp Tyr Gly Pro Gly Ser Tyr Gly Gly

20

25

30

ctg gat cgt gac tat ggc cat gga tcc tat ggg ggt cag aga tcc atg 262
 Leu Asp Arg Asp Tyr Gly His Gly Ser Tyr Gly Gly Gln Arg Ser Met

35

40

45

gat tcc tac cta aac cag tcc tat ggc atg gac aat cac agt ggt ggt 310
 Asp Ser Tyr Leu Asn Gln Ser Tyr Gly Met Asp Asn His Ser Gly Gly

50

55

60

65

ggg ggt agc agg ttt gga cct tat gag tct tac gac tcc agg tct 358
 Gly Gly Gly Ser Arg Phe Gly Pro Tyr Glu Ser Tyr Asp Ser Arg Ser

70

75

80

tct ctg ggt ggg cga gat ctg tac aga tct ggc tat ggt ttt aat gaa 406
 Ser Leu Gly Gly Arg Asp Leu Tyr Arg Ser Gly Tyr Gly Phe Asn Glu

166/617

85	90	95	
ccc gaa caa acc cgc ttc gga ggt agt tat ggt ggt cga ttt gag agc			454
Pro Glu Gln Thr Arg Phe Gly Gly Ser Tyr Gly Gly Arg Phe Glu Ser			
100	105	110	
tcc tac cgg aat agc ctt gac tct ttc gga ggt aga aac cag ggc ggg			502
Ser Tyr Arg Asn Ser Leu Asp Ser Phe Gly Gly Arg Asn Gln Gly Gly			
115	120	125	
tct agc tgg gaa gca cct tac tcc cgt tca aaa ttg agg cct ggg ttt			550
Ser Ser Trp Glu Ala Pro Tyr Ser Arg Ser Lys Leu Arg Pro Gly Phe			
130	135	140	145
atg gag gac aga gga aga gag aat tac tct tcc tac agc agt ttt tct			598
Met Glu Asp Arg Gly Arg Glu Asn Tyr Ser Ser Tyr Ser Ser Phe Ser			
150	155	160	
tca ccc cat atg aag cct gca cct gta ggc tct cgg ggg aga gga acg			646
Ser Pro His Met Lys Pro Ala Pro Val Gly Ser Arg Gly Arg Gly Thr			
165	170	175	
cct gct tat cct gaa agt acg ttt gga agc aga agc tat gat gct ttt			694
Pro Ala Tyr Pro Glu Ser Thr Phe Gly Ser Arg Ser Tyr Asp Ala Phe			
180	185	190	
gga gga cca tcc aca ggc aga ggc cga ggc cga gga cat atg ggt gat			742
Gly Gly Pro Ser Thr Gly Arg Gly Arg Gly Arg Gly His Met Gly Asp			
195	200	205	
ttt gga agc ttc cat aga cct gga att att gtt gac tat caa aac aaa			790
Phe Gly Ser Phe His Arg Pro Gly Ile Ile Val Asp Tyr Gln Asn Lys			
210	215	220	225
cct gcc aat gtg acg att gct act gca aga gga ata aaa aga aaa atg			838
Pro Ala Asn Val Thr Ile Ala Thr Ala Arg Gly Ile Lys Arg Lys Met			

167/617

230	235	240	
atg caa ata ttt att aag ccc ggg gga gcc ttt atc aag aag cct aag			886
Met Gln Ile Phe Ile Lys Pro Gly Gly Ala Phe Ile Lys Lys Pro Lys			
245	250	255	
cta gcg aaa cct atg gat aag atg aac ctc agc aaa tca cct aca aaa			934
Leu Ala Lys Pro Met Asp Lys Met Asn Leu Ser Lys Ser Pro Thr Lys			
260	265	270	
act gat cct aaa aat gaa gaa gaa gaa aag cgg cga att gag gct cgg			982
Thr Asp Pro Lys Asn Glu Glu Glu Glu Lys Arg Arg Ile Glu Ala Arg			
275	280	285	
cga gag aag caa aga cgt aga cga gaa aaa aac agt gaa aaa tat gga			1030
Arg Glu Lys Gln Arg Arg Arg Arg Glu Lys Asn Ser Glu Lys Tyr Gly			
290	295	300	305
gat gga tac aga atg gca ttc aca tgt tca ttt tgt aaa ttt cga acc			1078
Asp Gly Tyr Arg Met Ala Phe Thr Cys Ser Phe Cys Lys Phe Arg Thr			
310	315	320	
ttt gaa gaa aaa gat att gaa ctg cat ctg gaa agt tct tct cac cag			1126
Phe Glu Glu Lys Asp Ile Glu Leu His Leu Glu Ser Ser Ser His Gln			
325	330	335	
gaa aca tta gat cat att cag aaa caa acc aaa ttt gat aaa gta gtt			1174
Glu Thr Leu Asp His Ile Gln Lys Gln Thr Lys Phe Asp Lys Val Val			
340	345	350	
atg gag ttt tta cat gaa tgt atg gtg aat aaa ttt aaa aaa gca tct			1222
Met Glu Phe Leu His Glu Cys Met Val Asn Lys Phe Lys Lys Ala Ser			
355	360	365	
att cgt aag caa cag aca ctt aat cac cca gaa gct tac aaa ata att			1270
Ile Arg Lys Gln Gln Thr Leu Asn His Pro Glu Ala Tyr Lys Ile Ile			

370	375	380	385	
gaa aaa gat att atg gaa ggt gtt act gca gat gat cac atg atg aaa				1318
Glu Lys Asp Ile Met Glu Gly Val Thr Ala Asp Asp His Met Met Lys				
390	395	400		
gtg gag act gtt cac tgt agt gct tgt agc gtg tac atc cct gct tta				1366
Val Glu Thr Val His Cys Ser Ala Cys Ser Val Tyr Ile Pro Ala Leu				
405	410	415		
cac agc tca gtt cag ctg cac cta aag tct cct gac cac agc aaa ggg				1414
His Ser Ser Val Gln Leu His Leu Lys Ser Pro Asp His Ser Lys Gly				
420	425	430		
aag cag gct tat aag gaa cag ata aag agg gaa agt gtg ctg act gcc				1462
Lys Gln Ala Tyr Lys Glu Gln Ile Lys Arg Glu Ser Val Leu Thr Ala				
435	440	445		
aca agc atc tta aac aac ccg atc gtg aag gca cgg tat gag cgc ttt				1510
Thr Ser Ile Leu Asn Asn Pro Ile Val Lys Ala Arg Tyr Glu Arg Phe				
450	455	460	465	
gtt aag gga gag aat cct ttt gaa att caa gat cac cct cag gat cag				1558
Val Lys Gly Glu Asn Pro Phe Glu Ile Gln Asp His Pro Gln Asp Gln				
470	475	480		
cag ata gaa gga gat gaa gag gac gaa gag aag att ggt gaa ccc atc				1606
Gln Ile Glu Gly Asp Glu Glu Asp Glu Glu Lys Ile Gly Glu Pro Ile				
485	490	495		
gag gaa gag gaa gag gag gag gag gaa gag gag gag gaa ggg gag gaa				1654
Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Gly Glu Glu				
500	505	510		
gct gga tct gtg gag gaa gaa ggg gat gtg gag gga gag gag ggc aca				1702
Ala Gly Ser Val Glu Glu Glu Gly Asp Val Glu Gly Glu Glu Gly Thr				

515	520	525	
gca gaa gcc gca gca gca ggg gaa gct gac gca gtg gga gag gca gag			1750
Ala Glu Ala Ala Ala Ala Gly Glu Ala Asp Ala Val Gly Glu Ala Glu			
530	535	540	545
gga gca ggg gag gca gag gag gcg gag gag gag gag gaa gag gag gga			1798
Gly Ala Gly Glu Ala Glu Glu Ala Glu Glu Glu Glu Glu Glu Glu Gly			
550	555	560	
acc cag gag ttt gct gcc cag gcc tgt gct act gag cag tgc gag cac			1846
Thr Gln Glu Phe Ala Ala Gln Ala Cys Ala Thr Glu Gln Cys Glu His			
565	570	575	
agg cag atg taggcgccac acttcacagg ggccttactg gctgctaccg			1895
Arg Gln Met			
580			
tagagaatgg aagatgctga gtagcttatg atatgagttg acaccatggt gcatgcattc			1955
cacatattaa agcttgtttt atatcatttc taaatgtttg gcacttgttt aataaaatga			2015
agttaagatg atttcagttt agtttttata gataccaaat ttagatatga taaattgttt			2075
gtatggtttt taagcttagt ttttattacc ttattggtgt tcaggattct aggtgtgtgt			2135
tgctcctctg cccgttgtaa tcatttgaac ttaaaatgct gctcttgga gtgaaccttt			2195
aagtgtgcat tcagtttttg agtacttact ctagattgat tggacaagta ttctgtcctg			2255
atttagtat ttcttttttt acattgaata gcagttagca ttaagatggc ttaaaggatt			2315
ttgtgtacag ttccctttgt agcaataaaa tgttttcttt ctttttttta aaaaagaact			2375
tttcctttg attgcaattt aaacatttca tcaattaaat gagtatttaa aaatcaatat			2435
ctgccttaat gtataagttt agctcacaag tatttcaagt gattgagaag acttgaatta			2495
aaacattttt cctcagtcatt atttttaaaa agtgtgacta ctgtatatatt tctaacacat			2555
ttcagaggtc agtctgtaac tgatcttggt tatactagct ttagtttggt cttttctctg			2615
tgccatgtc aaaccttgga atcttctga aaatacaatt taatacaaat			2665

<210> 48

<211> 580

<212> PRT

<213> Mus musculus

<400> 48

Met Asp Phe Glu Asp Asp Tyr Val His Ser Thr Cys Arg Gly Ala Tyr
1 5 10 15
Gln Asp Phe Asn Gly Met Asp Arg Asp Tyr Gly Pro Gly Ser Tyr Gly
20 25 30
Gly Leu Asp Arg Asp Tyr Gly His Gly Ser Tyr Gly Gly Gln Arg Ser
35 40 45
Met Asp Ser Tyr Leu Asn Gln Ser Tyr Gly Met Asp Asn His Ser Gly
50 55 60
Gly Gly Gly Gly Ser Arg Phe Gly Pro Tyr Glu Ser Tyr Asp Ser Arg
65 70 75 80
Ser Ser Leu Gly Gly Arg Asp Leu Tyr Arg Ser Gly Tyr Gly Phe Asn
85 90 95
Glu Pro Glu Gln Thr Arg Phe Gly Gly Ser Tyr Gly Gly Arg Phe Glu
100 105 110
Ser Ser Tyr Arg Asn Ser Leu Asp Ser Phe Gly Gly Arg Asn Gln Gly
115 120 125
Gly Ser Ser Trp Glu Ala Pro Tyr Ser Arg Ser Lys Leu Arg Pro Gly
130 135 140
Phe Met Glu Asp Arg Gly Arg Glu Asn Tyr Ser Ser Tyr Ser Ser Phe
145 150 155 160
Ser Ser Pro His Met Lys Pro Ala Pro Val Gly Ser Arg Gly Arg Gly
165 170 175

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Thr Pro Ala Tyr Pro Glu Ser Thr Phe Gly Ser Arg Ser Tyr Asp Ala
180 185 190
Phe Gly Gly Pro Ser Thr Gly Arg Gly Arg Gly Arg Gly His Met Gly
195 200 205
Asp Phe Gly Ser Phe His Arg Pro Gly Ile Ile Val Asp Tyr Gln Asn
210 215 220
Lys Pro Ala Asn Val Thr Ile Ala Thr Ala Arg Gly Ile Lys Arg Lys
225 230 235 240
Met Met Gln Ile Phe Ile Lys Pro Gly Gly Ala Phe Ile Lys Lys Pro
245 250 255
Lys Leu Ala Lys Pro Met Asp Lys Met Asn Leu Ser Lys Ser Pro Thr
260 265 270
Lys Thr Asp Pro Lys Asn Glu Glu Glu Glu Lys Arg Arg Ile Glu Ala
275 280 285
Arg Arg Glu Lys Gln Arg Arg Arg Arg Glu Lys Asn Ser Glu Lys Tyr
290 295 300
Gly Asp Gly Tyr Arg Met Ala Phe Thr Cys Ser Phe Cys Lys Phe Arg
305 310 315 320
Thr Phe Glu Glu Lys Asp Ile Glu Leu His Leu Glu Ser Ser Ser His
325 330 335
Gln Glu Thr Leu Asp His Ile Gln Lys Gln Thr Lys Phe Asp Lys Val
340 345 350
Val Met Glu Phe Leu His Glu Cys Met Val Asn Lys Phe Lys Lys Ala
355 360 365
Ser Ile Arg Lys Gln Gln Thr Leu Asn His Pro Glu Ala Tyr Lys Ile
370 375 380
Ile Glu Lys Asp Ile Met Glu Gly Val Thr Ala Asp Asp His Met Met

385 390 395 400
Lys Val Glu Thr Val His Cys Ser Ala Cys Ser Val Tyr Ile Pro Ala
 405 410 415
Leu His Ser Ser Val Gln Leu His Leu Lys Ser Pro Asp His Ser Lys
 420 425 430
Gly Lys Gln Ala Tyr Lys Glu Gln Ile Lys Arg Glu Ser Val Leu Thr
 435 440 445
Ala Thr Ser Ile Leu Asn Asn Pro Ile Val Lys Ala Arg Tyr Glu Arg
 450 455 460
Phe Val Lys Gly Glu Asn Pro Phe Glu Ile Gln Asp His Pro Gln Asp
465 470 475 480
Gln Gln Ile Glu Gly Asp Glu Glu Asp Glu Glu Lys Ile Gly Glu Pro
 485 490 495
Ile Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu
 500 505 510
Glu Ala Gly Ser Val Glu Glu Glu Gly Asp Val Glu Gly Glu Glu Gly
 515 520 525
Thr Ala Glu Ala Ala Ala Ala Gly Glu Ala Asp Ala Val Gly Glu Ala
 530 535 540
Glu Gly Ala Gly Glu Ala Glu Glu Ala Glu Glu Glu Glu Glu Glu
545 550 555 560
Gly Thr Gln Glu Phe Ala Ala Gln Ala Cys Ala Thr Glu Gln Cys Glu
 565 570 575
His Arg Gln Met
 580

<210> 49

173/617

<211> 2706

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (122).. (1867)

<400> 49

gctggttagcg cgccgctctc ggtcgcgagg agtgatcgtg tggaatcgcg ggtcgcggac 60

gctcgcggcc ggccatagct cagcctagcg ccgccaaggc cgacggccct cagcctctgc 120

c atg gac ttc gag gac gat tac aca cac tcc gcc tgc agg aat act tat 169

Met Asp Phe Glu Asp Asp Tyr Thr His Ser Ala Cys Arg Asn Thr Tyr

1 5 10 15

cag ggc ttt aat gga atg gat cgt gat tat ggc cct gga tct tat gga 217

Gln Gly Phe Asn Gly Met Asp Arg Asp Tyr Gly Pro Gly Ser Tyr Gly

20 25 30

ggg atg gat cgt gac tat ggc cat gga tcc tat ggg ggt cag aga tcc 265

Gly Met Asp Arg Asp Tyr Gly His Gly Ser Tyr Gly Gly Gln Arg Ser

35 40 45

atg gat tcc tac cta aac cag tca tat ggc atg gac aat cac agt ggt 313

Met Asp Ser Tyr Leu Asn Gln Ser Tyr Gly Met Asp Asn His Ser Gly

50 55 60

ggt ggt ggg ggt agc agg ttt gga cct tat gag tct tac gac tcc agg 361

Gly Gly Gly Gly Ser Arg Phe Gly Pro Tyr Glu Ser Tyr Asp Ser Arg

65 70 75 80

tct tct ctg ggt ggg cga gat ctg tac aga tct ggc tat ggt ttt aat 409

Ser Ser Leu Gly Gly Arg Asp Leu Tyr Arg Ser Gly Tyr Gly Phe Asn

85 90 95

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gaa ccc gaa caa agc cgc ttc gga ggt agt tat ggt ggt cga ttt gag 457
 Glu Pro Glu Gln Ser Arg Phe Gly Gly Ser Tyr Gly Gly Arg Phe Glu
 100 105 110
 agc tcc tac cgg aat agc ctt gac tct ttc gga ggt aga aac cag ggc 505
 Ser Ser Tyr Arg Asn Ser Leu Asp Ser Phe Gly Gly Arg Asn Gln Gly
 115 120 125
 ggg tct agc tgg gaa gca cct tac tcc cgt tca aaa ttg agg cct ggg 553
 Gly Ser Ser Trp Glu Ala Pro Tyr Ser Arg Ser Lys Leu Arg Pro Gly
 130 135 140
 ttt atg gag gac aga gga aga gag aat tac tct tcc tac agc agt ttt 601
 Phe Met Glu Asp Arg Gly Arg Glu Asn Tyr Ser Ser Tyr Ser Ser Phe
 145 150 155 160
 tct tca ccc cat atg aag cct gca cct gta ggc tct cgg ggg aga gga 649
 Ser Ser Pro His Met Lys Pro Ala Pro Val Gly Ser Arg Gly Arg Gly
 165 170 175
 acg cct gct tat cct gaa agt acg ttt gga agc aga aac tat gat gct 697
 Thr Pro Ala Tyr Pro Glu Ser Thr Phe Gly Ser Arg Asn Tyr Asp Ala
 180 185 190
 ttt gga gga cca tca aca ggc aga ggc cga ggc cga gga cat atg ggt 745
 Phe Gly Gly Pro Ser Thr Gly Arg Gly Arg Gly Arg Gly His Met Gly
 195 200 205
 gat ttt gga agc att cat aga ccc gga att gtt gtt gac tat caa aac 793
 Asp Phe Gly Ser Ile His Arg Pro Gly Ile Val Val Asp Tyr Gln Asn
 210 215 220
 aaa tcc acc aat gtg aca gtt gct gct gca aga gga ata aag aga aaa 841
 Lys Ser Thr Asn Val Thr Val Ala Ala Ala Arg Gly Ile Lys Arg Lys
 225 230 235 240

atg atg cag cca ttt aat aag ccc agt gga acc ttt atc aag aaa ccc 889
Met Met Gln Pro Phe Asn Lys Pro Ser Gly Thr Phe Ile Lys Lys Pro
245 250 255

aaa cta gca aaa cct atg gag aag ata agc ctc agc aaa tca ccc aca 937
Lys Leu Ala Lys Pro Met Glu Lys Ile Ser Leu Ser Lys Ser Pro Thr
260 265 270

aaa act gat cct aaa aat gaa gag gaa gaa aag cgg cga att gag gct 985
Lys Thr Asp Pro Lys Asn Glu Glu Glu Glu Lys Arg Arg Ile Glu Ala
275 280 285

cgg cga gag aaa caa agg cgc aga aga gaa aaa aac agt gag aaa tac 1033
Arg Arg Glu Lys Gln Arg Arg Arg Arg Glu Lys Asn Ser Glu Lys Tyr
290 295 300

gga gat gga tac aga atg gca ttt aca tgt tca ttt tgt aaa ttt cga 1081
Gly Asp Gly Tyr Arg Met Ala Phe Thr Cys Ser Phe Cys Lys Phe Arg
305 310 315 320

aca ttt gaa gaa aaa gat att gaa ctg cat ctg gaa agt tct tca cat 1129
Thr Phe Glu Glu Lys Asp Ile Glu Leu His Leu Glu Ser Ser Ser His
325 330 335

cag gaa aca tta gat cat ata cag aaa caa act aaa ttt gat aaa gta 1177
Gln Glu Thr Leu Asp His Ile Gln Lys Gln Thr Lys Phe Asp Lys Val
340 345 350

gtt atg gag ttt ttg cat gag tgt atg gtg aat aaa ttc aag aaa aca 1225
Val Met Glu Phe Leu His Glu Cys Met Val Asn Lys Phe Lys Lys Thr
355 360 365

tct att cgt aag caa cag aca aat aat caa aca gaa gta gtt aaa ata 1273
Ser Ile Arg Lys Gln Gln Thr Asn Asn Gln Thr Glu Val Val Lys Ile
370 375 380

att gaa aaa gat gtt atg gaa ggt gtt act gta gat gat cac atg atg 1321
 Ile Glu Lys Asp Val Met Glu Gly Val Thr Val Asp Asp His Met Met
 385 390 395 400
 aag gta gag aca gtt cat tgc agc gct tgc agt gtt tat atc cct gct 1369
 Lys Val Glu Thr Val His Cys Ser Ala Cys Ser Val Tyr Ile Pro Ala
 405 410 415
 tta cat agt tca gtt cag cag cac tta aaa tct cct gat cat atc aaa 1417
 Leu His Ser Ser Val Gln Gln His Leu Lys Ser Pro Asp His Ile Lys
 420 425 430
 ggg aag cag gct tat aag gaa caa ata aaa aga gag agt gtc ttg act 1465
 Gly Lys Gln Ala Tyr Lys Glu Gln Ile Lys Arg Glu Ser Val Leu Thr
 435 440 445
 gct aca agc att tta aat aat cca ata gtg aag gcg cga tat gaa cgt 1513
 Ala Thr Ser Ile Leu Asn Asn Pro Ile Val Lys Ala Arg Tyr Glu Arg
 450 455 460
 ttt gtt aag ggt gag aat cct ttt gaa att caa gac cat tct cag gat 1561
 Phe Val Lys Gly Glu Asn Pro Phe Glu Ile Gln Asp His Ser Gln Asp
 465 470 475 480
 cag caa ata gaa gga gat gag gag gat gaa gag aag att gat gaa cct 1609
 Gln Gln Ile Glu Gly Asp Glu Glu Asp Glu Glu Lys Ile Asp Glu Pro
 485 490 495
 att gaa gaa gag gag gat gaa gat gag gaa gaa gaa gca gag gaa gtg 1657
 Ile Glu Glu Glu Glu Asp Glu Asp Glu Glu Glu Glu Ala Glu Glu Val
 500 505 510
 ggg gaa gta gag gaa gtg gaa gaa gta gag gaa gtg aga gaa gga gga 1705
 Gly Glu Val Glu Glu Val Glu Glu Val Glu Glu Val Arg Glu Gly Gly
 515 520 525

ata gag ggc gag gga aat ata cag gga gta ggg gaa gga ggg gaa gta 1753
 Ile Glu Gly Glu Gly Asn Ile Gln Gly Val Gly Glu Gly Gly Glu Val
 530 535 540
 ggg gta gtg gga gaa gta gag gga gtg ggg gaa gta gag gaa gta gag 1801
 Gly Val Val Gly Glu Val Glu Gly Val Gly Glu Val Glu Glu Val Glu
 545 550 555 560
 gaa tta gag gaa gag aca gca aag gaa gaa cct gct gac ttc cct gtt 1849
 Glu Leu Glu Glu Glu Thr Ala Lys Glu Glu Pro Ala Asp Phe Pro Val
 565 570 575
 gag caa cct gaa gaa aat taaatataag gtattagatt taaaaggagc 1897
 Glu Gln Pro Glu Glu Asn
 580
 ttacatttc ggttctaag taaaaaagg taagaaattt aatagcttaa aatatgaatt 1957
 aacacccatg ttgcatgcat tccacatatt aaaatttggt ttatataatt tctaaatgtt 2017
 taacatttgt ttaataaaat gaaggcaaaa ctattttagt ttagttttta tagctaccag 2077
 acttagatcc gataaattgt ttgtataatt ttaagctta atttttatta ctttattggt 2137
 gttaaggata acaaattgtg attgttagta tatctattct aatcatttta tcttaaatgc 2197
 tgctcttggg agtgaatatt caagtgtgca tcaatttttt gaatacttac cctggaagat 2257
 ataaactggg caagtatttt gtgctctgtg tattttttta ctgcattaga cattgaatag 2317
 taatttgcgt taagatacgc ttaaaggctc ttgtgacca tgtttccctt tgtagcaata 2377
 aatgttttt tacgaaaact ttctccctgg attagcagtt taaatgaaac agagttcatc 2437
 aatgaaatga gtattttaaaa taaaatttg ccttaatgta tcagttcagc tcacaagtat 2497
 ttaaatga ttgagaagac ttgaattaaa gaaaaaaaaa ttctcaatca tatttttaaa 2557
 atataagact aaaattgttt ttaaaacaca ttcaaataag aagtgaagtt gaactgacct 2617
 tatttatact ctttttaagt ttgttccttt tccctgtgcc tgtgtcaaata cttcaagtct 2677
 tgctgaaaat acatttgata caaagtttt 2706

<210> 50

<211> 582

<212> PRT

<213> Homo sapiens

<400> 50

Met Asp Phe Glu Asp Asp Tyr Thr His Ser Ala Cys Arg Asn Thr Tyr

1 5 10 15

Gln Gly Phe Asn Gly Met Asp Arg Asp Tyr Gly Pro Gly Ser Tyr Gly

20 25 30

Gly Met Asp Arg Asp Tyr Gly His Gly Ser Tyr Gly Gly Gln Arg Ser

35 40 45

Met Asp Ser Tyr Leu Asn Gln Ser Tyr Gly Met Asp Asn His Ser Gly

50 55 60

Gly Gly Gly Gly Ser Arg Phe Gly Pro Tyr Glu Ser Tyr Asp Ser Arg

65 70 75 80

Ser Ser Leu Gly Gly Arg Asp Leu Tyr Arg Ser Gly Tyr Gly Phe Asn

85 90 95

Glu Pro Glu Gln Ser Arg Phe Gly Gly Ser Tyr Gly Gly Arg Phe Glu

100 105 110

Ser Ser Tyr Arg Asn Ser Leu Asp Ser Phe Gly Gly Arg Asn Gln Gly

115 120 125

Gly Ser Ser Trp Glu Ala Pro Tyr Ser Arg Ser Lys Leu Arg Pro Gly

130 135 140

Phe Met Glu Asp Arg Gly Arg Glu Asn Tyr Ser Ser Tyr Ser Ser Phe

145 150 155 160

Ser Ser Pro His Met Lys Pro Ala Pro Val Gly Ser Arg Gly Arg Gly

165 170 175

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Thr Pro Ala Tyr Pro Glu Ser Thr Phe Gly Ser Arg Asn Tyr Asp Ala
180 185 190

Phe Gly Gly Pro Ser Thr Gly Arg Gly Arg Gly Arg Gly His Met Gly
195 200 205

Asp Phe Gly Ser Ile His Arg Pro Gly Ile Val Val Asp Tyr Gln Asn
210 215 220

Lys Ser Thr Asn Val Thr Val Ala Ala Ala Arg Gly Ile Lys Arg Lys
225 230 235 240

Met Met Gln Pro Phe Asn Lys Pro Ser Gly Thr Phe Ile Lys Lys Pro
245 250 255

Lys Leu Ala Lys Pro Met Glu Lys Ile Ser Leu Ser Lys Ser Pro Thr
260 265 270

Lys Thr Asp Pro Lys Asn Glu Glu Glu Glu Lys Arg Arg Ile Glu Ala
275 280 285

Arg Arg Glu Lys Gln Arg Arg Arg Arg Glu Lys Asn Ser Glu Lys Tyr
290 295 300

Gly Asp Gly Tyr Arg Met Ala Phe Thr Cys Ser Phe Cys Lys Phe Arg
305 310 315 320

Thr Phe Glu Glu Lys Asp Ile Glu Leu His Leu Glu Ser Ser Ser His
325 330 335

Gln Glu Thr Leu Asp His Ile Gln Lys Gln Thr Lys Phe Asp Lys Val
340 345 350

Val Met Glu Phe Leu His Glu Cys Met Val Asn Lys Phe Lys Lys Thr
355 360 365

Ser Ile Arg Lys Gln Gln Thr Asn Asn Gln Thr Glu Val Val Lys Ile
370 375 380

Ile Glu Lys Asp Val Met Glu Gly Val Thr Val Asp Asp His Met Met

385 390 395 400
Lys Val Glu Thr Val His Cys Ser Ala Cys Ser Val Tyr Ile Pro Ala
 405 410 415
Leu His Ser Ser Val Gln Gln His Leu Lys Ser Pro Asp His Ile Lys
 420 425 430
Gly Lys Gln Ala Tyr Lys Glu Gln Ile Lys Arg Glu Ser Val Leu Thr
 435 440 445
Ala Thr Ser Ile Leu Asn Asn Pro Ile Val Lys Ala Arg Tyr Glu Arg
 450 455 460
Phe Val Lys Gly Glu Asn Pro Phe Glu Ile Gln Asp His Ser Gln Asp
465 470 475 480
Gln Gln Ile Glu Gly Asp Glu Glu Asp Glu Glu Lys Ile Asp Glu Pro
 485 490 495
Ile Glu Glu Glu Glu Asp Glu Asp Glu Glu Glu Glu Ala Glu Glu Val
 500 505 510
Gly Glu Val Glu Glu Val Glu Glu Val Glu Glu Val Arg Glu Gly Gly
 515 520 525
Ile Glu Gly Glu Gly Asn Ile Gln Gly Val Gly Glu Gly Gly Glu Val
 530 535 540
Gly Val Val Gly Glu Val Glu Gly Val Gly Glu Val Glu Glu Val Glu
545 550 555 560
Glu Leu Glu Glu Glu Thr Ala Lys Glu Glu Pro Ala Asp Phe Pro Val
 565 570 575
Glu Gln Pro Glu Glu Asn
 580

<210> 51

<211> 3493

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (178).. (2706)

<400> 51

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gcctgaagcc caagagagtg gagcctcgcg aagtgaggaa cctggcaciaa ggtggaggcc 120
tgaattttga tctatgttct acctacatcc agctggctga aagtacttga ggatcac 177
atg acc ctg gac atg gat gct gtt ctg tca gat ttt gtc cgt tcc aca 225
Met Thr Leu Asp Met Asp Ala Val Leu Ser Asp Phe Val Arg Ser Thr
      1             5             10             15
gga gca gag cca ggg cta gcg cga gat ctc cta gaa gga aag aat tgg 273
Gly Ala Glu Pro Gly Leu Ala Arg Asp Leu Leu Glu Gly Lys Asn Trp
              20             25             30
gat gtg aat gcc gcc ctc agt gat ttt gaa cag cta cgt caa gtc cat 321
Asp Val Asn Ala Ala Leu Ser Asp Phe Glu Gln Leu Arg Gln Val His
              35             40             45
gct gga aac cta ccc cca tcc ttt agt gag ggg agt ggt ggc tcc agg 369
Ala Gly Asn Leu Pro Pro Ser Phe Ser Glu Gly Ser Gly Gly Ser Arg
              50             55             60
acc cct gaa aaa ggg ttt tct gac aga gag cct act cgc ccc ccc cga 417
Thr Pro Glu Lys Gly Phe Ser Asp Arg Glu Pro Thr Arg Pro Pro Arg
              65             70             75             80
ccc atc ctc cag cgg cag gat gac atc gtt caa gaa aaa cgc ctg tct 465
Pro Ile Leu Gln Arg Gln Asp Asp Ile Val Gln Glu Lys Arg Leu Ser

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182/617

85	90	95	
agg ggc atc tcc cac gcc agc tcc agc att gtt tcc ctg gcc cgg tcc			513
Arg Gly Ile Ser His Ala Ser Ser Ser Ile Val Ser Leu Ala Arg Ser			
100	105	110	
cat gtc tcc tcc aat ggt ggg ggt ggg ggg agc aat gag cac ccc ctg			561
His Val Ser Ser Asn Gly Gly Gly Gly Gly Ser Asn Glu His Pro Leu			
115	120	125	
gaa atg ccc atc tgt gcc ttc cag ctt cca gat ctc act gta tac aat			609
Glu Met Pro Ile Cys Ala Phe Gln Leu Pro Asp Leu Thr Val Tyr Asn			
130	135	140	
gaa gac ttc cgc agc ttc ata gag aga gac ctc att gag cag tcc atg			657
Glu Asp Phe Arg Ser Phe Ile Glu Arg Asp Leu Ile Glu Gln Ser Met			
145	150	155	160
ctg gtt gcc ttg gaa cag gca ggg cgt ttg aac tgg tgg gtg agt gtg			705
Leu Val Ala Leu Glu Gln Ala Gly Arg Leu Asn Trp Trp Val Ser Val			
165	170	175	
gat ccc acc tct cag agg ctg ctt cct ttg gca act act gga gat ggg			753
Asp Pro Thr Ser Gln Arg Leu Leu Pro Leu Ala Thr Thr Gly Asp Gly			
180	185	190	
aac tgc ctc ctg cat gca gcc tcc ctt gga atg tgg ggt ttc cat gat			801
Asn Cys Leu Leu His Ala Ala Ser Leu Gly Met Trp Gly Phe His Asp			
195	200	205	
cgg gac ttg atg ctg cgg aaa gct ttg tat gca ctg atg gag aag gga			849
Arg Asp Leu Met Leu Arg Lys Ala Leu Tyr Ala Leu Met Glu Lys Gly			
210	215	220	
gtt gag aag gaa gcg ttg aaa agg cgc tgg agg tgg cag cag aca cag			897
Val Glu Lys Glu Ala Leu Lys Arg Arg Trp Arg Trp Gln Gln Thr Gln			

225	230	235	240	
cag aat aaa gag tca ggg ctg gta tac aca gaa gat gaa tgg cag aag	945			
Gln Asn Lys Glu Ser Gly Leu Val Tyr Thr Glu Asp Glu Trp Gln Lys				
245	250	255		
gag tgg aat gaa ctg atc aag ctt gcc tca agt gaa ccc cga atg cat	993			
Glu Trp Asn Glu Leu Ile Lys Leu Ala Ser Ser Glu Pro Arg Met His				
260	265	270		
cta ggt acc aat gga gcc aac tgt ggt ggg gtg gag agt tct gag gag	1041			
Leu Gly Thr Asn Gly Ala Asn Cys Gly Gly Val Glu Ser Ser Glu Glu				
275	280	285		
cct gta tat gag agc ctt gaa gag ttt cac gtc ttt gtc ctt gct cat	1089			
Pro Val Tyr Glu Ser Leu Glu Glu Phe His Val Phe Val Leu Ala His				
290	295	300		
gtg ctt agg agg ccc ata gtc gtc gtg gca gac acc atg ctg agg gac	1137			
Val Leu Arg Arg Pro Ile Val Val Val Ala Asp Thr Met Leu Arg Asp				
305	310	315	320	
tcc gga ggg gaa gca ttt gcc cct att ccc ttt gga gga atc tat ctg	1185			
Ser Gly Gly Glu Ala Phe Ala Pro Ile Pro Phe Gly Gly Ile Tyr Leu				
325	330	335		
cct ttg gag gtc cca gcc agc cag tgt cac cgc tcc cct ctg gtg ctc	1233			
Pro Leu Glu Val Pro Ala Ser Gln Cys His Arg Ser Pro Leu Val Leu				
340	345	350		
gcc tat gat cag gcc cac ttt tct gca ctc gtg tcc atg gag cag aag	1281			
Ala Tyr Asp Gln Ala His Phe Ser Ala Leu Val Ser Met Glu Gln Lys				
355	360	365		
gag aat acc aag gaa caa gct gtg atc cca ctt aca gat tca gag tat	1329			
Glu Asn Thr Lys Glu Gln Ala Val Ile Pro Leu Thr Asp Ser Glu Tyr				

370	375	380	
aag ctg ctg ccc ttg cac ttt gct gtg gac cct gga aag ggc tgg gag	1377		
Lys Leu Leu Pro Leu His Phe Ala Val Asp Pro Gly Lys Gly Trp Glu			
385	390	395	400
tgg ggc aaa gat gat agt gac aat gtc cga ttg gcc agt gta att ctg	1425		
Trp Gly Lys Asp Asp Ser Asp Asn Val Arg Leu Ala Ser Val Ile Leu			
405	410	415	
tcc cta gag gtc aaa ttg cat ctg ctg cat agc tac atg aat gtg aag	1473		
Ser Leu Glu Val Lys Leu His Leu Leu His Ser Tyr Met Asn Val Lys			
420	425	430	
tgg atc cca ctg tcc tct gat gca cag gct cct ctg gcc cag cct gag	1521		
Trp Ile Pro Leu Ser Ser Asp Ala Gln Ala Pro Leu Ala Gln Pro Glu			
435	440	445	
tcc ccc acc gcc tca gct gga gat gag ccc cgg tcc act cct gag tct	1569		
Ser Pro Thr Ala Ser Ala Gly Asp Glu Pro Arg Ser Thr Pro Glu Ser			
450	455	460	
gga gac tca gac aag gag tca gtt ggc agc agt tcc acc agc aac gag	1617		
Gly Asp Ser Asp Lys Glu Ser Val Gly Ser Ser Ser Thr Ser Asn Glu			
465	470	475	480
ggc ggc cgg cgg aag gag aag tca aag cga gat cgg gag aag gac aag	1665		
Gly Gly Arg Arg Lys Glu Lys Ser Lys Arg Asp Arg Glu Lys Asp Lys			
485	490	495	
aag aga gca gat tct gtg gct aac aaa ctg ggc agc ttt ggc aaa acc	1713		
Lys Arg Ala Asp Ser Val Ala Asn Lys Leu Gly Ser Phe Gly Lys Thr			
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ttg ggc agc aag ctc aag aag aac atg ggg ggc ctg atg cac agc aag	1761		
Leu Gly Ser Lys Leu Lys Lys Asn Met Gly Gly Leu Met His Ser Lys			

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515	520	525	
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Gly Ser Lys Pro Gly Gly Val Gly Thr Gly Leu Gly Gly Ser Ser Gly			
530	535	540	
act gag aca ctg gag aag aag aag aaa aac tca ctg aag agc tgg aag	1857		
Thr Glu Thr Leu Glu Lys Lys Lys Lys Asn Ser Leu Lys Ser Trp Lys			
545	550	555	560
ggt ggc aag gag gag gca gct ggg gat ggg cct gtg tct gag aag ccc	1905		
Gly Gly Lys Glu Glu Ala Ala Gly Asp Gly Pro Val Ser Glu Lys Pro			
565	570	575	
cca gct gag tct gtt ggt aac gga ggg agc aag tat agc cag gag gtg	1953		
Pro Ala Glu Ser Val Gly Asn Gly Gly Ser Lys Tyr Ser Gln Glu Val			
580	585	590	
atg cag agc ctg agc att ctg agg act gcc atg caa ggg gag ggg aag	2001		
Met Gln Ser Leu Ser Ile Leu Arg Thr Ala Met Gln Gly Glu Gly Lys			
595	600	605	
ttt att ttt gtt gga acc ctg aag atg ggt cac cgt cac cag tat cag	2049		
Phe Ile Phe Val Gly Thr Leu Lys Met Gly His Arg His Gln Tyr Gln			
610	615	620	
gag gaa atg atc cag cgc tac ctt tct gat gct gag gag aga ttc ctg	2097		
Glu Glu Met Ile Gln Arg Tyr Leu Ser Asp Ala Glu Glu Arg Phe Leu			
625	630	635	640
gca gaa cag aag cag aag gag gca gag agg aag atc atg aat gga gga	2145		
Ala Glu Gln Lys Gln Lys Glu Ala Glu Arg Lys Ile Met Asn Gly Gly			
645	650	655	
ata ggg ggt ggc cct cct cca gcc aaa aag cca gag cca gat gct agg	2193		
Ile Gly Gly Gly Pro Pro Pro Ala Lys Lys Pro Glu Pro Asp Ala Arg			

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gaa gag cag ccg acc ggt ccc cca gca gag tcc agg gca atg gca ttt			2241
Glu Glu Gln Pro Thr Gly Pro Pro Ala Glu Ser Arg Ala Met Ala Phe			
675	680	685	
tcc act ggc tac cct ggg gac ttt act atc cct cgg ccg tct ggg ggc			2289
Ser Thr Gly Tyr Pro Gly Asp Phe Thr Ile Pro Arg Pro Ser Gly Gly			
690	695	700	
gga gtc cac tgc cag gaa ccc cgg agg cag ttg gca ggg ggt cca tgt			2337
Gly Val His Cys Gln Glu Pro Arg Arg Gln Leu Ala Gly Gly Pro Cys			
705	710	715	720
gtc ggg ggc cta cca cca tat gcc acc ttc ccc aga cag tgc cct cct			2385
Val Gly Gly Leu Pro Pro Tyr Ala Thr Phe Pro Arg Gln Cys Pro Pro			
725	730	735	
ggg cga ccc tac ccc cac cag gac agc atc cct tct ctg gag cca ggc			2433
Gly Arg Pro Tyr Pro His Gln Asp Ser Ile Pro Ser Leu Glu Pro Gly			
740	745	750	
agc cac tct aag gat gga ctt cac agg ggt gcc ttg tta cca ccc ccc			2481
Ser His Ser Lys Asp Gly Leu His Arg Gly Ala Leu Leu Pro Pro Pro			
755	760	765	
tac cga gtg gct gat tcc tat agc aat ggc tac aga gag ccc cct gag			2529
Tyr Arg Val Ala Asp Ser Tyr Ser Asn Gly Tyr Arg Glu Pro Pro Glu			
770	775	780	
cca gat gga tgg gct gga ggt ctc cgg ggc ctt ccc cca act cag acc			2577
Pro Asp Gly Trp Ala Gly Gly Leu Arg Gly Leu Pro Pro Thr Gln Thr			
785	790	795	800
aaa tgc aaa caa ccg aac tgc agc ttc tat gga cac cct ggg aca aac			2625
Lys Cys Lys Gln Pro Asn Cys Ser Phe Tyr Gly His Pro Gly Thr Asn			

805	810	815	
aac ttc tgt tcc tgt tgt tac agg gaa gaa ctg agg agg agg gag cgg			2673
Asn Phe Cys Ser Cys Cys Tyr Arg Glu Glu Leu Arg Arg Arg Glu Arg			
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gaa ccg gat ggg gag ctc ctg gtg cac agg ttc tgaacgggtg gaacactgaa			2726
Glu Pro Asp Gly Glu Leu Leu Val His Arg Phe			
835	840		
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tgcacacagg agtgctgccg ggctggcaag agcaggtcgg ggctggatgg cacctcaggg			2906
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atgtcatctg ttacagtttg agaagagatt gctgattacc ccctgtcttt tcctcatcta			3446
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<211> 843

<212> PRT

<213> Homo sapiens

<400> 52

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35 40 45
Ala Gly Asn Leu Pro Pro Ser Phe Ser Glu Gly Ser Gly Gly Ser Arg
50 55 60
Thr Pro Glu Lys Gly Phe Ser Asp Arg Glu Pro Thr Arg Pro Pro Arg
65 70 75 80
Pro Ile Leu Gln Arg Gln Asp Asp Ile Val Gln Glu Lys Arg Leu Ser
85 90 95
Arg Gly Ile Ser His Ala Ser Ser Ser Ile Val Ser Leu Ala Arg Ser
100 105 110
His Val Ser Ser Asn Gly Gly Gly Gly Ser Asn Glu His Pro Leu
115 120 125
Glu Met Pro Ile Cys Ala Phe Gln Leu Pro Asp Leu Thr Val Tyr Asn
130 135 140
Glu Asp Phe Arg Ser Phe Ile Glu Arg Asp Leu Ile Glu Gln Ser Met
145 150 155 160
Leu Val Ala Leu Glu Gln Ala Gly Arg Leu Asn Trp Trp Val Ser Val
165 170 175
Asp Pro Thr Ser Gln Arg Leu Leu Pro Leu Ala Thr Thr Gly Asp Gly
180 185 190
Asn Cys Leu Leu His Ala Ala Ser Leu Gly Met Trp Gly Phe His Asp
195 200 205
Arg Asp Leu Met Leu Arg Lys Ala Leu Tyr Ala Leu Met Glu Lys Gly
210 215 220

Val Glu Lys Glu Ala Leu Lys Arg Arg Trp Arg Trp Gln Gln Thr Gln
225 230 235 240
Gln Asn Lys Glu Ser Gly Leu Val Tyr Thr Glu Asp Glu Trp Gln Lys
245 250 255
Glu Trp Asn Glu Leu Ile Lys Leu Ala Ser Ser Glu Pro Arg Met His
260 265 270
Leu Gly Thr Asn Gly Ala Asn Cys Gly Gly Val Glu Ser Ser Glu Glu
275 280 285
Pro Val Tyr Glu Ser Leu Glu Glu Phe His Val Phe Val Leu Ala His
290 295 300
Val Leu Arg Arg Pro Ile Val Val Val Ala Asp Thr Met Leu Arg Asp
305 310 315 320
Ser Gly Gly Glu Ala Phe Ala Pro Ile Pro Phe Gly Gly Ile Tyr Leu
325 330 335
Pro Leu Glu Val Pro Ala Ser Gln Cys His Arg Ser Pro Leu Val Leu
340 345 350
Ala Tyr Asp Gln Ala His Phe Ser Ala Leu Val Ser Met Glu Gln Lys
355 360 365
Glu Asn Thr Lys Glu Gln Ala Val Ile Pro Leu Thr Asp Ser Glu Tyr
370 375 380
Lys Leu Leu Pro Leu His Phe Ala Val Asp Pro Gly Lys Gly Trp Glu
385 390 395 400
Trp Gly Lys Asp Asp Ser Asp Asn Val Arg Leu Ala Ser Val Ile Leu
405 410 415
Ser Leu Glu Val Lys Leu His Leu Leu His Ser Tyr Met Asn Val Lys
420 425 430
Trp Ile Pro Leu Ser Ser Asp Ala Gln Ala Pro Leu Ala Gln Pro Glu

435 440 445
Ser Pro Thr Ala Ser Ala Gly Asp Glu Pro Arg Ser Thr Pro Glu Ser
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Gly Asp Ser Asp Lys Glu Ser Val Gly Ser Ser Ser Thr Ser Asn Glu
465 470 475 480
Gly Gly Arg Arg Lys Glu Lys Ser Lys Arg Asp Arg Glu Lys Asp Lys
485 490 495
Lys Arg Ala Asp Ser Val Ala Asn Lys Leu Gly Ser Phe Gly Lys Thr
500 505 510
Leu Gly Ser Lys Leu Lys Lys Asn Met Gly Gly Leu Met His Ser Lys
515 520 525
Gly Ser Lys Pro Gly Gly Val Gly Thr Gly Leu Gly Gly Ser Ser Gly
530 535 540
Thr Glu Thr Leu Glu Lys Lys Lys Lys Asn Ser Leu Lys Ser Trp Lys
545 550 555 560
Gly Gly Lys Glu Glu Ala Ala Gly Asp Gly Pro Val Ser Glu Lys Pro
565 570 575
Pro Ala Glu Ser Val Gly Asn Gly Gly Ser Lys Tyr Ser Gln Glu Val
580 585 590
Met Gln Ser Leu Ser Ile Leu Arg Thr Ala Met Gln Gly Glu Gly Lys
595 600 605
Phe Ile Phe Val Gly Thr Leu Lys Met Gly His Arg His Gln Tyr Gln
610 615 620
Glu Glu Met Ile Gln Arg Tyr Leu Ser Asp Ala Glu Glu Arg Phe Leu
625 630 635 640
Ala Glu Gln Lys Gln Lys Glu Ala Glu Arg Lys Ile Met Asn Gly Gly
645 650 655

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Ile Gly Gly Gly Pro Pro Pro Ala Lys Lys Pro Glu Pro Asp Ala Arg
660 665 670

Glu Glu Gln Pro Thr Gly Pro Pro Ala Glu Ser Arg Ala Met Ala Phe
675 680 685

Ser Thr Gly Tyr Pro Gly Asp Phe Thr Ile Pro Arg Pro Ser Gly Gly
690 695 700

Gly Val His Cys Gln Glu Pro Arg Arg Gln Leu Ala Gly Gly Pro Cys
705 710 715 720

Val Gly Gly Leu Pro Pro Tyr Ala Thr Phe Pro Arg Gln Cys Pro Pro
725 730 735

Gly Arg Pro Tyr Pro His Gln Asp Ser Ile Pro Ser Leu Glu Pro Gly
740 745 750

Ser His Ser Lys Asp Gly Leu His Arg Gly Ala Leu Leu Pro Pro Pro
755 760 765

Tyr Arg Val Ala Asp Ser Tyr Ser Asn Gly Tyr Arg Glu Pro Pro Glu
770 775 780

Pro Asp Gly Trp Ala Gly Gly Leu Arg Gly Leu Pro Pro Thr Gln Thr
785 790 795 800

Lys Cys Lys Gln Pro Asn Cys Ser Phe Tyr Gly His Pro Gly Thr Asn
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tgaattttga tctatgttct acctacatcc agctggctga aagtacttga ggatcac 177
atg acc ctg gac atg gat gct gtt ctg tca gat ttt gtc cgt tcc aca 225
Met Thr Leu Asp Met Asp Ala Val Leu Ser Asp Phe Val Arg Ser Thr
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Gly Ala Glu Pro Gly Leu Ala Arg Asp Leu Leu Glu Gly Lys Asn Trp
      20             25             30
gat gtg aat gcc gcc ctc agt gat ttt gaa cag cta cgt caa gtc cat 321
Asp Val Asn Ala Ala Leu Ser Asp Phe Glu Gln Leu Arg Gln Val His
      35             40             45
gct gga aac cta ccc cca tcc ttt agt gag ggg agt ggt ggc tcc agg 369
Ala Gly Asn Leu Pro Pro Ser Phe Ser Glu Gly Ser Gly Gly Ser Arg
      50             55             60
acc cct gaa aaa ggg ttt tct gac aga gag cct act cgc ccc ccc cga 417
Thr Pro Glu Lys Gly Phe Ser Asp Arg Glu Pro Thr Arg Pro Pro Arg
      65             70             75             80
ccc atc ctc cag cgg cag gat gac atc gtt caa gaa aaa cgc ctg tct 465
Pro Ile Leu Gln Arg Gln Asp Asp Ile Val Gln Glu Lys Arg Leu Ser
      85             90             95

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Arg Gly Ile Ser His Ala Ser Ser Ser Ile Val Ser Leu Ala Arg Ser
      100              105              110
cat gtc tcc tcc aat ggt ggg ggt ggg ggg agc aat gag cac ccc ctg 561
His Val Ser Ser Asn Gly Gly Gly Gly Gly Ser Asn Glu His Pro Leu
      115              120              125
gaa atg ccc atc tgt gcc ttc cag ctt cca gat ctc act gta tac aat 609
Glu Met Pro Ile Cys Ala Phe Gln Leu Pro Asp Leu Thr Val Tyr Asn
      130              135              140
gaa gac ttc cgc agc ttc ata gag aga gac ctc att gag cag tcc atg 657
Glu Asp Phe Arg Ser Phe Ile Glu Arg Asp Leu Ile Glu Gln Ser Met
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gat ccc acc tct cag agg ctg ctt cct ttg gca act act gga gat ggg 753
Asp Pro Thr Ser Gln Arg Leu Leu Pro Leu Ala Thr Thr Gly Asp Gly
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Asn Cys Leu Leu His Ala Ala Ser Leu Gly Met Trp Gly Phe His Asp
      195              200              205
cgg gac ttg atg ctg cgg aaa gct ttg tat gca ctg atg gag aag gga 849
Arg Asp Leu Met Leu Arg Lys Ala Leu Tyr Ala Leu Met Glu Lys Gly
      210              215              220
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Val Glu Lys Glu Ala Leu Lys Arg Arg Trp Arg Trp Gln Gln Thr Gln
225              230              235              240

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cag aat aaa gag tca ggg ctg gta tac aca gaa gat gaa tgg cag aag 945
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 gag tgg aat gaa ctg atc aag ctt gcc tca agt gaa ccc cga atg cat 993
 Glu Trp Asn Glu Leu Ile Lys Leu Ala Ser Ser Glu Pro Arg Met His
 260 265 270
 cta ggt acc aat gga gcc aac tgt ggt ggg gtg gag agt tct gag gag 1041
 Leu Gly Thr Asn Gly Ala Asn Cys Gly Gly Val Glu Ser Ser Glu Glu
 275 280 285
 cct gta tat gag agc ctt gaa gag ttt cac gtc ttt gtc ctt gct cat 1089
 Pro Val Tyr Glu Ser Leu Glu Glu Phe His Val Phe Val Leu Ala His
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 Val Leu Arg Arg Pro Ile Val Val Val Ala Asp Thr Met Leu Arg Asp
 305 310 315 320
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 Ser Gly Gly Glu Ala Phe Ala Pro Ile Pro Phe Gly Gly Ile Tyr Leu
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 cct ttg gag gtc cca gcc agc cag tgt cac cgc tcc cct ctg gtg etc 1233
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 Ala Tyr Asp Gln Ala His Phe Ser Ala Leu Val Ser Met Glu Gln Lys
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 Glu Asn Thr Lys Glu Gln Ala Val Ile Pro Leu Thr Asp Ser Glu Tyr
 370 375 380

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tgg ggc aaa gat gat agt gac aat gtc cga ttg gcc agt gta att ctg 1425
Trp Gly Lys Asp Asp Ser Asp Asn Val Arg Leu Ala Ser Val Ile Leu
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Ser Leu Glu Val Lys Leu His Leu Leu His Ser Tyr Met Asn Val Lys
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Gly Asp Ser Asp Lys Glu Ser Val Gly Ser Ser Ser Thr Ser Asn Glu
465 470 475 480
ggc ggc cgg cgg aag gag aag tca aag cga gat cgg gag aag gac aag 1665
Gly Gly Arg Arg Lys Glu Lys Ser Lys Arg Asp Arg Glu Lys Asp Lys
485 490 495
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Lys Arg Ala Asp Ser Val Ala Asn Lys Leu Gly Ser Phe Gly Lys Thr
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ttg ggc agc aag ctc aag aag aac atg ggg ggc ctg atg cac agc aag 1761
Leu Gly Ser Lys Leu Lys Lys Asn Met Gly Gly Leu Met His Ser Lys
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 Met Gln Ser Leu Ser Ile Leu Arg Thr Ala Met Gln Gly Glu Gly Lys
 595 600 605
 ttt att ttt gtt gga acc ctg aag atg ggt cac cgt cac cag tat cag 2049
 Phe Ile Phe Val Gly Thr Leu Lys Met Gly His Arg His Gln Tyr Gln
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 645 650 655
 ata ggg ggt ggc cct cct cca gcc aaa aag cca gag cca gat gct agg 2193
 Ile Gly Gly Gly Pro Pro Pro Ala Lys Lys Pro Glu Pro Asp Ala Arg
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197/617

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tcc act ggc tac cct ggg gac ttt act atc cct cgg ccg tct ggg ggc 2289
Ser Thr Gly Tyr Pro Gly Asp Phe Thr Ile Pro Arg Pro Ser Gly Gly
690 695 700
gga gtc cac tgc cag gaa ccc cgg agg cag ttg gca ggg ggt cca tgt 2337
Gly Val His Cys Gln Glu Pro Arg Arg Gln Leu Ala Gly Gly Pro Cys
705 710 715 720
gtc ggg ggc cta cca cca tat gcc acc ttc ccc aga cag tgc cct cct 2385
Val Gly Gly Leu Pro Pro Tyr Ala Thr Phe Pro Arg Gln Cys Pro Pro
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755 760 765
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770 775 780
cca gat gga tgg gct gga ggt ctc cgg ggc ctt ccc cca act cag acc 2577
Pro Asp Gly Trp Ala Gly Gly Leu Arg Gly Leu Pro Pro Thr Gln Thr
785 790 795 800
aaa tgc aaa caa ccg aac tgc agc ttc tat gga cac cct gag aca aac 2625
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 Asn Phe Cys Ser Cys Cys Tyr Arg Glu Glu Leu Arg Arg Arg Glu Arg

820

825

830

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835

840

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<400> 54

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5

10

15

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Ala Gly Asn Leu Pro Pro Ser Phe Ser Glu Gly Ser Gly Gly Ser Arg
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Thr Pro Glu Lys Gly Phe Ser Asp Arg Glu Pro Thr Arg Pro Pro Arg
65 70 75 80
Pro Ile Leu Gln Arg Gln Asp Asp Ile Val Gln Glu Lys Arg Leu Ser
85 90 95
Arg Gly Ile Ser His Ala Ser Ser Ser Ile Val Ser Leu Ala Arg Ser
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His Val Ser Ser Asn Gly Gly Gly Gly Gly Ser Asn Glu His Pro Leu
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Glu Met Pro Ile Cys Ala Phe Gln Leu Pro Asp Leu Thr Val Tyr Asn
130 135 140
Glu Asp Phe Arg Ser Phe Ile Glu Arg Asp Leu Ile Glu Gln Ser Met
145 150 155 160
Leu Val Ala Leu Glu Gln Ala Gly Arg Leu Asn Trp Trp Val Ser Val
165 170 175
Asp Pro Thr Ser Gln Arg Leu Leu Pro Leu Ala Thr Thr Gly Asp Gly
180 185 190
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210 215 220
Val Glu Lys Glu Ala Leu Lys Arg Arg Trp Arg Trp Gln Gln Thr Gln

225 230 235 240
Gln Asn Lys Glu Ser Gly Leu Val Tyr Thr Glu Asp Glu Trp Gln Lys
245 250 255
Glu Trp Asn Glu Leu Ile Lys Leu Ala Ser Ser Glu Pro Arg Met His
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Leu Gly Thr Asn Gly Ala Asn Cys Gly Gly Val Glu Ser Ser Glu Glu
275 280 285
Pro Val Tyr Glu Ser Leu Glu Glu Phe His Val Phe Val Leu Ala His
290 295 300
Val Leu Arg Arg Pro Ile Val Val Val Ala Asp Thr Met Leu Arg Asp
305 310 315 320
Ser Gly Gly Glu Ala Phe Ala Pro Ile Pro Phe Gly Gly Ile Tyr Leu
325 330 335
Pro Leu Glu Val Pro Ala Ser Gln Cys His Arg Ser Pro Leu Val Leu
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Ala Tyr Asp Gln Ala His Phe Ser Ala Leu Val Ser Met Glu Gln Lys
355 360 365
Glu Asn Thr Lys Glu Gln Ala Val Ile Pro Leu Thr Asp Ser Glu Tyr
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Trp Gly Lys Asp Asp Ser Asp Asn Val Arg Leu Ala Ser Val Ile Leu
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Ser Leu Glu Val Lys Leu His Leu Leu His Ser Tyr Met Asn Val Lys
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Trp Ile Pro Leu Ser Ser Asp Ala Gln Ala Pro Leu Ala Gln Pro Glu
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Lys Arg Ala Asp Ser Val Ala Asn Lys Leu Gly Ser Phe Gly Lys Thr
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Thr Glu Thr Leu Glu Lys Lys Lys Lys Asn Ser Leu Lys Ser Trp Lys
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565 570 575
Pro Ala Glu Ser Val Gly Asn Gly Gly Ser Lys Tyr Ser Gln Glu Val
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Met Gln Ser Leu Ser Ile Leu Arg Thr Ala Met Gln Gly Glu Gly Lys
595 600 605
Phe Ile Phe Val Gly Thr Leu Lys Met Gly His Arg His Gln Tyr Gln
610 615 620
Glu Glu Met Ile Gln Arg Tyr Leu Ser Asp Ala Glu Glu Arg Phe Leu
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Ala Glu Gln Lys Gln Lys Glu Ala Glu Arg Lys Ile Met Asn Gly Gly
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675 680 685
Ser Thr Gly Tyr Pro Gly Asp Phe Thr Ile Pro Arg Pro Ser Gly Gly
690 695 700
Gly Val His Cys Gln Glu Pro Arg Arg Gln Leu Ala Gly Gly Pro Cys
705 710 715 720
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725 730 735
Gly Arg Pro Tyr Pro His Gln Asp Ser Ile Pro Ser Leu Glu Pro Gly
740 745 750
Ser His Ser Lys Asp Gly Leu His Arg Gly Ala Leu Leu Pro Pro Pro
755 760 765
Tyr Arg Val Ala Asp Ser Tyr Ser Asn Gly Tyr Arg Glu Pro Pro Glu
770 775 780
Pro Asp Gly Trp Ala Gly Gly Leu Arg Gly Leu Pro Pro Thr Gln Thr
785 790 795 800
Lys Cys Lys Gln Pro Asn Cys Ser Phe Tyr Gly His Pro Glu Thr Asn
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<210> 55

<211> 3437

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<222> (100).. (846)

<400> 55

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Met Pro Met Glu Gly

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ttt ggg aaa gtc acc ctg tcc aaa gag ctg ctg gta gat gct gtg aat 162

Phe Gly Lys Val Thr Leu Ser Lys Glu Leu Leu Val Asp Ala Val Asn

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20

ata gcc att cct gcc tct ctg gag att tcc tcc cta ttg ggg ttt tgg 210

Ile Ala Ile Pro Ala Ser Leu Glu Ile Ser Ser Leu Leu Gly Phe Trp

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cag ctc ccc cct cct act ccc cag aat ggc ttt gtg aat agc acc atc 258

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cct gtg ggg cct ggg gag cca ctg ccc cat agg ata acc tgt ctg gcg 306

Pro Val Gly Pro Gly Glu Pro Leu Pro His Arg Ile Thr Cys Leu Ala

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60

65

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Gln Gln Gln Pro Pro Pro Leu Gln Pro Pro Pro Pro Leu Pro Leu Pro

70

75

80

85

cag cca ctg cca gtg cca cag cca cta cca cag cca cag atg cag cca 402

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90

95

100

204/617

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 Gln Pro Leu Gln Leu Gln Leu Pro Gln Leu Leu Pro Gln Leu Gln Pro
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 Glu Gly Ala Glu Glu Gly Ala Glu Pro Glu Ala Gln Ala Glu Glu Glu
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 gaa gag gaa gag gaa gcg gaa gag cca cag cca gaa gaa gcc caa ata 738
 Glu Glu Glu Glu Glu Ala Glu Glu Pro Gln Pro Glu Glu Ala Gln Ile
 200 205 210
 gca gtg agt gct gtg aat ctg ggc cag ccc ccc cta ccc cca act ccc 786
 Ala Val Ser Ala Val Asn Leu Gly Gln Pro Pro Leu Pro Pro Thr Pro
 215 220 225
 cat att ttc aca gct ggc tcc aac act gct atc ctg ccc cat ttc cat 834
 His Ile Phe Thr Ala Gly Ser Asn Thr Ala Ile Leu Pro His Phe His
 230 235 240 245

cac gca ttt aga taaattgggt ttttaagagg tgcttctctt gtgggagatg 886

His Ala Phe Arg

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<211> 249

<212> PRT

<213> Mus musculus

<400> 56

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Val Asn Ser Thr Ile Pro Val Gly Pro Gly Glu Pro Leu Pro His Arg			
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Ile Thr Cys Leu Ala Gln Gln Gln Pro Pro Pro Leu Gln Pro Pro Pro			
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Pro Leu Pro Leu Pro Gln Pro Leu Pro Val Pro Gln Pro Leu Pro Gln			
85	90	95	
Pro Gln Met Gln Pro Gln Phe Gln Leu Gln Ile Gln Pro Gln Met Gln			
100	105	110	
Pro Gln Met Gln Leu Gln Pro Leu Gln Leu Gln Leu Pro Gln Leu Leu			
115	120	125	
Pro Gln Leu Gln Pro Gln Gln Gln Pro Asp Pro Glu Pro Glu Pro Glu			
130	135	140	
Pro Glu Pro Glu Pro Glu Pro Glu Pro Gly Pro Glu Pro Glu Pro Glu			
145	150	155	160
Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Glu Glu Gln Glu Glu Ala			
165	170	175	
Glu Glu Glu Ala Glu Glu Gly Ala Glu Glu Gly Ala Glu Pro Glu Ala			
180	185	190	
Gln Ala Glu Glu Glu Glu Glu Glu Glu Ala Glu Glu Pro Gln Pro			
195	200	205	
Glu Glu Ala Gln Ile Ala Val Ser Ala Val Asn Leu Gly Gln Pro Pro			
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Leu Pro His Phe His His Ala Phe Arg

245

<210> 57

<211> 3437

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (100).. (846)

<400> 57

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                                     Met Pro Met Glu Gly
                                     1           5
ttt ggg aaa gtc acc ctg tcc aaa gag ctg ctg gta gat gct gtg aat    162
Phe Gly Lys Val Thr Leu Ser Lys Glu Leu Leu Val Asp Ala Val Asn
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ata gcc att cct gcc tct ctg gag att tcc tcc cta ttg ggg ttt tgg    210
Ile Ala Ile Pro Ala Ser Leu Glu Ile Ser Ser Leu Leu Gly Phe Trp
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cag ctc ccc cct cct act ccc cag aat ggc ttt gtg aat agc acc atc    258
Gln Leu Pro Pro Pro Thr Pro Gln Asn Gly Phe Val Asn Ser Thr Ile
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cct gtg ggg cct ggg gag cca ctg ccc cat agg ata acc tgt ctg gcg    306
Pro Val Gly Pro Gly Glu Pro Leu Pro His Arg Ile Thr Cys Leu Ala
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209/617

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 cag cca ctg cca gtg cca cag cca cta cca cag cca cag atg cag cca 402
 Gln Pro Leu Pro Val Pro Gln Pro Leu Pro Gln Pro Gln Met Gln Pro
 90 95 100
 cag ttt cag ttg cag atc cag ccc cag atg cag ccc cag atg cag ctg 450
 Gln Phe Gln Leu Gln Ile Gln Pro Gln Met Gln Pro Gln Met Gln Leu
 105 110 115
 cag cca ctg cag ctg cag cta cca cag ctg ctg ccg caa ctg caa cct 498
 Gln Pro Leu Gln Leu Gln Leu Pro Gln Leu Leu Pro Gln Leu Gln Pro
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 135 140 145
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 150 155 160 165
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 Glu Pro Glu Pro Glu Glu Glu Gln Glu Glu Ala Glu Glu Glu Ala Glu
 170 175 180
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 gaa gag gaa gag gaa gcg gaa gag cca cag cca gaa gaa gcc caa ata 738
 Glu Glu Glu Glu Glu Ala Glu Glu Pro Gln Pro Glu Glu Ala Gln Ile
 200 205 210

210/617

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<211> 249

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<213> Mus musculus

<400> 58

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 Val Asn Ser Thr Ile Pro Val Gly Pro Gly Glu Pro Leu Pro His Arg
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 Ile Thr Cys Leu Ala Gln Gln Gln Pro Pro Pro Leu Pro Pro Pro Pro
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 85 90 95
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 Glu Glu Glu Ala Glu Glu Gly Ala Glu Glu Gly Ala Glu Pro Glu Ala
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213/617

Gln Ala Glu Glu Glu Glu Glu Glu Glu Ala Glu Glu Pro Gln Pro

195

200

205

Glu Glu Ala Gln Ile Ala Val Ser Ala Val Asn Leu Gly Gln Pro Pro

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240

Leu Pro His Phe His His Ala Phe Arg

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<210> 59

<211> 3975

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (249).. (2360)

<400> 59

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15

20

25

30

214/617

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 Tyr Lys Leu Met Arg His Met Ala Thr His Ser Pro Gln Lys Ile His
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 Gln Cys Thr His Cys Glu Lys Thr Phe Asn Arg Lys Asp His Leu Lys
 65 70 75
 aac cac ctc cag acc cac gat ccc aac aag atc tcc tac gcg tgt gac 530
 Asn His Leu Gln Thr His Asp Pro Asn Lys Ile Ser Tyr Ala Cys Asp
 80 85 90
 gat tgc ggc aag aag tac cac acc atg ctg ggc tac aag agg cac ctg 578
 Asp Cys Gly Lys Lys Tyr His Thr Met Leu Gly Tyr Lys Arg His Leu
 95 100 105 110
 gcc ctg cac tcg gcg agc aat ggc gat ctc acc tgt ggg gtg tgc acc 626
 Ala Leu His Ser Ala Ser Asn Gly Asp Leu Thr Cys Gly Val Cys Thr
 115 120 125
 ctg gag ctg ggg agc acc gag gtc ctg ctg gac cac ctc aag tct cac 674
 Leu Glu Leu Gly Ser Thr Glu Val Leu Leu Asp His Leu Lys Ser His
 130 135 140
 gcg gaa gaa aag gcc aac cag gca ccc agg gag aag aaa tac cag tgc 722
 Ala Glu Glu Lys Ala Asn Gln Ala Pro Arg Glu Lys Lys Tyr Gln Cys
 145 150 155
 gac cac tgt gat aga tgc ttc tac acc cgg aaa gat gtg cgt cgc cac 770
 Asp His Cys Asp Arg Cys Phe Tyr Thr Arg Lys Asp Val Arg Arg His
 160 165 170

ctg gtg gtc cac aca gga tgc aag gac ttc ctg tgt cag ttc tgt gcc 818
 Leu Val Val His Thr Gly Cys Lys Asp Phe Leu Cys Gln Phe Cys Ala
 175 180 185 190
 cag aga ttt ggg cgc aaa gac cac ctc act cgt cac acc aag aag acc 866
 Gln Arg Phe Gly Arg Lys Asp His Leu Thr Arg His Thr Lys Lys Thr
 195 200 205
 cac tcc cag gag ctg atg caa gag aat atg cag gca gga gat tac cag 914
 His Ser Gln Glu Leu Met Gln Glu Asn Met Gln Ala Gly Asp Tyr Gln
 210 215 220
 agc aat ttc caa ctc att gcg cct tca act tcg ttc cag ata aag gtt 962
 Ser Asn Phe Gln Leu Ile Ala Pro Ser Thr Ser Phe Gln Ile Lys Val
 225 230 235
 gat ccc atg cct cct ttc cag cta gga gcg gct ccc gag aac ggg ctt 1010
 Asp Pro Met Pro Pro Phe Gln Leu Gly Ala Ala Pro Glu Asn Gly Leu
 240 245 250
 gat ggt ggc ttg cca ccc gag gtt cat ggt cta gtg ctt gct gcc cca 1058
 Asp Gly Gly Leu Pro Pro Glu Val His Gly Leu Val Leu Ala Ala Pro
 255 260 265 270
 gaa gaa gct ccc caa ccc atg ccg ccc ttg gag cct ttg gag cct ttg 1106
 Glu Glu Ala Pro Gln Pro Met Pro Pro Leu Glu Pro Leu Glu Pro Leu
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 gag cct ttg gag cct ttg gag ccg atg cag tct ttg gag cct ttg cag 1154
 Glu Pro Leu Glu Pro Leu Glu Pro Met Gln Ser Leu Glu Pro Leu Gln
 290 295 300
 cct ttg gag ccg atg cag cct ttg gag cca atg cag cct ttg gag ccg 1202
 Pro Leu Glu Pro Met Gln Pro Leu Glu Pro Met Gln Pro Leu Glu Pro
 305 310 315

atg cag cct tta gag cct ttg gag cct ctg gag ccg atg cag cct ttg 1250
 Met Gln Pro Leu Glu Pro Leu Glu Pro Leu Glu Pro Met Gln Pro Leu
 320 325 330
 gag ccg atg cag cct ttg gag cct atg cag cca atg ctg cca atg cag 1298
 Glu Pro Met Gln Pro Leu Glu Pro Met Gln Pro Met Leu Pro Met Gln
 335 340 345 350
 cca atg cag cca atg cag cca atg cag cca atg ctg cca atg cag cca 1346
 Pro Met Gln Pro Met Gln Pro Met Gln Pro Met Leu Pro Met Gln Pro
 355 360 365
 atg ctg cca atg cag cca atg cag cca atg cag cca atg ctg cca atg 1394
 Met Leu Pro Met Gln Pro Met Gln Pro Met Gln Pro Met Leu Pro Met
 370 375 380
 cca gag ccg tct ttc act ctg cac cct ggc gta gtt ccc acc tct cct 1442
 Pro Glu Pro Ser Phe Thr Leu His Pro Gly Val Val Pro Thr Ser Pro
 385 390 395
 ccc cca att att ctt cag gag cat aag tat aat cct gtt cct acc tca 1490
 Pro Pro Ile Ile Leu Gln Glu His Lys Tyr Asn Pro Val Pro Thr Ser
 400 405 410
 tat gcc cca ttt gta ggc atg ccc gtc aaa gca gat ggc aag gcc ttt 1538
 Tyr Ala Pro Phe Val Gly Met Pro Val Lys Ala Asp Gly Lys Ala Phe
 415 420 425 430
 tgc aac gtg ggt ttc ttt gag gaa ttt cct ctg caa gag cct cag gcg 1586
 Cys Asn Val Gly Phe Phe Glu Glu Phe Pro Leu Gln Glu Pro Gln Ala
 435 440 445
 cct ctc aag ttc aac cca tgt ttt gag atg cct atg gag ggg ttt ggg 1634
 Pro Leu Lys Phe Asn Pro Cys Phe Glu Met Pro Met Glu Gly Phe Gly
 450 455 460

aaa gtc acc ctg tcc aaa gag ctg ctg gta gat gct gtg aat ata gcc 1682
 Lys Val Thr Leu Ser Lys Glu Leu Leu Val Asp Ala Val Asn Ile Ala
 465 470 475
 att cct gcc tct ctg gag att tcc tcc cta ttg ggg ttt tgg cag ctc 1730
 Ile Pro Ala Ser Leu Glu Ile Ser Ser Leu Leu Gly Phe Trp Gln Leu
 480 485 490
 ccc cct cct act ccc cag aat ggc ttt gtg aat agc acc atc cct gtg 1778
 Pro Pro Pro Thr Pro Gln Asn Gly Phe Val Asn Ser Thr Ile Pro Val
 495 500 505 510
 ggg cct ggg gag cca ctg ccc cat agg ata acc tgt ctg gcg cag cag 1826
 Gly Pro Gly Glu Pro Leu Pro His Arg Ile Thr Cys Leu Ala Gln Gln
 515 520 525
 cag cca ccg cca ctg ccg ccg cca cca ccg ctg cca ctg cca cag cca 1874
 Gln Pro Pro Pro Leu Pro Pro Pro Pro Pro Leu Pro Leu Pro Gln Pro
 530 535 540
 ctg cca gtg cca cag cca cta cca cag cca cag atg cag cca cag ttt 1922
 Leu Pro Val Pro Gln Pro Leu Pro Gln Pro Gln Met Gln Pro Gln Phe
 545 550 555
 cag ttg cag atc cag ccc cag atg cag ccc cag atg cag ctg cag cca 1970
 Gln Leu Gln Ile Gln Pro Gln Met Gln Pro Gln Met Gln Leu Gln Pro
 560 565 570
 ctg cag ctg cag cta cca cag ctg ctg ccg caa ctg caa cct cag cag 2018
 Leu Gln Leu Gln Leu Pro Gln Leu Leu Pro Gln Leu Gln Pro Gln Gln
 575 580 585 590
 cag cct gat cct gag cca gag cca gag cca gag cca gag cca gag cca 2066
 Gln Pro Asp Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro
 595 600 605

gag cca gag ccg gaa ccg gaa ccg gag cca gag cca gag cca gaa cca 2114
 Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro
 610 615 620
 gag cca gag gaa gaa cag gaa gag gca gaa gaa gag gca gag gaa gga 2162
 Glu Pro Glu Glu Glu Gln Glu Glu Ala Glu Glu Glu Ala Glu Glu Gly
 625 630 635
 gca gag gaa gga gca gaa cca gag gca cag gca gaa gaa gag gaa gag 2210
 Ala Glu Glu Gly Ala Glu Pro Glu Ala Gln Ala Glu Glu Glu Glu Glu
 640 645 650
 gaa gag gaa gcg gaa gag cca cag cca gaa gaa gcc caa ata gca gtg 2258
 Glu Glu Glu Ala Glu Glu Pro Gln Pro Glu Glu Ala Gln Ile Ala Val
 655 660 665 670
 agt gct gtg aat ctg ggc cag ccc ccc cta ccc cca act ccc cat att 2306
 Ser Ala Val Asn Leu Gly Gln Pro Pro Leu Pro Pro Thr Pro His Ile
 675 680 685
 ttc aca gct ggc tcc aac act gct atc ctg ccc cat ttc cat cac gca 2354
 Phe Thr Ala Gly Ser Asn Thr Ala Ile Leu Pro His Phe His His Ala
 690 695 700
 ttt aga taaattggtt ttttaagagg tgcttctctt gtgggagatg ttttaaacat 2410
 Phe Arg
 cagttacagt ttgaggagaa gcattggaaa acaggaatgg ggtttttagct tatttgtcat 2470
 aagtagcttg agaaaaagaa ttctctaact gcatgcgttg tgccaatata tacccttagt 2530
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 atcctcatta tcttataatc acgtgattac gtgataagat ccaaaacatg agctgctatt 2710
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actgtgtaac caagtcaagt ggccaactaa ttgaagaaga atcaatcaaa gtgtttgtgg 3190
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ttccc 3975

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<211> 704

<212> PRT

<213> Mus musculus

<400> 60

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Lys Cys Ser Lys Ala Glu Cys Gly Lys Ala Phe Val Ser Lys Tyr Lys
35 40 45
Leu Met Arg His Met Ala Thr His Ser Pro Gln Lys Ile His Gln Cys
50 55 60
Thr His Cys Glu Lys Thr Phe Asn Arg Lys Asp His Leu Lys Asn His
65 70 75 80
Leu Gln Thr His Asp Pro Asn Lys Ile Ser Tyr Ala Cys Asp Asp Cys
85 90 95
Gly Lys Lys Tyr His Thr Met Leu Gly Tyr Lys Arg His Leu Ala Leu
100 105 110
His Ser Ala Ser Asn Gly Asp Leu Thr Cys Gly Val Cys Thr Leu Glu
115 120 125
Leu Gly Ser Thr Glu Val Leu Leu Asp His Leu Lys Ser His Ala Glu
130 135 140
Glu Lys Ala Asn Gln Ala Pro Arg Glu Lys Lys Tyr Gln Cys Asp His
145 150 155 160
Cys Asp Arg Cys Phe Tyr Thr Arg Lys Asp Val Arg Arg His Leu Val
165 170 175
Val His Thr Gly Cys Lys Asp Phe Leu Cys Gln Phe Cys Ala Gln Arg
180 185 190
Phe Gly Arg Lys Asp His Leu Thr Arg His Thr Lys Lys Thr His Ser
195 200 205
Gln Glu Leu Met Gln Glu Asn Met Gln Ala Gly Asp Tyr Gln Ser Asn
210 215 220

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Phe Gln Leu Ile Ala Pro Ser Thr Ser Phe Gln Ile Lys Val Asp Pro
 225 230 235 240
 Met Pro Pro Phe Gln Leu Gly Ala Ala Pro Glu Asn Gly Leu Asp Gly
 245 250 255
 Gly Leu Pro Pro Glu Val His Gly Leu Val Leu Ala Ala Pro Glu Glu
 260 265 270
 Ala Pro Gln Pro Met Pro Pro Leu Glu Pro Leu Glu Pro Leu Glu Pro
 275 280 285
 Leu Glu Pro Leu Glu Pro Met Gln Ser Leu Glu Pro Leu Gln Pro Leu
 290 295 300
 Glu Pro Met Gln Pro Leu Glu Pro Met Gln Pro Leu Glu Pro Met Gln
 305 310 315 320
 Pro Leu Glu Pro Leu Glu Pro Leu Glu Pro Met Gln Pro Leu Glu Pro
 325 330 335
 Met Gln Pro Leu Glu Pro Met Gln Pro Met Leu Pro Met Gln Pro Met
 340 345 350
 Gln Pro Met Gln Pro Met Gln Pro Met Leu Pro Met Gln Pro Met Leu
 355 360 365
 Pro Met Gln Pro Met Gln Pro Met Gln Pro Met Leu Pro Met Pro Glu
 370 375 380
 Pro Ser Phe Thr Leu His Pro Gly Val Val Pro Thr Ser Pro Pro Pro
 385 390 395 400
 Ile Ile Leu Gln Glu His Lys Tyr Asn Pro Val Pro Thr Ser Tyr Ala
 405 410 415
 Pro Phe Val Gly Met Pro Val Lys Ala Asp Gly Lys Ala Phe Cys Asn
 420 425 430
 Val Gly Phe Phe Glu Glu Phe Pro Leu Gln Glu Pro Gln Ala Pro Leu

435 440 445
Lys Phe Asn Pro Cys Phe Glu Met Pro Met Glu Gly Phe Gly Lys Val
450 455 460
Thr Leu Ser Lys Glu Leu Leu Val Asp Ala Val Asn Ile Ala Ile Pro
465 470 475 480
Ala Ser Leu Glu Ile Ser Ser Leu Leu Gly Phe Trp Gln Leu Pro Pro
485 490 495
Pro Thr Pro Gln Asn Gly Phe Val Asn Ser Thr Ile Pro Val Gly Pro
500 505 510
Gly Glu Pro Leu Pro His Arg Ile Thr Cys Leu Ala Gln Gln Gln Pro
515 520 525
Pro Pro Leu Pro Pro Pro Pro Pro Leu Pro Leu Pro Gln Pro Leu Pro
530 535 540
Val Pro Gln Pro Leu Pro Gln Pro Gln Met Gln Pro Gln Phe Gln Leu
545 550 555 560
Gln Ile Gln Pro Gln Met Gln Pro Gln Met Gln Leu Gln Pro Leu Gln
565 570 575
Leu Gln Leu Pro Gln Leu Leu Pro Gln Leu Gln Pro Gln Gln Gln Pro
580 585 590
Asp Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro
595 600 605
Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro
610 615 620
Glu Glu Glu Gln Glu Glu Ala Glu Glu Glu Ala Glu Glu Gly Ala Glu
625 630 635 640
Glu Gly Ala Glu Pro Glu Ala Gln Ala Glu Glu Glu Glu Glu Glu
645 650 655

Glu Ala Glu Glu Pro Gln Pro Glu Glu Ala Gln Ile Ala Val Ser Ala

660

665

670

Val Asn Leu Gly Gln Pro Pro Leu Pro Pro Thr Pro His Ile Phe Thr

675

680

685

Ala Gly Ser Asn Thr Ala Ile Leu Pro His Phe His His Ala Phe Arg

690

695

700

<210> 61

<211> 3150

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (225).. (1835)

<400> 61

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catgtgcagg ggccagttag aaaaagaaat ttttgagtga cgtcagaatc aagttcgagc 120

acaacgggga gaggcgaatt atagcgttca gccggcctgt gaaatatgaa gatgtggagc 180

acaaggtgac aacagtattt ggacaacctc ttgatctaca ttac atg aac aat gag 236

Met Asn Asn Glu

1

ctc tcc atc ctg ctg aaa aac caa gat gat ctt gat aaa gca att gac 284

Leu Ser Ile Leu Leu Lys Asn Gln Asp Asp Leu Asp Lys Ala Ile Asp

5

10

15

20

att tta gat aga agc tca agc atg aaa agc ctt agg ata ttg ctg ttg 332

Ile Leu Asp Arg Ser Ser Ser Met Lys Ser Leu Arg Ile Leu Leu Leu

25

30

35

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tcc cag gac aga aac cat aac agt tcc tct ccc cac tct ggg gtg tcc 380
 Ser Gln Asp Arg Asn His Asn Ser Ser Ser Pro His Ser Gly Val Ser
 40 45 50
 aga cag gtg cgg atc aag gct tcc cag tcc gca ggg gat ata aat act 428
 Arg Gln Val Arg Ile Lys Ala Ser Gln Ser Ala Gly Asp Ile Asn Thr
 55 60 65
 atc tac cag ccc ccc gag ccc aga agc agg cac ctc tct gtc agc tcc 476
 Ile Tyr Gln Pro Pro Glu Pro Arg Ser Arg His Leu Ser Val Ser Ser
 70 75 80
 cag aac cct ggc cga agc tca cct ccc cct ggc tat gtt cct gag cgg 524
 Gln Asn Pro Gly Arg Ser Ser Pro Pro Pro Gly Tyr Val Pro Glu Arg
 85 90 95 100
 cag cag cac att gcc cgg cag ggg tcc tac acc agc atc aac agt gag 572
 Gln Gln His Ile Ala Arg Gln Gly Ser Tyr Thr Ser Ile Asn Ser Glu
 105 110 115
 ggg gag ttc atc cca gag acc agc gag cag tgc atg ctg gat ccc ctg 620
 Gly Glu Phe Ile Pro Glu Thr Ser Glu Gln Cys Met Leu Asp Pro Leu
 120 125 130
 agc agt gca gaa aat tcc ttg tct gga agc tgc caa tcc ttg gac agc 668
 Ser Ser Ala Glu Asn Ser Leu Ser Gly Ser Cys Gln Ser Leu Asp Ser
 135 140 145
 cca tcc ttc cgg aaa tca cga atg tcc cgt gcc cag agc ttc cct gac 716
 Pro Ser Phe Arg Lys Ser Arg Met Ser Arg Ala Gln Ser Phe Pro Asp
 150 155 160
 aac aga cag gaa tac tca gat cgg gaa act cag ctt tat gac aaa ggg 764
 Asn Arg Gln Glu Tyr Ser Asp Arg Glu Thr Gln Leu Tyr Asp Lys Gly
 165 170 175 180

gtc aaa ggt gga acc tac ccc cgg cgc tac cac gtg tct gtg cac cac 812
 Val Lys Gly Gly Thr Tyr Pro Arg Arg Tyr His Val Ser Val His His
 185 190 195
 aag gac tac agt gat ggc aga aga aca ttt ccc cga ata cgg cgt cat 860
 Lys Asp Tyr Ser Asp Gly Arg Arg Thr Phe Pro Arg Ile Arg Arg His
 200 205 210
 caa ggc aac ttg ttc acc ctg gtg ccc tcc agc cgc tcc ctg agc aca 908
 Gln Gly Asn Leu Phe Thr Leu Val Pro Ser Ser Arg Ser Leu Ser Thr
 215 220 225
 aat ggc gag aac atg ggt ctg gct gtg caa tac ctg gac ccc cgt ggg 956
 Asn Gly Glu Asn Met Gly Leu Ala Val Gln Tyr Leu Asp Pro Arg Gly
 230 235 240
 cgc ctg cgg agt gcg gac agc gag aat gcc ctc tct gtg cag gag agg 1004
 Arg Leu Arg Ser Ala Asp Ser Glu Asn Ala Leu Ser Val Gln Glu Arg
 245 250 255 260
 aat gtg cca acc aag tct ccc agt gcc ccc atc aac tgg cgc cgg gga 1052
 Asn Val Pro Thr Lys Ser Pro Ser Ala Pro Ile Asn Trp Arg Arg Gly
 265 270 275
 aag ctc ctg ggc cag ggt gcc ttc ggc agg gtc tat ttg tgc tat gac 1100
 Lys Leu Leu Gly Gln Gly Ala Phe Gly Arg Val Tyr Leu Cys Tyr Asp
 280 285 290
 gtg gac acg gga cgt gaa ctt gct tcc aag cag gtc caa ttt gat cca 1148
 Val Asp Thr Gly Arg Glu Leu Ala Ser Lys Gln Val Gln Phe Asp Pro
 295 300 305
 gac agt cct gag aca agc aag gag gtg agt gct ctg gag tgc gag atc 1196
 Asp Ser Pro Glu Thr Ser Lys Glu Val Ser Ala Leu Glu Cys Glu Ile
 310 315 320

cag ttg cta aag aac ttg cag cat gag cgc atc gtg cag tac tat ggc 1244
 Gln Leu Leu Lys Asn Leu Gln His Glu Arg Ile Val Gln Tyr Tyr Gly
 325 330 335 340
 tgt ctg cgg gac cgc gct gag aag acc ctg acc atc ttc atg gag tac 1292
 Cys Leu Arg Asp Arg Ala Glu Lys Thr Leu Thr Ile Phe Met Glu Tyr
 345 350 355
 atg cca ggg ggc tcg gtg aaa gac cag ttg aag gct tac ggt gct ctg 1340
 Met Pro Gly Gly Ser Val Lys Asp Gln Leu Lys Ala Tyr Gly Ala Leu
 360 365 370
 aca gag agc gtg acc cga aag tac acg cgg cag atc ctg gag ggc atg 1388
 Thr Glu Ser Val Thr Arg Lys Tyr Thr Arg Gln Ile Leu Glu Gly Met
 375 380 385
 tcc tac ctg cac agc aac atg att gtt cac cgg gac att aag gga gcc 1436
 Ser Tyr Leu His Ser Asn Met Ile Val His Arg Asp Ile Lys Gly Ala
 390 395 400
 aac atc ctc cga gac tct gct ggg aat gta aag ctg ggg gac ttt ggg 1484
 Asn Ile Leu Arg Asp Ser Ala Gly Asn Val Lys Leu Gly Asp Phe Gly
 405 410 415 420
 gcc agc aaa cgc ctg cag acg atc tgt atg tcg ggg acg ggc atg cgc 1532
 Ala Ser Lys Arg Leu Gln Thr Ile Cys Met Ser Gly Thr Gly Met Arg
 425 430 435
 tcc gtc act ggc aca ccc tac tgg atg agc cct gag gtg atc agc ggc 1580
 Ser Val Thr Gly Thr Pro Tyr Trp Met Ser Pro Glu Val Ile Ser Gly
 440 445 450
 gag ggc tat gga agg aaa gca gac gtg tgg agc ctg ggc tgc act gtg 1628
 Glu Gly Tyr Gly Arg Lys Ala Asp Val Trp Ser Leu Gly Cys Thr Val
 455 460 465

gtg gag atg ctg aca gag aaa cca ccg tgg gca gag tat gaa gct atg 1676
Val Glu Met Leu Thr Glu Lys Pro Pro Trp Ala Glu Tyr Glu Ala Met

470

475

480

gcc gcc atc ttc aag att gcc acc cag ccc acc aat cct cag ctg ccc 1724
Ala Ala Ile Phe Lys Ile Ala Thr Gln Pro Thr Asn Pro Gln Leu Pro

485

490

495

500

tcc cac atc tct gaa cat ggc cgg gac ttc ctg agg cgc att ttt gtg 1772
Ser His Ile Ser Glu His Gly Arg Asp Phe Leu Arg Arg Ile Phe Val

505

510

515

gag gct cgc cag aga cct tca gct gag gag ctg ctc aca cac cac ttt 1820
Glu Ala Arg Gln Arg Pro Ser Ala Glu Glu Leu Leu Thr His His Phe

520

525

530

gca cag ctc atg tac tgagctctca cgGCCacaca gctGCCggtc GCCctttgct 1875
Ala Gln Leu Met Tyr

535

gcatggcagg gggctgctgc tgggctcagt gaagtgtctg cttctcccag gcaaggctgt 1935
ggaccatgga gtggcagccc agccagcgtc ggtctgtgcc cttccgcca ctggggctca 1995
gagccgggggt ggggtggtgc cagcctcagg actgggagcc cccagcctgt cagatccagg 2055
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 agttgtcatt aaagg 3150

<210> 62

<211> 537

<212> PRT

<213> Homo sapiens

<400> 62

Met Asn Asn Glu Leu Ser Ile Leu Leu Lys Asn Gln Asp Asp Leu Asp
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 Lys Ala Ile Asp Ile Leu Asp Arg Ser Ser Ser Met Lys Ser Leu Arg
 20 25 30
 Ile Leu Leu Leu Ser Gln Asp Arg Asn His Asn Ser Ser Ser Pro His
 35 40 45
 Ser Gly Val Ser Arg Gln Val Arg Ile Lys Ala Ser Gln Ser Ala Gly
 50 55 60
 Asp Ile Asn Thr Ile Tyr Gln Pro Pro Glu Pro Arg Ser Arg His Leu
 65 70 75 80
 Ser Val Ser Ser Gln Asn Pro Gly Arg Ser Ser Pro Pro Pro Gly Tyr

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	85	90	95
Val Pro Glu Arg Gln Gln His Ile Ala Arg Gln Gly Ser Tyr Thr Ser			
100	105	110	
Ile Asn Ser Glu Gly Glu Phe Ile Pro Glu Thr Ser Glu Gln Cys Met			
115	120	125	
Leu Asp Pro Leu Ser Ser Ala Glu Asn Ser Leu Ser Gly Ser Cys Gln			
130	135	140	
Ser Leu Asp Ser Pro Ser Phe Arg Lys Ser Arg Met Ser Arg Ala Gln			
145	150	155	160
Ser Phe Pro Asp Asn Arg Gln Glu Tyr Ser Asp Arg Glu Thr Gln Leu			
165	170	175	
Tyr Asp Lys Gly Val Lys Gly Gly Thr Tyr Pro Arg Arg Tyr His Val			
180	185	190	
Ser Val His His Lys Asp Tyr Ser Asp Gly Arg Arg Thr Phe Pro Arg			
195	200	205	
Ile Arg Arg His Gln Gly Asn Leu Phe Thr Leu Val Pro Ser Ser Arg			
210	215	220	
Ser Leu Ser Thr Asn Gly Glu Asn Met Gly Leu Ala Val Gln Tyr Leu			
225	230	235	240
Asp Pro Arg Gly Arg Leu Arg Ser Ala Asp Ser Glu Asn Ala Leu Ser			
245	250	255	
Val Gln Glu Arg Asn Val Pro Thr Lys Ser Pro Ser Ala Pro Ile Asn			
260	265	270	
Trp Arg Arg Gly Lys Leu Leu Gly Gln Gly Ala Phe Gly Arg Val Tyr			
275	280	285	
Leu Cys Tyr Asp Val Asp Thr Gly Arg Glu Leu Ala Ser Lys Gln Val			
290	295	300	

Gln Phe Asp Pro Asp Ser Pro Glu Thr Ser Lys Glu Val Ser Ala Leu
305 310 315 320
Glu Cys Glu Ile Gln Leu Leu Lys Asn Leu Gln His Glu Arg Ile Val
325 330 335
Gln Tyr Tyr Gly Cys Leu Arg Asp Arg Ala Glu Lys Thr Leu Thr Ile
340 345 350
Phe Met Glu Tyr Met Pro Gly Gly Ser Val Lys Asp Gln Leu Lys Ala
355 360 365
Tyr Gly Ala Leu Thr Glu Ser Val Thr Arg Lys Tyr Thr Arg Gln Ile
370 375 380
Leu Glu Gly Met Ser Tyr Leu His Ser Asn Met Ile Val His Arg Asp
385 390 395 400
Ile Lys Gly Ala Asn Ile Leu Arg Asp Ser Ala Gly Asn Val Lys Leu
405 410 415
Gly Asp Phe Gly Ala Ser Lys Arg Leu Gln Thr Ile Cys Met Ser Gly
420 425 430
Thr Gly Met Arg Ser Val Thr Gly Thr Pro Tyr Trp Met Ser Pro Glu
435 440 445
Val Ile Ser Gly Glu Gly Tyr Gly Arg Lys Ala Asp Val Trp Ser Leu
450 455 460
Gly Cys Thr Val Val Glu Met Leu Thr Glu Lys Pro Pro Trp Ala Glu
465 470 475 480
Tyr Glu Ala Met Ala Ala Ile Phe Lys Ile Ala Thr Gln Pro Thr Asn
485 490 495
Pro Gln Leu Pro Ser His Ile Ser Glu His Gly Arg Asp Phe Leu Arg
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Arg Ile Phe Val Glu Ala Arg Gln Arg Pro Ser Ala Glu Glu Leu Leu

515 520 525
 Thr His His Phe Ala Gln Leu Met Tyr

530 535

<210> 63

<211> 3352

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (97).. (2037)

<400> 63

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Met Asn Asp Leu Val Ala

1

5

ctc cag atg aac cga cgt cac cgg atg cct gga tat gag acc atg aag 162
 Leu Gln Met Asn Arg Arg His Arg Met Pro Gly Tyr Glu Thr Met Lys

10

15

20

aac aaa gac aca ggt cac tca aat agg cag aaa aaa cac aac agc agc 210
 Asn Lys Asp Thr Gly His Ser Asn Arg Gln Lys Lys His Asn Ser Ser

25

30

35

agc tca gcc ctt ctg aac agc ccc aca gta aca aca agc tca tgt gca 258
 Ser Ser Ala Leu Leu Asn Ser Pro Thr Val Thr Thr Ser Ser Cys Ala

40

45

50

ggg gcc agt gag aaa aag aaa ttt ttg agt gac gtc aga atc aag ttc 306

232/617

Gly Ala Ser Glu Lys Lys Lys Phe Leu Ser Asp Val Arg Ile Lys Phe
 55 60 65 70
 gag cac aac ggg gag agg cga att ata gcg ttc agc cgg cct gtg aaa 354
 Glu His Asn Gly Glu Arg Arg Ile Ile Ala Phe Ser Arg Pro Val Lys
 75 80 85
 tat gaa gat gtg gag cac aag gtg aca aca gta ttt gga caa cct ctt 402
 Tyr Glu Asp Val Glu His Lys Val Thr Thr Val Phe Gly Gln Pro Leu
 90 95 100
 gat cta cat tac atg aac aat gag ctc tcc atc ctg ctg aaa aac caa 450
 Asp Leu His Tyr Met Asn Asn Glu Leu Ser Ile Leu Leu Lys Asn Gln
 105 110 115
 gat gat ctt gat aaa gca att gac att tta gat aga agc tca agc atg 498
 Asp Asp Leu Asp Lys Ala Ile Asp Ile Leu Asp Arg Ser Ser Ser Met
 120 125 130
 aaa agc ctt agg ata ttg ctg ttg tcc cag gac aga aac cat aac agt 546
 Lys Ser Leu Arg Ile Leu Leu Leu Ser Gln Asp Arg Asn His Asn Ser
 135 140 145 150
 tcc tct ccc cac tct ggg gtg tcc aga cag gtg cgg atc aag gct tcc 594
 Ser Ser Pro His Ser Gly Val Ser Arg Gln Val Arg Ile Lys Ala Ser
 155 160 165
 cag tcc gca ggg gat ata aat act atc tac cag ccc ccc gag ccc aga 642
 Gln Ser Ala Gly Asp Ile Asn Thr Ile Tyr Gln Pro Pro Glu Pro Arg
 170 175 180
 agc agg cac ctc tct gtc agc tcc cag aac cct ggc cga agc tca cct 690
 Ser Arg His Leu Ser Val Ser Ser Gln Asn Pro Gly Arg Ser Ser Pro
 185 190 195
 ccc cct ggc tat gtt cct gag cgg cag cag cac att gcc cgg cag ggg 738

Pro Pro Gly Tyr Val Pro Glu Arg Gln Gln His Ile Ala Arg Gln Gly
 200 205 210
 tcc tac acc agc atc aac agt gag ggg gag ttc atc cca gag acc agc 786
 Ser Tyr Thr Ser Ile Asn Ser Glu Gly Glu Phe Ile Pro Glu Thr Ser
 215 220 225 230
 gag cag tgc atg ctg gat ccc ctg agc agt gca gaa aat tcc ttg tct 834
 Glu Gln Cys Met Leu Asp Pro Leu Ser Ser Ala Glu Asn Ser Leu Ser
 235 240 245
 gga agc tgc caa tcc ttg gac agg tca gca gac agc cca tcc ttc cgg 882
 Gly Ser Cys Gln Ser Leu Asp Arg Ser Ala Asp Ser Pro Ser Phe Arg
 250 255 260
 aaa tca cga atg tcc cgt gcc cag agc ttc cct gac aac aga cag gaa 930
 Lys Ser Arg Met Ser Arg Ala Gln Ser Phe Pro Asp Asn Arg Gln Glu
 265 270 275
 tac tca gat cgg gaa act cag ctt tat gac aaa ggg gtc aaa ggt gga 978
 Tyr Ser Asp Arg Glu Thr Gln Leu Tyr Asp Lys Gly Val Lys Gly Gly
 280 285 290
 acc tac ccc cgg cgc tac cac gtg tct gtg cac cac aag gac tac agt 1026
 Thr Tyr Pro Arg Arg Tyr His Val Ser Val His His Lys Asp Tyr Ser
 295 300 305 310
 gat ggc aga aga aca ttt ccc cga ata cgg cgt cat caa ggc aac ttg 1074
 Asp Gly Arg Arg Thr Phe Pro Arg Ile Arg Arg His Gln Gly Asn Leu
 315 320 325
 ttc acc ctg gtg ccc tcc agc cgc tcc ctg agc aca aat ggc gag aac 1122
 Phe Thr Leu Val Pro Ser Ser Arg Ser Leu Ser Thr Asn Gly Glu Asn
 330 335 340
 atg ggt ctg gct gtg caa tac ctg gac ccc cgt ggg cgc ctg cgg agt 1170

Met Gly Leu Ala Val Gln Tyr Leu Asp Pro Arg Gly Arg Leu Arg Ser
 345 350 355
 gcg gac agc gag aat gcc ctc tct gtg cag gag agg aat gtg cca acc 1218
 Ala Asp Ser Glu Asn Ala Leu Ser Val Gln Glu Arg Asn Val Pro Thr
 360 365 370
 aag tct ccc agt gcc ccc atc aac tgg cgc cgg gga aag ctc ctg ggc 1266
 Lys Ser Pro Ser Ala Pro Ile Asn Trp Arg Arg Gly Lys Leu Leu Gly
 375 380 385 390
 cag ggt gcc ttc ggc agg gtc tat ttg tgc tat gac gtg gac acg gga 1314
 Gln Gly Ala Phe Gly Arg Val Tyr Leu Cys Tyr Asp Val Asp Thr Gly
 395 400 405
 cgt gaa ctt gct tcc aag cag gtc caa ttt gat cca gac agt cct gag 1362
 Arg Glu Leu Ala Ser Lys Gln Val Gln Phe Asp Pro Asp Ser Pro Glu
 410 415 420
 aca agc aag gag gtg agt gct ctg gag tgc gag atc cag ttg cta aag 1410
 Thr Ser Lys Glu Val Ser Ala Leu Glu Cys Glu Ile Gln Leu Leu Lys
 425 430 435
 aac ttg cag cat gag cgc atc gtg cag tac tat ggc tgt ctg cgg gac 1458
 Asn Leu Gln His Glu Arg Ile Val Gln Tyr Tyr Gly Cys Leu Arg Asp
 440 445 450
 cgc gct gag aag acc ctg acc atc ttc atg gag tac atg cca ggg ggc 1506
 Arg Ala Glu Lys Thr Leu Thr Ile Phe Met Glu Tyr Met Pro Gly Gly
 455 460 465 470
 tcg gtg aaa gac cag ttg aag gct tac ggt gct ctg aca gag agc gtg 1554
 Ser Val Lys Asp Gln Leu Lys Ala Tyr Gly Ala Leu Thr Glu Ser Val
 475 480 485
 acc cga aag tac acg cgg cag atc ctg gag ggc atg tcc tac ctg cac 1602

Thr Arg Lys Tyr Thr Arg Gln Ile Leu Glu Gly Met Ser Tyr Leu His
 490 495 500
 agc aac atg att gtt cac cgg gac att aag gga gcc aac atc ctc cga 1650
 Ser Asn Met Ile Val His Arg Asp Ile Lys Gly Ala Asn Ile Leu Arg
 505 510 515
 gac tct gct ggg aat gta aag ctg ggg gac ttt ggg gcc agc aaa cgc 1698
 Asp Ser Ala Gly Asn Val Lys Leu Gly Asp Phe Gly Ala Ser Lys Arg
 520 525 530
 ctg cag acg atc tgt atg tcg ggg acg ggc atg cgc tcc gtc act ggc 1746
 Leu Gln Thr Ile Cys Met Ser Gly Thr Gly Met Arg Ser Val Thr Gly
 535 540 545 550
 act ccc tac tgg atg agc cct gag gtg atc agc ggc gag ggc tat gga 1794
 Thr Pro Tyr Trp Met Ser Pro Glu Val Ile Ser Gly Glu Gly Tyr Gly
 555 560 565
 agg aaa gca gac gtg tgg agc ctg ggc tgc act gtg gtg gag atg ctg 1842
 Arg Lys Ala Asp Val Trp Ser Leu Gly Cys Thr Val Val Glu Met Leu
 570 575 580
 aca gag aaa cca ccg tgg gca gag tat gaa gct atg gcc gcc atc ttc 1890
 Thr Glu Lys Pro Pro Trp Ala Glu Tyr Glu Ala Met Ala Ala Ile Phe
 585 590 595
 aag att gcc acc cag ccc acc aat cct cag ctg ccc tcc cac atc tct 1938
 Lys Ile Ala Thr Gln Pro Thr Asn Pro Gln Leu Pro Ser His Ile Ser
 600 605 610
 gaa cat ggc cgg gac ttc ctg agg cgc att ttt gtg gag gct cgc cag 1986
 Glu His Gly Arg Asp Phe Leu Arg Arg Ile Phe Val Glu Ala Arg Gln
 615 620 625 630
 aga cct tca gct gag gag ctg ctc aca cac cac ttt gca cag ctc atg 2034

Arg Pro Ser Ala Glu Glu Leu Leu Thr His His Phe Ala Gln Leu Met

635

640

645

tac tgagctctca cgccacaca gctgccggtc gccctttgct gcatggcagg 2087

Tyr

gggctgctgc tgggctcagt gaagttgctg cttctcccag gcaaggctgt ggaccatgga 2147
 gtggcagccc agccagcgtc ggtctgtgcc ccttccgcca ctggggctca gagccggggt 2207
 ggggtggctg cagcctcagg actgggagcc cccagcctgt cagatccagg agctccagt 2267
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 caccctcggg gatgtgtcct gacactgcaa ttggcaccga agcccagagg gtctgggggc 2387
 acaagactga cgccagggtg tgaagagtgt tattttcatt caaagtgtta tttgttttt 2447
 ccttccaatg tctggagacc accagggcat ctctgggctg gatgagctcc cacaagcctg 2507
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 aaagg 3352

<210> 64

<211> 647

<212> PRT

<213> Homo sapiens

<400> 64

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Gly Tyr Glu Thr Met Lys Asn Lys Asp Thr Gly His Ser Asn Arg Gln

20 25 30

Lys Lys His Asn Ser Ser Ser Ser Ala Leu Leu Asn Ser Pro Thr Val

35 40 45

Thr Thr Ser Ser Cys Ala Gly Ala Ser Glu Lys Lys Lys Phe Leu Ser

50 55 60

Asp Val Arg Ile Lys Phe Glu His Asn Gly Glu Arg Arg Ile Ile Ala

65 70 75 80

Phe Ser Arg Pro Val Lys Tyr Glu Asp Val Glu His Lys Val Thr Thr

85 90 95

Val Phe Gly Gln Pro Leu Asp Leu His Tyr Met Asn Asn Glu Leu Ser

100 105 110

Ile Leu Leu Lys Asn Gln Asp Asp Leu Asp Lys Ala Ile Asp Ile Leu

115 120 125

Asp Arg Ser Ser Ser Met Lys Ser Leu Arg Ile Leu Leu Leu Ser Gln

130 135 140

Asp Arg Asn His Asn Ser Ser Ser Pro His Ser Gly Val Ser Arg Gln

145 150 155 160

Val Arg Ile Lys Ala Ser Gln Ser Ala Gly Asp Ile Asn Thr Ile Tyr

165 170 175

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Gln Pro Pro Glu Pro Arg Ser Arg His Leu Ser Val Ser Ser Gln Asn
180 185 190
Pro Gly Arg Ser Ser Pro Pro Pro Gly Tyr Val Pro Glu Arg Gln Gln
195 200 205
His Ile Ala Arg Gln Gly Ser Tyr Thr Ser Ile Asn Ser Glu Gly Glu
210 215 220
Phe Ile Pro Glu Thr Ser Glu Gln Cys Met Leu Asp Pro Leu Ser Ser
225 230 235 240
Ala Glu Asn Ser Leu Ser Gly Ser Cys Gln Ser Leu Asp Arg Ser Ala
245 250 255
Asp Ser Pro Ser Phe Arg Lys Ser Arg Met Ser Arg Ala Gln Ser Phe
260 265 270
Pro Asp Asn Arg Gln Glu Tyr Ser Asp Arg Glu Thr Gln Leu Tyr Asp
275 280 285
Lys Gly Val Lys Gly Gly Thr Tyr Pro Arg Arg Tyr His Val Ser Val
290 295 300
His His Lys Asp Tyr Ser Asp Gly Arg Arg Thr Phe Pro Arg Ile Arg
305 310 315 320
Arg His Gln Gly Asn Leu Phe Thr Leu Val Pro Ser Ser Arg Ser Leu
325 330 335
Ser Thr Asn Gly Glu Asn Met Gly Leu Ala Val Gln Tyr Leu Asp Pro
340 345 350
Arg Gly Arg Leu Arg Ser Ala Asp Ser Glu Asn Ala Leu Ser Val Gln
355 360 365
Glu Arg Asn Val Pro Thr Lys Ser Pro Ser Ala Pro Ile Asn Trp Arg
370 375 380
Arg Gly Lys Leu Leu Gly Gln Gly Ala Phe Gly Arg Val Tyr Leu Cys

385 390 395 400
Tyr Asp Val Asp Thr Gly Arg Glu Leu Ala Ser Lys Gln Val Gln Phe
 405 410 415
Asp Pro Asp Ser Pro Glu Thr Ser Lys Glu Val Ser Ala Leu Glu Cys
 420 425 430
Glu Ile Gln Leu Leu Lys Asn Leu Gln His Glu Arg Ile Val Gln Tyr
 435 440 445
Tyr Gly Cys Leu Arg Asp Arg Ala Glu Lys Thr Leu Thr Ile Phe Met
 450 455 460
Glu Tyr Met Pro Gly Gly Ser Val Lys Asp Gln Leu Lys Ala Tyr Gly
465 470 475 480
Ala Leu Thr Glu Ser Val Thr Arg Lys Tyr Thr Arg Gln Ile Leu Glu
 485 490 495
Gly Met Ser Tyr Leu His Ser Asn Met Ile Val His Arg Asp Ile Lys
 500 505 510
Gly Ala Asn Ile Leu Arg Asp Ser Ala Gly Asn Val Lys Leu Gly Asp
 515 520 525
Phe Gly Ala Ser Lys Arg Leu Gln Thr Ile Cys Met Ser Gly Thr Gly
 530 535 540
Met Arg Ser Val Thr Gly Thr Pro Tyr Trp Met Ser Pro Glu Val Ile
545 550 555 560
Ser Gly Glu Gly Tyr Gly Arg Lys Ala Asp Val Trp Ser Leu Gly Cys
 565 570 575
Thr Val Val Glu Met Leu Thr Glu Lys Pro Pro Trp Ala Glu Tyr Glu
 580 585 590
Ala Met Ala Ala Ile Phe Lys Ile Ala Thr Gln Pro Thr Asn Pro Gln
 595 600 605

Leu Pro Ser His Ile Ser Glu His Gly Arg Asp Phe Leu Arg Arg Ile

610

615

620

Phe Val Glu Ala Arg Gln Arg Pro Ser Ala Glu Glu Leu Leu Thr His

625

630

635

640

His Phe Ala Gln Leu Met Tyr

645

<210> 65

<211> 3352

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (67).. (2037)

<400> 65

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gccacc atg gac gaa cag gag gca ttg aac tca atc atg aac gat ctg 108

Met Asp Glu Gln Glu Ala Leu Asn Ser Ile Met Asn Asp Leu

1

5

10

gtg gcc ctc cag atg aac cga cgt cac cgg atg cct gga tat gag acc 156

Val Ala Leu Gln Met Asn Arg Arg His Arg Met Pro Gly Tyr Glu Thr

15

20

25

30

atg aag aac aaa gac aca ggt cac tca aat agg cag aaa aaa cac aac 204

Met Lys Asn Lys Asp Thr Gly His Ser Asn Arg Gln Lys Lys His Asn

35

40

45

agc agc agc tca gcc ctt ctg aac agc ccc aca gta aca aca agc tca 252

Ser Ser Ser Ser Ala Leu Leu Asn Ser Pro Thr Val Thr Thr Ser Ser

241/617

50	55	60	
tgt gca ggg gcc agt gag aaa aag aaa ttt ttg agt gac gtc aga atc	300		
Cys Ala Gly Ala Ser Glu Lys Lys Lys Phe Leu Ser Asp Val Arg Ile			
65	70	75	
aag ttc gag cac aac ggg gag agg cga att ata gcg ttc agc cgg cct	348		
Lys Phe Glu His Asn Gly Glu Arg Arg Ile Ile Ala Phe Ser Arg Pro			
80	85	90	
gtg aaa tat gaa gat gtg gag cac aag gtg aca aca gta ttt gga caa	396		
Val Lys Tyr Glu Asp Val Glu His Lys Val Thr Thr Val Phe Gly Gln			
95	100	105	110
cct ctt gat cta cat tac atg aac aat gag ctc tcc atc ctg ctg aaa	444		
Pro Leu Asp Leu His Tyr Met Asn Asn Glu Leu Ser Ile Leu Leu Lys			
115	120	125	
aac caa gat gat ctt gat aaa gca att gac att tta gat aga agc tca	492		
Asn Gln Asp Asp Leu Asp Lys Ala Ile Asp Ile Leu Asp Arg Ser Ser			
130	135	140	
agc atg aaa agc ctt agg ata ttg ctg ttg tcc cag gac aga aac cat	540		
Ser Met Lys Ser Leu Arg Ile Leu Leu Leu Ser Gln Asp Arg Asn His			
145	150	155	
aac agt tcc tct ccc cac tct ggg gtg tcc aga cag gtg cgg atc aag	588		
Asn Ser Ser Ser Pro His Ser Gly Val Ser Arg Gln Val Arg Ile Lys			
160	165	170	
gct tcc cag tcc gca ggg gat ata aat act atc tac cag ccc ccc gag	636		
Ala Ser Gln Ser Ala Gly Asp Ile Asn Thr Ile Tyr Gln Pro Pro Glu			
175	180	185	190
ccc aga agc agg cac ctc tct gtc agc tcc cag aac cct ggc cga agc	684		
Pro Arg Ser Arg His Leu Ser Val Ser Ser Gln Asn Pro Gly Arg Ser			

195	200	205	
tca cct ccc cct ggc tat gtt cct gag cgg cag cag cac att gcc cgg			732
Ser Pro Pro Pro Gly Tyr Val Pro Glu Arg Gln Gln His Ile Ala Arg			
210	215	220	
cag ggg tcc tac acc agc atc aac agt gag ggg gag ttc atc cca gag			780
Gln Gly Ser Tyr Thr Ser Ile Asn Ser Glu Gly Glu Phe Ile Pro Glu			
225	230	235	
acc agc gag cag tgc atg ctg gat ccc ctg agc agt gca gaa aat tcc			828
Thr Ser Glu Gln Cys Met Leu Asp Pro Leu Ser Ser Ala Glu Asn Ser			
240	245	250	
ttg tct gga agc tgc caa tcc ttg gac agg tca gca gac agc cca tcc			876
Leu Ser Gly Ser Cys Gln Ser Leu Asp Arg Ser Ala Asp Ser Pro Ser			
255	260	265	270
ttc cgg aaa tca cga atg tcc cgt gcc cag agc ttc cct gac aac aga			924
Phe Arg Lys Ser Arg Met Ser Arg Ala Gln Ser Phe Pro Asp Asn Arg			
275	280	285	
cag gaa tac tca gat cgg gaa act cag ctt tat gac aaa ggg gtc aaa			972
Gln Glu Tyr Ser Asp Arg Glu Thr Gln Leu Tyr Asp Lys Gly Val Lys			
290	295	300	
ggt gga acc tac ccc cgg cgc tac cac gtg tct gtg cac cac aag gac			1020
Gly Gly Thr Tyr Pro Arg Arg Tyr His Val Ser Val His His Lys Asp			
305	310	315	
tac agt gat ggc aga aga aca ttt ccc cga ata cgg cgt cat caa ggc			1068
Tyr Ser Asp Gly Arg Arg Thr Phe Pro Arg Ile Arg Arg His Gln Gly			
320	325	330	
aac ttg ttc acc ctg gtg ccc tcc agc cgc tcc ctg agc aca aat ggc			1116
Asn Leu Phe Thr Leu Val Pro Ser Ser Arg Ser Leu Ser Thr Asn Gly			

335	340	345	350	
gag aac atg ggt ctg gct gtg caa tac ctg gac ccc cgt ggg cgc ctg				1164
Glu Asn Met Gly Leu Ala Val Gln Tyr Leu Asp Pro Arg Gly Arg Leu				
	355	360	365	
cgg agt gcg gac agc gag aat gcc ctc tct gtg cag gag agg aat gtg				1212
Arg Ser Ala Asp Ser Glu Asn Ala Leu Ser Val Gln Glu Arg Asn Val				
	370	375	380	
cca acc aag tct ccc agt gcc ccc atc aac tgg cgc cgg gga aag ctc				1260
Pro Thr Lys Ser Pro Ser Ala Pro Ile Asn Trp Arg Arg Gly Lys Leu				
	385	390	395	
ctg ggc cag ggt gcc ttc ggc agg gtc tat ttg tgc tat gac gtg gac				1308
Leu Gly Gln Gly Ala Phe Gly Arg Val Tyr Leu Cys Tyr Asp Val Asp				
	400	405	410	
acg gga cgt gaa ctt gct tcc aag cag gtc caa ttt gat cca gac agt				1356
Thr Gly Arg Glu Leu Ala Ser Lys Gln Val Gln Phe Asp Pro Asp Ser				
415	420	425	430	
cct gag aca agc aag gag gtg agt gct ctg gag tgc gag atc cag ttg				1404
Pro Glu Thr Ser Lys Glu Val Ser Ala Leu Glu Cys Glu Ile Gln Leu				
	435	440	445	
cta aag aac ttg cag cat gag cgc atc gtg cag tac tat ggc tgt ctg				1452
Leu Lys Asn Leu Gln His Glu Arg Ile Val Gln Tyr Tyr Gly Cys Leu				
	450	455	460	
cgg gac cgc gct gag aag acc ctg acc atc ttc atg gag tac atg cca				1500
Arg Asp Arg Ala Glu Lys Thr Leu Thr Ile Phe Met Glu Tyr Met Pro				
	465	470	475	
ggg ggc tcg gtg aaa gac cag ttg aag gct tac ggt gct ctg aca gag				1548
Gly Gly Ser Val Lys Asp Gln Leu Lys Ala Tyr Gly Ala Leu Thr Glu				

480	485	490	
agc gtg acc cga aag tac acg cgg cag atc ctg gag ggc atg tcc tac			1596
Ser Val Thr Arg Lys Tyr Thr Arg Gln Ile Leu Glu Gly Met Ser Tyr			
495	500	505	510
ctg cac agc aac atg att gtt cac cgg gac att aag gga gcc aac atc			1644
Leu His Ser Asn Met Ile Val His Arg Asp Ile Lys Gly Ala Asn Ile			
515	520	525	
ctc cga gac tct gct ggg aat gta aag ctg ggg gac ttt ggg gcc agc			1692
Leu Arg Asp Ser Ala Gly Asn Val Lys Leu Gly Asp Phe Gly Ala Ser			
530	535	540	
aaa cgc ctg cag acg atc tgt atg tcg ggg acg ggc atg cgc tcc gtc			1740
Lys Arg Leu Gln Thr Ile Cys Met Ser Gly Thr Gly Met Arg Ser Val			
545	550	555	
act ggc act ccc tac tgg atg agc cct gag gtg atc agc ggc gag ggc			1788
Thr Gly Thr Pro Tyr Trp Met Ser Pro Glu Val Ile Ser Gly Glu Gly			
560	565	570	
tat gga agg aaa gca gac gtg tgg agc ctg ggc tgc act gtg gtg gag			1836
Tyr Gly Arg Lys Ala Asp Val Trp Ser Leu Gly Cys Thr Val Val Glu			
575	580	585	590
atg ctg aca gag aaa cca ccg tgg gca gag tat gaa gct atg gcc gcc			1884
Met Leu Thr Glu Lys Pro Pro Trp Ala Glu Tyr Glu Ala Met Ala Ala			
595	600	605	
atc ttc aag att gcc acc cag ccc acc aat cct cag ctg ccc tcc cac			1932
Ile Phe Lys Ile Ala Thr Gln Pro Thr Asn Pro Gln Leu Pro Ser His			
610	615	620	
atc tct gaa cat ggc cgg gac ttc ctg agg cgc att ttt gtg gag gct			1980
Ile Ser Glu His Gly Arg Asp Phe Leu Arg Arg Ile Phe Val Glu Ala			

625 630 635
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 Arg Gln Arg Pro Ser Ala Glu Glu Leu Leu Thr His His Phe Ala Gln
 640 645 650
 ctc atg tac tgagctctca cggccacaca gctgccggtc gccctttgct 2077
 Leu Met Tyr
 655
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 ggaccatgga gtggcagccc agccagcgtc ggtctgtgcc cttccgcca ctggggctca 2197
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 gtctgggggc acaagactga cgccagggtg tgaagagtgt tattttcatt caaagtgtta 2437
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 cacaagcctg agggaaaggc cagcactcgc tagcagtggc aggcagaggc ccaggctgcc 2557
 gtcccctaga gtcccaggtt ggctctgcca gtccgtgcct ttaccaaaga tgaatgaagc 2617
 aaatgtcatg ctgccttatt cagggaagga ggagcctgtc ctgcctgtgg ccatgaccct 2677
 gcctctccca ggcagggggc cgcgatgtgg aactgctgcc actgaggggg gatccagttt 2737
 tgtcaatgca gttgtctctg ttttacaagt tggagtcaact cttatgctgt acccagtttc 2797
 taaactggag actgtgtgtg ccctctgggc tctgagtacc cctgctttgg gcttgggcct 2857
 aggctgcatt gaaaagagct gaaggttgtg gcctttgcgc tcctggccca gcctttgttc 2917
 cccactggag cagaagggga gatggacgac acggtcggga catctggcct ggccagtgcc 2977
 ctgateccag agagcccag gaggtgtctc aggtgcctg agtcgtgacc tgctaggcca 3037
 gagcccactc catctggtag aagggaagc ccatatgcta ccaccagctg tgtccaaaac 3097
 cgccagctct gttcttctc agccagcctc gccatcccc ttgaggtctc agccccttc 3157
 ccttgtagct cctcccctgg agggggaatg gcagcagggg ttggggaaac agcatctcca 3217
 agcagcttag agttggccat atttacctca gcctgggcgc tggtcctttc ttccggcccc 3277

tccccctccaa aatgtgccta ttgctagagc tcctccctct caacacccag tttccttggg 3337
 agttgtcatt aaagg 3352

<210> 66

<211> 657

<212> PRT

<213> Homo sapiens

<400> 66

Met Asp Glu Gln Glu Ala Leu Asn Ser Ile Met Asn Asp Leu Val Ala
 1 5 10 15
 Leu Gln Met Asn Arg Arg His Arg Met Pro Gly Tyr Glu Thr Met Lys
 20 25 30
 Asn Lys Asp Thr Gly His Ser Asn Arg Gln Lys Lys His Asn Ser Ser
 35 40 45
 Ser Ser Ala Leu Leu Asn Ser Pro Thr Val Thr Thr Ser Ser Cys Ala
 50 55 60
 Gly Ala Ser Glu Lys Lys Lys Phe Leu Ser Asp Val Arg Ile Lys Phe
 65 70 75 80
 Glu His Asn Gly Glu Arg Arg Ile Ile Ala Phe Ser Arg Pro Val Lys
 85 90 95
 Tyr Glu Asp Val Glu His Lys Val Thr Thr Val Phe Gly Gln Pro Leu
 100 105 110
 Asp Leu His Tyr Met Asn Asn Glu Leu Ser Ile Leu Leu Lys Asn Gln
 115 120 125
 Asp Asp Leu Asp Lys Ala Ile Asp Ile Leu Asp Arg Ser Ser Ser Met
 130 135 140
 Lys Ser Leu Arg Ile Leu Leu Leu Ser Gln Asp Arg Asn His Asn Ser

247/617

145 150 155 160
Ser Ser Pro His Ser Gly Val Ser Arg Gln Val Arg Ile Lys Ala Ser
 165 170 175
Gln Ser Ala Gly Asp Ile Asn Thr Ile Tyr Gln Pro Pro Glu Pro Arg
 180 185 190
Ser Arg His Leu Ser Val Ser Ser Gln Asn Pro Gly Arg Ser Ser Pro
 195 200 205
Pro Pro Gly Tyr Val Pro Glu Arg Gln Gln His Ile Ala Arg Gln Gly
 210 215 220
Ser Tyr Thr Ser Ile Asn Ser Glu Gly Glu Phe Ile Pro Glu Thr Ser
225 230 235 240
Glu Gln Cys Met Leu Asp Pro Leu Ser Ser Ala Glu Asn Ser Leu Ser
 245 250 255
Gly Ser Cys Gln Ser Leu Asp Arg Ser Ala Asp Ser Pro Ser Phe Arg
 260 265 270
Lys Ser Arg Met Ser Arg Ala Gln Ser Phe Pro Asp Asn Arg Gln Glu
 275 280 285
Tyr Ser Asp Arg Glu Thr Gln Leu Tyr Asp Lys Gly Val Lys Gly Gly
 290 295 300
Thr Tyr Pro Arg Arg Tyr His Val Ser Val His His Lys Asp Tyr Ser
305 310 315 320
Asp Gly Arg Arg Thr Phe Pro Arg Ile Arg Arg His Gln Gly Asn Leu
 325 330 335
Phe Thr Leu Val Pro Ser Ser Arg Ser Leu Ser Thr Asn Gly Glu Asn
 340 345 350
Met Gly Leu Ala Val Gln Tyr Leu Asp Pro Arg Gly Arg Leu Arg Ser
 355 360 365

Ala Asp Ser Glu Asn Ala Leu Ser Val Gln Glu Arg Asn Val Pro Thr
 370 375 380
 Lys Ser Pro Ser Ala Pro Ile Asn Trp Arg Arg Gly Lys Leu Leu Gly
 385 390 395 400
 Gln Gly Ala Phe Gly Arg Val Tyr Leu Cys Tyr Asp Val Asp Thr Gly
 405 410 415
 Arg Glu Leu Ala Ser Lys Gln Val Gln Phe Asp Pro Asp Ser Pro Glu
 420 425 430
 Thr Ser Lys Glu Val Ser Ala Leu Glu Cys Glu Ile Gln Leu Leu Lys
 435 440 445
 Asn Leu Gln His Glu Arg Ile Val Gln Tyr Tyr Gly Cys Leu Arg Asp
 450 455 460
 Arg Ala Glu Lys Thr Leu Thr Ile Phe Met Glu Tyr Met Pro Gly Gly
 465 470 475 480
 Ser Val Lys Asp Gln Leu Lys Ala Tyr Gly Ala Leu Thr Glu Ser Val
 485 490 495
 Thr Arg Lys Tyr Thr Arg Gln Ile Leu Glu Gly Met Ser Tyr Leu His
 500 505 510
 Ser Asn Met Ile Val His Arg Asp Ile Lys Gly Ala Asn Ile Leu Arg
 515 520 525
 Asp Ser Ala Gly Asn Val Lys Leu Gly Asp Phe Gly Ala Ser Lys Arg
 530 535 540
 Leu Gln Thr Ile Cys Met Ser Gly Thr Gly Met Arg Ser Val Thr Gly
 545 550 555 560
 Thr Pro Tyr Trp Met Ser Pro Glu Val Ile Ser Gly Glu Gly Tyr Gly
 565 570 575
 Arg Lys Ala Asp Val Trp Ser Leu Gly Cys Thr Val Val Glu Met Leu

580 585 590
 Thr Glu Lys Pro Pro Trp Ala Glu Tyr Glu Ala Met Ala Ala Ile Phe
 595 600 605
 Lys Ile Ala Thr Gln Pro Thr Asn Pro Gln Leu Pro Ser His Ile Ser
 610 615 620
 Glu His Gly Arg Asp Phe Leu Arg Arg Ile Phe Val Glu Ala Arg Gln
 625 630 635 640
 Arg Pro Ser Ala Glu Glu Leu Leu Thr His His Phe Ala Gln Leu Met
 645 650 655
 Tyr

<210> 67

<211> 3259

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (67).. (1944)

<400> 67

ttgttttttcg gagcgttcct gaggtgacac tcacggacct tagccaccgc cgccgccatc 60

gccacc atg gac gaa cag gag gca ttg aac tca atc atg aac gat ctg 108

Met Asp Glu Gln Glu Ala Leu Asn Ser Ile Met Asn Asp Leu

1

5

10

gtg gcc ctc cag atg aac cga cgt cac cgg atg cct gga tat gag acc 156

Val Ala Leu Gln Met Asn Arg Arg His Arg Met Pro Gly Tyr Glu Thr

15

20

25

30

atg aag aac aaa gac aca ggt cac tca aat agg cag agt gac gtc aga 204

250/617

251/617

Ser Ser Pro Pro Pro Gly Tyr Val Pro Glu Arg Gln Gln His Ile Ala
 175 180 185 190
 cgg cag ggg tcc tac acc agc atc aac agt gag ggg gag ttc atc cca 684
 Arg Gln Gly Ser Tyr Thr Ser Ile Asn Ser Glu Gly Glu Phe Ile Pro
 195 200 205
 gag acc agc gag cag tgc atg ctg gat ccc ctg agc agt gca gaa aat 732
 Glu Thr Ser Glu Gln Cys Met Leu Asp Pro Leu Ser Ser Ala Glu Asn
 210 215 220
 tcc ttg tct gga agc tgc caa tcc ttg gac agg tca gca gac agc cca 780
 Ser Leu Ser Gly Ser Cys Gln Ser Leu Asp Arg Ser Ala Asp Ser Pro
 225 230 235
 tcc ttc cgg aaa tca cga atg tcc cgt gcc cag agc ttc cct gac aac 828
 Ser Phe Arg Lys Ser Arg Met Ser Arg Ala Gln Ser Phe Pro Asp Asn
 240 245 250
 aga cag gaa tac tca gat cgg gaa act cag ctt tat gac aaa ggg gtc 876
 Arg Gln Glu Tyr Ser Asp Arg Glu Thr Gln Leu Tyr Asp Lys Gly Val
 255 260 265 270
 aaa ggt gga acc tac ccc cgg cgc tac cac gtg tct gtg cac cac aag 924
 Lys Gly Gly Thr Tyr Pro Arg Arg Tyr His Val Ser Val His His Lys
 275 280 285
 gac tac agt gat ggc aga aga aca ttt ccc cga ata cgg cgt cat caa 972
 Asp Tyr Ser Asp Gly Arg Arg Thr Phe Pro Arg Ile Arg Arg His Gln
 290 295 300
 ggc aac ttg ttc acc ctg gtg ccc tcc agc cgc tcc ctg agc aca aat 1020
 Gly Asn Leu Phe Thr Leu Val Pro Ser Ser Arg Ser Leu Ser Thr Asn
 305 310 315
 ggc gag aac atg ggt ctg gct gtg caa tac ctg gac ccc cgt ggg cgc 1068

Gly Glu Asn Met Gly Leu Ala Val Gln Tyr Leu Asp Pro Arg Gly Arg
 320 325 330
 ctg cgg agt gcg gac agc gag aat gcc ctc tct gtg cag gag agg aat 1116
 Leu Arg Ser Ala Asp Ser Glu Asn Ala Leu Ser Val Gln Glu Arg Asn
 335 340 345 350
 gtg cca acc aag tct ccc agt gcc ccc atc aac tgg cgc cgg gga aag 1164
 Val Pro Thr Lys Ser Pro Ser Ala Pro Ile Asn Trp Arg Arg Gly Lys
 355 360 365
 ctc ctg ggc cag ggt gcc ttc ggc agg gtc tat ttg tgc tat gac gtg 1212
 Leu Leu Gly Gln Gly Ala Phe Gly Arg Val Tyr Leu Cys Tyr Asp Val
 370 375 380
 gac acg gga cgt gaa ctt gct tcc aag cag gtc caa ttt gat cca gac 1260
 Asp Thr Gly Arg Glu Leu Ala Ser Lys Gln Val Gln Phe Asp Pro Asp
 385 390 395
 agt cct gag aca agc aag gag gtg agt gct ctg gag tgc gag atc cag 1308
 Ser Pro Glu Thr Ser Lys Glu Val Ser Ala Leu Glu Cys Glu Ile Gln
 400 405 410
 ttg cta aag aac ttg cag cat gag cgc atc gtg cag tac tat ggc tgt 1356
 Leu Leu Lys Asn Leu Gln His Glu Arg Ile Val Gln Tyr Tyr Gly Cys
 415 420 425 430
 ctg cgg gac cgc gct gag aag acc ctg acc atc ttc atg gag tac atg 1404
 Leu Arg Asp Arg Ala Glu Lys Thr Leu Thr Ile Phe Met Glu Tyr Met
 435 440 445
 cca ggg ggc tcg gtg aaa gac cag ttg aag gct tac ggt gct ctg aca 1452
 Pro Gly Gly Ser Val Lys Asp Gln Leu Lys Ala Tyr Gly Ala Leu Thr
 450 455 460
 gag agc gtg acc cga aag tac acg cgg cag atc ctg gag ggc atg tcc 1500

Glu Ser Val Thr Arg Lys Tyr Thr Arg Gln Ile Leu Glu Gly Met Ser

465

470

475

tac ctg cac agc aac atg att gtt cac cgg gac att aag gga gcc aac 1548

Tyr Leu His Ser Asn Met Ile Val His Arg Asp Ile Lys Gly Ala Asn

480

485

490

atc ctc cga gac tct gct ggg aat gta aag ctg ggg gac ttt ggg gcc 1596

Ile Leu Arg Asp Ser Ala Gly Asn Val Lys Leu Gly Asp Phe Gly Ala

495

500

505

510

agc aaa cgc ctg cag acg atc tgt atg tcg ggg acg ggc atg cgc tcc 1644

Ser Lys Arg Leu Gln Thr Ile Cys Met Ser Gly Thr Gly Met Arg Ser

515

520

525

gtc act ggc act ccc tac tgg atg agc cct gag gtg atc agc ggc gag 1692

Val Thr Gly Thr Pro Tyr Trp Met Ser Pro Glu Val Ile Ser Gly Glu

530

535

540

ggc tat gga agg aaa gca gac gtg tgg agc ctg ggc tgc act gtg gtg 1740

Gly Tyr Gly Arg Lys Ala Asp Val Trp Ser Leu Gly Cys Thr Val Val

545

550

555

gag atg ctg aca gag aaa cca ccg tgg gca gag tat gaa gct atg gcc 1788

Glu Met Leu Thr Glu Lys Pro Pro Trp Ala Glu Tyr Glu Ala Met Ala

560

565

570

gcc atc ttc aag att gcc acc cag ccc acc aat cct cag ctg ccc tcc 1836

Ala Ile Phe Lys Ile Ala Thr Gln Pro Thr Asn Pro Gln Leu Pro Ser

575

580

585

590

cac atc tct gaa cat ggc cgg gac ttc ctg agg cgc att ttt gtg gag 1884

His Ile Ser Glu His Gly Arg Asp Phe Leu Arg Arg Ile Phe Val Glu

595

600

605

gct cgc cag aga cct tca gct gag gag ctg ctc aca cac cac ttt gca 1932

Ala Arg Gln Arg Pro Ser Ala Glu Glu Leu Leu Thr His His Phe Ala

610

615

620

cag ctc atg tac tgagctctca cggccacaca gctgccggtc gccctttgct 1984

Gln Leu Met Tyr

625

gcatggcagg gggctgctgc tgggctcagt gaagttgctg cttctcccag gcaaggctgt 2044

ggaccatgga gtggcagccc agccagcgtc ggtctgtgcc cttccgcca ctggggctca 2104

gagccggggt ggggtggctg cagcctcagg actgggagcc cccagcctgt cagatccagg 2164

agctccagtg tcttgagctc agcgtggagg ggtaggggct gggaacagtg tgcaaggcag 2224

ccgtgggccc caccctcggg gatgtgtcct gacactgcaa ttggcaccga agcccagagg 2284

gtctgggggc acaagactga cgccagggtg tgaagagtgt tattttcatt caaagtgtta 2344

ttttgttttt ctttccaatg tctggagacc accagggtcat ctctgggctg gatgagctcc 2404

cacaagcctg agggaaaggc cagcactcgc tagcagtggc aggcagaggc ccaggctgcc 2464

gtcccctaga gtcccagggtt ggctctgcca gtctgtcct ttaccaaaga tgaatgaagc 2524

aaatgtcatg ctgccttatt cagggaagga ggagcctgtc ctgcctgtgg ccatgaccct 2584

gcctctccca ggcagggggc cgcgatgtgg aactgtgcc actgaggggg gatccagttt 2644

tgtcaatgca gtgtgtctg ttttacaagt tggagtcact cttatgtctg acccagtttc 2704

taaactggag actgtgtgtg ccctctgggc tctgagtacc cctgctttgg gcttgggcct 2764

aggctgcatt gaaaagagct gaaggttgtg gcctttgcgc tcttgccca gcctttgttc 2824

cccactggag cagaagggga gatggacgac acggtcggga catctggcct ggccagtgcc 2884

ctgatcccag agagcccagag gaggtgtctc aggctgcctg agtcgtgacc tgctaggcca 2944

gagcccactc catctggtag aagggaagc ccatatgcta ccaccagctg tgtccaaaac 3004

cgccagctct gtcttctctc agccagcctc gccatcccc ttgaggtctc agcccctttc 3064

cctttagctt cctcccctgg agggggaatg gcagcagggg ttggggaaac agcatctcca 3124

agcagcttag agttggccat atttacctca gcctgggcgc tggctcttcc ttccggcccc 3184

tcccctccaa aatgtgccta ttgctagagc tcctccctct caacaccag tttccttggg 3244

agttgtcatt aaagg 3259

<210> 68

<211> 626

<212> PRT

<213> Homo sapiens

<400> 68

Met Asp Glu Gln Glu Ala Leu Asn Ser Ile Met Asn Asp Leu Val Ala

1 5 10 15

Leu Gln Met Asn Arg Arg His Arg Met Pro Gly Tyr Glu Thr Met Lys

20 25 30

Asn Lys Asp Thr Gly His Ser Asn Arg Gln Ser Asp Val Arg Ile Lys

35 40 45

Phe Glu His Asn Gly Glu Arg Arg Ile Ile Ala Phe Ser Arg Pro Val

50 55 60

Lys Tyr Glu Asp Val Glu His Lys Val Thr Thr Val Phe Gly Gln Pro

65 70 75 80

Leu Asp Leu His Tyr Met Asn Asn Glu Leu Ser Ile Leu Leu Lys Asn

85 90 95

Gln Asp Asp Leu Asp Lys Ala Ile Asp Ile Leu Asp Arg Ser Ser Ser

100 105 110

Met Lys Ser Leu Arg Ile Leu Leu Leu Ser Gln Asp Arg Asn His Asn

115 120 125

Ser Ser Ser Pro His Ser Gly Val Ser Arg Gln Val Arg Ile Lys Ala

130 135 140

Ser Gln Ser Ala Gly Asp Ile Asn Thr Ile Tyr Gln Pro Pro Glu Pro

145 150 155 160

Arg Ser Arg His Leu Ser Val Ser Ser Gln Asn Pro Gly Arg Ser Ser

256/617

	165	170	175
Pro Pro Pro Gly Tyr Val Pro Glu Arg Gln Gln His Ile Ala Arg Gln			
	180	185	190
Gly Ser Tyr Thr Ser Ile Asn Ser Glu Gly Glu Phe Ile Pro Glu Thr			
	195	200	205
Ser Glu Gln Cys Met Leu Asp Pro Leu Ser Ser Ala Glu Asn Ser Leu			
	210	215	220
Ser Gly Ser Cys Gln Ser Leu Asp Arg Ser Ala Asp Ser Pro Ser Phe			
225	230	235	240
Arg Lys Ser Arg Met Ser Arg Ala Gln Ser Phe Pro Asp Asn Arg Gln			
	245	250	255
Glu Tyr Ser Asp Arg Glu Thr Gln Leu Tyr Asp Lys Gly Val Lys Gly			
	260	265	270
Gly Thr Tyr Pro Arg Arg Tyr His Val Ser Val His His Lys Asp Tyr			
	275	280	285
Ser Asp Gly Arg Arg Thr Phe Pro Arg Ile Arg Arg His Gln Gly Asn			
	290	295	300
Leu Phe Thr Leu Val Pro Ser Ser Arg Ser Leu Ser Thr Asn Gly Glu			
305	310	315	320
Asn Met Gly Leu Ala Val Gln Tyr Leu Asp Pro Arg Gly Arg Leu Arg			
	325	330	335
Ser Ala Asp Ser Glu Asn Ala Leu Ser Val Gln Glu Arg Asn Val Pro			
	340	345	350
Thr Lys Ser Pro Ser Ala Pro Ile Asn Trp Arg Arg Gly Lys Leu Leu			
	355	360	365
Gly Gln Gly Ala Phe Gly Arg Val Tyr Leu Cys Tyr Asp Val Asp Thr			
	370	375	380

Gly Arg Glu Leu Ala Ser Lys Gln Val Gln Phe Asp Pro Asp Ser Pro
385 390 395 400
Glu Thr Ser Lys Glu Val Ser Ala Leu Glu Cys Glu Ile Gln Leu Leu
405 410 415
Lys Asn Leu Gln His Glu Arg Ile Val Gln Tyr Tyr Gly Cys Leu Arg
420 425 430
Asp Arg Ala Glu Lys Thr Leu Thr Ile Phe Met Glu Tyr Met Pro Gly
435 440 445
Gly Ser Val Lys Asp Gln Leu Lys Ala Tyr Gly Ala Leu Thr Glu Ser
450 455 460
Val Thr Arg Lys Tyr Thr Arg Gln Ile Leu Glu Gly Met Ser Tyr Leu
465 470 475 480
His Ser Asn Met Ile Val His Arg Asp Ile Lys Gly Ala Asn Ile Leu
485 490 495
Arg Asp Ser Ala Gly Asn Val Lys Leu Gly Asp Phe Gly Ala Ser Lys
500 505 510
Arg Leu Gln Thr Ile Cys Met Ser Gly Thr Gly Met Arg Ser Val Thr
515 520 525
Gly Thr Pro Tyr Trp Met Ser Pro Glu Val Ile Ser Gly Glu Gly Tyr
530 535 540
Gly Arg Lys Ala Asp Val Trp Ser Leu Gly Cys Thr Val Val Glu Met
545 550 555 560
Leu Thr Glu Lys Pro Pro Trp Ala Glu Tyr Glu Ala Met Ala Ala Ile
565 570 575
Phe Lys Ile Ala Thr Gln Pro Thr Asn Pro Gln Leu Pro Ser His Ile
580 585 590
Ser Glu His Gly Arg Asp Phe Leu Arg Arg Ile Phe Val Glu Ala Arg

595 600 605
 Gln Arg Pro Ser Ala Glu Glu Leu Leu Thr His His Phe Ala Gln Leu

610 615 620
 Met Tyr
 625

<210> 69

<211> 1069

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (144).. (620)

<400> 69

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 tcccctcagg aacccaaggt tccgggtcct cctcccaaatt tccagctact ctcccccatc 120
 agtgtctctc cccaagtcca ggg atg gag gct gaa aga ccc cag gaa gaa gat 173

Met Glu Ala Glu Arg Pro Gln Glu Glu Asp

1 5 10

ggt gaa cag agt ctc ccg cag gat gat cag gga tgg ccc cct gtg aat 221

Gly Glu Gln Ser Leu Pro Gln Asp Asp Gln Gly Trp Pro Pro Val Asn

15 20 25

gcc acc gct cgg cct tgg aga tct gct cct ccc tcc cct cct cct 269

Ala Thr Ala Arg Pro Trp Arg Ser Ala Pro Pro Ser Pro Pro Pro Pro

30 35 40

gga acc cga cac aca gcc cta ggg ccc cgt tct ggc tcc ctg ctc tcc 317

Gly Thr Arg His Thr Ala Leu Gly Pro Arg Ser Gly Ser Leu Leu Ser

259/617

45 50 55
 ctg cag act gag ctc ctt ctg gac cta gtg gcc gaa gcc cag tcc cgc 365
 Leu Gln Thr Glu Leu Leu Leu Asp Leu Val Ala Glu Ala Gln Ser Arg
 60 65 70
 cgc cta gag gaa cag agg gcc acc ttc cac acc ccc gag gcc cca cca 413
 Arg Leu Glu Glu Gln Arg Ala Thr Phe His Thr Pro Glu Ala Pro Pro
 75 80 85 90
 aac cta gcc cca gcc cca ccc cgg ctt ctt gaa gac aaa gaa cag ctc 461
 Asn Leu Ala Pro Ala Pro Pro Arg Leu Leu Glu Asp Lys Glu Gln Leu
 95 100 105
 tac agc acc atc ctt agt cac cag tgc cag cgg att gaa gcc caa cgg 509
 Tyr Ser Thr Ile Leu Ser His Gln Cys Gln Arg Ile Glu Ala Gln Arg
 110 115 120
 tct gac ccg ccc ctt ccc ccc ggg ggg cag gag ctt ctg gag ttg ctg 557
 Ser Asp Pro Pro Leu Pro Pro Gly Gly Gln Glu Leu Leu Glu Leu Leu
 125 130 135
 ctg aga gtt cag ggt gga ggt cga atg gag gag cag aga tcc cgg cct 605
 Leu Arg Val Gln Gly Gly Gly Arg Met Glu Glu Gln Arg Ser Arg Pro
 140 145 150
 cct aca cac acc tgc tgagaccgga gtcctcacc agtccttct ctctgggact 660
 Pro Thr His Thr Cys
 155
 caaagctggg acactccccg aaggctttca accctgtttg gcaggggtaa ccagagatgg 720
 aagaccgggc taaaattgct gtatttacca cccactttcc ctggggactg gacttgggac 780
 aagtactcta accatgaaga taagcaaggt aggttgga caactcccga ggacagttaa 840
 agagtctcta tcctgagctg tcaagctact aaacagggtg tgagggtgc ggctgcccc 900
 tgcctagtga gaaaaaagg gaagagtaag acaattgtcc agcactagca gtctcaggcc 960

ccaaggcaga ggggcccaga ggcagtgaag cgactcttac cccgccccca ccctgctgct 1020
 gagtctgtct gatgttttgg ttgtatgaat aaacataatt cccctctgg 1069

<210> 70

<211> 159

<212> PRT

<213> Mus musculus

<400> 70

Met Glu Ala Glu Arg Pro Gln Glu Glu Asp Gly Glu Gln Ser Leu Pro

1 5 10 15

Gln Asp Asp Gln Gly Trp Pro Pro Val Asn Ala Thr Ala Arg Pro Trp

20 25 30

Arg Ser Ala Pro Pro Ser Pro Pro Pro Gly Thr Arg His Thr Ala

35 40 45

Leu Gly Pro Arg Ser Gly Ser Leu Leu Ser Leu Gln Thr Glu Leu Leu

50 55 60

Leu Asp Leu Val Ala Glu Ala Gln Ser Arg Arg Leu Glu Glu Gln Arg

65 70 75 80

Ala Thr Phe His Thr Pro Glu Ala Pro Pro Asn Leu Ala Pro Ala Pro

85 90 95

Pro Arg Leu Leu Glu Asp Lys Glu Gln Leu Tyr Ser Thr Ile Leu Ser

100 105 110

His Gln Cys Gln Arg Ile Glu Ala Gln Arg Ser Asp Pro Pro Leu Pro

115 120 125

Pro Gly Gly Gln Glu Leu Leu Glu Leu Leu Arg Val Gln Gly Gly

130 135 140

Gly Arg Met Glu Glu Gln Arg Ser Arg Pro Pro Thr His Thr Cys

261/617

145

150

155

<210> 71

<211> 1147

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (66).. (545)

<400> 71

caaggttcca gccctcctcc caaatcccag ccacctctcc cccaccagtt tctcccctct 60

agggg atg gag gct gag aga ccc cag gaa gaa gag gat ggt gag cag ggc 110

Met Glu Ala Glu Arg Pro Gln Glu Glu Glu Asp Gly Glu Gln Gly

1

5

10

15

ccc cct cag gat gag gaa ggc tgg ccc cct cca aac tcc acc act cgg 158

Pro Pro Gln Asp Glu Glu Gly Trp Pro Pro Pro Asn Ser Thr Thr Arg

20

25

30

cct tgg cga tct gct cct cca tcc cct cct cct cca ggg acc cgc cac 206

Pro Trp Arg Ser Ala Pro Pro Ser Pro Pro Pro Pro Gly Thr Arg His

35

40

45

aca gcc ctg gga ccc cgc tcg gcc tcc ctg ctc tcc ctg cag act gaa 254

Thr Ala Leu Gly Pro Arg Ser Ala Ser Leu Leu Ser Leu Gln Thr Glu

50

55

60

ctc ctt ctg gac ctg gtg gct gaa gcc cag tcc cgc cgc ctg gag gag 302

Leu Leu Leu Asp Leu Val Ala Glu Ala Gln Ser Arg Arg Leu Glu Glu

65

70

75

cag agg gcc acc ttc tac acc ccc caa aac ccc tca agc cta gcc cct 350

262/617

Gln Arg Ala Thr Phe Tyr Thr Pro Gln Asn Pro Ser Ser Leu Ala Pro
 80 85 90 95
 gcc cca ctc cgt cct ctc gag gac aga gaa cag ctt tac agc act atc 398
 Ala Pro Leu Arg Pro Leu Glu Asp Arg Glu Gln Leu Tyr Ser Thr Ile
 100 105 110
 ctc agt cac cag tgc cag cgg atg gaa gcc cag cgg tca gag cct ccc 446
 Leu Ser His Gln Cys Gln Arg Met Glu Ala Gln Arg Ser Glu Pro Pro
 115 120 125
 ctc cct cca ggg ggg caa gag ctc ctg gag ttg ctg ctg aga gtt cag 494
 Leu Pro Pro Gly Gly Gln Glu Leu Leu Glu Leu Leu Leu Arg Val Gln
 130 135 140
 ggt ggg ggt cga atg gag gag caa agg tcc cgg ccc ccc aca cac acc 542
 Gly Gly Gly Arg Met Glu Glu Gln Arg Ser Arg Pro Pro Thr His Thr
 145 150 155
 tgc tgagacttga gcccacaacca gcccttcctt gccactggtc tcaaagctgg 595
 Cys
 160
 gcagcccatt gcatgccctc aactcttget tggcaggggt accagagact gaaagacacg 655
 gcacaaatct caatattcat ctccacatc accttcctg ggaactggac aggggtgaaag 715
 tcctcaaact ctgggaacag gcgagatgga acagggattt aactccccgc ccacaggtcc 775
 atgggagctt gaggcagtaa gggggatccc aggcacccat ctcaaggagt ggctgggagt 835
 cttttcccta acttgtgggg acaccaccag ttgtcaagct actaggcagt aggggtctgag 895
 ggctcaggcc tccacctgag aggttataac ctgagagaca gctctacct tcctccagt 955
 aagaaggga ggtgggtggg cacctgagag attaagacta ttctccagt cccactacca 1015
 gcacccccga tcctgagac tgaggggttt acgggctgtg aatggacctt cagccctgcc 1075
 caccctccct cccactgct gctgagtctg tctgatgtt tggttgtgtg aataaatata 1135
 attccctct gg 1147

<210> 72

<211> 160

<212> PRT

<213> Homo sapiens

<400> 72

Met Glu Ala Glu Arg Pro Gln Glu Glu Glu Asp Gly Glu Gln Gly Pro

1 5 10 15

Pro Gln Asp Glu Glu Gly Trp Pro Pro Pro Asn Ser Thr Thr Arg Pro

20 25 30

Trp Arg Ser Ala Pro Pro Ser Pro Pro Pro Gly Thr Arg His Thr

35 40 45

Ala Leu Gly Pro Arg Ser Ala Ser Leu Leu Ser Leu Gln Thr Glu Leu

50 55 60

Leu Leu Asp Leu Val Ala Glu Ala Gln Ser Arg Arg Leu Glu Glu Gln

65 70 75 80

Arg Ala Thr Phe Tyr Thr Pro Gln Asn Pro Ser Ser Leu Ala Pro Ala

85 90 95

Pro Leu Arg Pro Leu Glu Asp Arg Glu Gln Leu Tyr Ser Thr Ile Leu

100 105 110

Ser His Gln Cys Gln Arg Met Glu Ala Gln Arg Ser Glu Pro Pro Leu

115 120 125

Pro Pro Gly Gly Gln Glu Leu Leu Glu Leu Leu Arg Val Gln Gly

130 135 140

Gly Gly Arg Met Glu Glu Gln Arg Ser Arg Pro Pro Thr His Thr Cys

145 150 155 160

<210> 73

<211> 1987

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (255)..(1433)

<400> 73

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 tacataggga acttctgccg gaggacagca acgtttttgt cctaggaaga aaggggtgac 180
 gttccaggaa ggccactaac atcgaatcac acataataac tcctctggat caggctgctc 240
 cactactccc caac atg gca gag acc cat tat gct ccc ctg agc tca gcc 290

Met Ala Glu Thr His Tyr Ala Pro Leu Ser Ser Ala

1

5

10

ttc ccc ttt gtc acg tca tac caa aca ggc tcc agc agg tta cct gag 338

Phe Pro Phe Val Thr Ser Tyr Gln Thr Gly Ser Ser Arg Leu Pro Glu

15

20

25

gtc agt agg agc acc gaa aga gct tta aga gaa gga aaa cta ctg gaa 386

Val Ser Arg Ser Thr Glu Arg Ala Leu Arg Glu Gly Lys Leu Leu Glu

30

35

40

ctg gtc tac gga atc aag gag act gtg gca aca ttg tcc cag att cca 434

Leu Val Tyr Gly Ile Lys Glu Thr Val Ala Thr Leu Ser Gln Ile Pro

45

50

55

60

gtg agc atc ttt gtg act ggg gac tct ggc aat ggc atg tca tct ttc 482

Val Ser Ile Phe Val Thr Gly Asp Ser Gly Asn Gly Met Ser Ser Phe

65

70

75

265/617

atc aat gca ctt cga gtc atc ggc cat gat gaa gat gcc tcg gct ccc 530
 Ile Asn Ala Leu Arg Val Ile Gly His Asp Glu Asp Ala Ser Ala Pro
 80 85 90
 act ggg gtg gtg agg acc acg aag acg cgg act gag tac tct tca tcc 578
 Thr Gly Val Val Arg Thr Thr Lys Thr Arg Thr Glu Tyr Ser Ser Ser
 95 100 105
 cac ttt ccc aat gtg gtg ctg tgg gac tta cct gga ttg ggg gcc aca 626
 His Phe Pro Asn Val Val Leu Trp Asp Leu Pro Gly Leu Gly Ala Thr
 110 115 120
 gcc caa acc gta gag gac tat gtg gaa gag atg aaa ttt agc aca tgt 674
 Ala Gln Thr Val Glu Asp Tyr Val Glu Glu Met Lys Phe Ser Thr Cys
 125 130 135 140
 gac tta ttc atc atc att gcc tct gag cag ttc agc tcg aat cat gtg 722
 Asp Leu Phe Ile Ile Ile Ala Ser Glu Gln Phe Ser Ser Asn His Val
 145 150 155
 aag ctg tcc aaa att atc cag agc atg gga aag agg ttc tat att gtc 770
 Lys Leu Ser Lys Ile Ile Gln Ser Met Gly Lys Arg Phe Tyr Ile Val
 160 165 170
 tgg acc aag ctg gac agg gac ctc agc acc agt gtc cta tca gag gtc 818
 Trp Thr Lys Leu Asp Arg Asp Leu Ser Thr Ser Val Leu Ser Glu Val
 175 180 185
 cgg ctc cta cag aat atc cag gag aat atc cga gag aat ctg cag aag 866
 Arg Leu Leu Gln Asn Ile Gln Glu Asn Ile Arg Glu Asn Leu Gln Lys
 190 195 200
 gag aaa gtg aag tac ccc ccc gtg ttc ctg gta tcc agt cta gac cct 914
 Glu Lys Val Lys Tyr Pro Pro Val Phe Leu Val Ser Ser Leu Asp Pro
 205 210 215 220

tta cta tat gac ttc ccg aag ctt agg gac aca ctt cat aaa gat ctc	962
Leu Leu Tyr Asp Phe Pro Lys Leu Arg Asp Thr Leu His Lys Asp Leu	
225 230 235	
tcc aac atc agg tgc tgt gaa ccc tta aag acc ctt tac ggc act tat	1010
Ser Asn Ile Arg Cys Cys Glu Pro Leu Lys Thr Leu Tyr Gly Thr Tyr	
240 245 250	
gag aag atc gtt ggt gat aaa gta gca gtc tgg aag cag aga ata gcc	1058
Glu Lys Ile Val Gly Asp Lys Val Ala Val Trp Lys Gln Arg Ile Ala	
255 260 265	
aac gag tcc ttg aag aat tct ctc ggt gtc aga gat gat gac aac atg	1106
Asn Glu Ser Leu Lys Asn Ser Leu Gly Val Arg Asp Asp Asp Asn Met	
270 275 280	
ggc gag tgt ctg aaa gtg tac cga ctg ata ttt ggt gta gat gac gaa	1154
Gly Glu Cys Leu Lys Val Tyr Arg Leu Ile Phe Gly Val Asp Asp Glu	
285 290 295 300	
tca gtt cag cag gta gcc cag agt atg ggg aca gta gtc atg gag tac	1202
Ser Val Gln Gln Val Ala Gln Ser Met Gly Thr Val Val Met Glu Tyr	
305 310 315	
aag gac aac atg aag tcc caa aac ttt tat act ctc cgc aga gag gac	1250
Lys Asp Asn Met Lys Ser Gln Asn Phe Tyr Thr Leu Arg Arg Glu Asp	
320 325 330	
tgg aaa ctg agg ctg atg aca tgt gca att gtg aat gca ttc ttc cgt	1298
Trp Lys Leu Arg Leu Met Thr Cys Ala Ile Val Asn Ala Phe Phe Arg	
335 340 345	
ttg ttg aga ttt ctc cca tgc gta tgc tgc tgt tta aga cgc ttg aga	1346
Leu Leu Arg Phe Leu Pro Cys Val Cys Cys Cys Leu Arg Arg Leu Arg	
350 355 360	

cat aaa cgc atg ctt ttc tta gtt gcc cag gac acc aag aac atc cta 1394

His Lys Arg Met Leu Phe Leu Val Ala Gln Asp Thr Lys Asn Ile Leu

365 370 375 380

gag aaa atc ctg agg gac tcc atc ttc cct ccg cag atc tagtataagg 1443

Glu Lys Ile Leu Arg Asp Ser Ile Phe Pro Pro Gln Ile

385 390

gcagcctggt acccttcttc ttccacagaa gccagggttac cttagatctc tttcctagat 1503

ccctattttct ccaccagaaa tcaagagata caaaaatgct tcctgtaagg gttttagatt 1563

ctctgagagg agttaaaatc actcatctcc cctgtctcga ttctaatagca ttgttccact 1623

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agaaattttg tttttgggca gagatggctt agcagttaag aacaccaact gcttttccga 1743

aggtcatgag ttcaaattccc agcaaccacg tgatgggtca caaccatccg tagtgagatc 1803

tgatgccctc ttctgagatg tctgaagaca gctacagtgt acttacatat aataaataaa 1863

taaataaata aataaataaa taaatctttg ggaaaaaaat tagaaatttt gttttcagct 1923

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catt 1987

<210> 74

<211> 393

<212> PRT

<213> Mus musculus

<400> 74

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Thr Ser Tyr Gln Thr Gly Ser Ser Arg Leu Pro Glu Val Ser Arg Ser

20 25 30

Thr Glu Arg Ala Leu Arg Glu Gly Lys Leu Leu Glu Leu Val Tyr Gly

268/617

35 40 45
 Ile Lys Glu Thr Val Ala Thr Leu Ser Gln Ile Pro Val Ser Ile Phe
 50 55 60
 Val Thr Gly Asp Ser Gly Asn Gly Met Ser Ser Phe Ile Asn Ala Leu
 65 70 75 80
 Arg Val Ile Gly His Asp Glu Asp Ala Ser Ala Pro Thr Gly Val Val
 85 90 95
 Arg Thr Thr Lys Thr Arg Thr Glu Tyr Ser Ser Ser His Phe Pro Asn
 100 105 110
 Val Val Leu Trp Asp Leu Pro Gly Leu Gly Ala Thr Ala Gln Thr Val
 115 120 125
 Glu Asp Tyr Val Glu Glu Met Lys Phe Ser Thr Cys Asp Leu Phe Ile
 130 135 140
 Ile Ile Ala Ser Glu Gln Phe Ser Ser Asn His Val Lys Leu Ser Lys
 145 150 155 160
 Ile Ile Gln Ser Met Gly Lys Arg Phe Tyr Ile Val Trp Thr Lys Leu
 165 170 175
 Asp Arg Asp Leu Ser Thr Ser Val Leu Ser Glu Val Arg Leu Leu Gln
 180 185 190
 Asn Ile Gln Glu Asn Ile Arg Glu Asn Leu Gln Lys Glu Lys Val Lys
 195 200 205
 Tyr Pro Pro Val Phe Leu Val Ser Ser Leu Asp Pro Leu Leu Tyr Asp
 210 215 220
 Phe Pro Lys Leu Arg Asp Thr Leu His Lys Asp Leu Ser Asn Ile Arg
 225 230 235 240
 Cys Cys Glu Pro Leu Lys Thr Leu Tyr Gly Thr Tyr Glu Lys Ile Val
 245 250 255

Gly Asp Lys Val Ala Val Trp Lys Gln Arg Ile Ala Asn Glu Ser Leu

260 265 270

Lys Asn Ser Leu Gly Val Arg Asp Asp Asp Asn Met Gly Glu Cys Leu

275 280 285

Lys Val Tyr Arg Leu Ile Phe Gly Val Asp Asp Glu Ser Val Gln Gln

290 295 300

Val Ala Gln Ser Met Gly Thr Val Val Met Glu Tyr Lys Asp Asn Met

305 310 315 320

Lys Ser Gln Asn Phe Tyr Thr Leu Arg Arg Glu Asp Trp Lys Leu Arg

325 330 335

Leu Met Thr Cys Ala Ile Val Asn Ala Phe Phe Arg Leu Leu Arg Phe

340 345 350

Leu Pro Cys Val Cys Cys Cys Leu Arg Arg Leu Arg His Lys Arg Met

355 360 365

Leu Phe Leu Val Ala Gln Asp Thr Lys Asn Ile Leu Glu Lys Ile Leu

370 375 380

Arg Asp Ser Ile Phe Pro Pro Gln Ile

385 390

<210> 75

<211> 2250

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (468).. (1694)

<400> 75

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 tcattcttca acatccgggt ctatattcca gttttggatc tctacatagg gaacttctgc 180
 cggaggacag caacgttttt gtcctaggaa gaaaggggtg acgttccagg aaggccacta 240
 acatcgaatc acacataata actcctctgg atcagggttt gaggagtatt aagttagata 300
 aggcatcga aggaaccaac tcagattcac agacagagga cctgtgtgct taaagtctaa 360
 gaggaggagga agaacctgag gagcggcttc ctacagagacc ctaataaaac cagagagcct 420
 caccagggag ctgaaaggtc cacagacagc gtcactcgga tcttatac atg aaa cca 476

Met Lys Pro

1

tca cac agt tcc tgc gag gct gct cca cta ctc ccc aac atg gca gag 524
 Ser His Ser Ser Cys Glu Ala Ala Pro Leu Leu Pro Asn Met Ala Glu
 5 10 15
 acc cat tat gct ccc ctg agc tca gcc ttc ccc ttt gtc acg tca tac 572
 Thr His Tyr Ala Pro Leu Ser Ser Ala Phe Pro Phe Val Thr Ser Tyr
 20 25 30 35
 caa aca ggc tcc agc agg tta cct gag gtc agt agg agc acc gaa aga 620
 Gln Thr Gly Ser Ser Arg Leu Pro Glu Val Ser Arg Ser Thr Glu Arg
 40 45 50
 gct tta aga gaa gga aaa cta ctg gaa ctg gtc tac gga atc aag gag 668
 Ala Leu Arg Glu Gly Lys Leu Leu Glu Leu Val Tyr Gly Ile Lys Glu
 55 60 65
 act gtg gca aca ttg tcc cag att cca gtg agc atc ttt gtg act ggg 716
 Thr Val Ala Thr Leu Ser Gln Ile Pro Val Ser Ile Phe Val Thr Gly
 70 75 80
 gac tct ggc aat ggc atg tca tct ttc atc aat gca ctt cga gtc atc 764
 Asp Ser Gly Asn Gly Met Ser Ser Phe Ile Asn Ala Leu Arg Val Ile

271/617

85	90	95	
ggc cat gat gaa gat gcc tcg gct ccc act ggg gtg gtg agg acc acg	812		
Gly His Asp Glu Asp Ala Ser Ala Pro Thr Gly Val Val Arg Thr Thr			
100	105	110	115
aag acg cgg act gag tac tct tca tcc cac ttt ccc aat gtg gtg ctg	860		
Lys Thr Arg Thr Glu Tyr Ser Ser Ser His Phe Pro Asn Val Val Leu			
120	125	130	
tgg gac tta cct gga ttg ggg gcc aca gcc caa acc gta gag gac tat	908		
Trp Asp Leu Pro Gly Leu Gly Ala Thr Ala Gln Thr Val Glu Asp Tyr			
135	140	145	
gtg gaa gag atg aaa ttt agc aca tgt gac tta ttc atc atc att gcc	956		
Val Glu Glu Met Lys Phe Ser Thr Cys Asp Leu Phe Ile Ile Ile Ala			
150	155	160	
tct gag cag ttc agc tcg aat cat gtg aag ctg tcc aaa att atc cag	1004		
Ser Glu Gln Phe Ser Ser Asn His Val Lys Leu Ser Lys Ile Ile Gln			
165	170	175	
agc atg gga aag agg ttc tat att gtc tgg acc aag ctg gac agg gac	1052		
Ser Met Gly Lys Arg Phe Tyr Ile Val Trp Thr Lys Leu Asp Arg Asp			
180	185	190	195
ctc agc acc agt gtc cta tca gag gtc cgg ctc cta cag aat atc cag	1100		
Leu Ser Thr Ser Val Leu Ser Glu Val Arg Leu Leu Gln Asn Ile Gln			
200	205	210	
gag aat atc cga gag aat ctg cag aag gag aaa gtg aag tac ccc ccc	1148		
Glu Asn Ile Arg Glu Asn Leu Gln Lys Glu Lys Val Lys Tyr Pro Pro			
215	220	225	
gtg ttc ctg gta tcc agt cta gac cct tta cta tat gac ttc ccg aag	1196		
Val Phe Leu Val Ser Ser Leu Asp Pro Leu Leu Tyr Asp Phe Pro Lys			

230	235	240	
ctt agg gac aca ctt cat aaa gat ctc tcc aac atc agg tgc tgt gaa			1244
Leu Arg Asp Thr Leu His Lys Asp Leu Ser Asn Ile Arg Cys Cys Glu			
245	250	255	
ccc tta aag acc ctt tat ggc act tat gag aag atc gtt ggt gat aaa			1292
Pro Leu Lys Thr Leu Tyr Gly Thr Tyr Glu Lys Ile Val Gly Asp Lys			
260	265	270	275
gta gca gtc tgg aag cag aga ata gcc aac gag tcc ttg aag aat tct			1340
Val Ala Val Trp Lys Gln Arg Ile Ala Asn Glu Ser Leu Lys Asn Ser			
280	285	290	
ctc ggt gtc aga gat gat gac aac atg ggc gag tgt ctg aaa gtg tac			1388
Leu Gly Val Arg Asp Asp Asp Asn Met Gly Glu Cys Leu Lys Val Tyr			
295	300	305	
cga ctg ata ttt ggt gta gat gac gaa tca gtt cag cag gta gcc cag			1436
Arg Leu Ile Phe Gly Val Asp Asp Glu Ser Val Gln Gln Val Ala Gln			
310	315	320	
agt atg ggg aca gta gtc atg gag tac aag gac aac atg aag tcc caa			1484
Ser Met Gly Thr Val Val Met Glu Tyr Lys Asp Asn Met Lys Ser Gln			
325	330	335	
aac ttt tat act ctc cgc aga gag gac tgg aaa ctg agg ctg atg aca			1532
Asn Phe Tyr Thr Leu Arg Arg Glu Asp Trp Lys Leu Arg Leu Met Thr			
340	345	350	355
tgt gca att gtg aat gca ttc ttc cgt ttg ttg aga ttt ctc cca tgc			1580
Cys Ala Ile Val Asn Ala Phe Phe Arg Leu Leu Arg Phe Leu Pro Cys			
360	365	370	
gta tgc tgc tgt tta aga cgc ttg aga cat aaa cgc atg ctt ttc tta			1628
Val Cys Cys Cys Leu Arg Arg Leu Arg His Lys Arg Met Leu Phe Leu			

375 380 385
 gtt gcc cag gac acc aag aac atc cta gag aaa atc ctg agg gac tcc 1676
 Val Ala Gln Asp Thr Lys Asn Ile Leu Glu Lys Ile Leu Arg Asp Ser
 390 395 400
 atc ttc cct ccg cag atc tagtataagg gcagcctggt acccttcttc 1724
 Ile Phe Pro Pro Gln Ile
 405
 ttccacagaa gccaggttac cttagatctc tttcctagat ccctatttct ccaccagaaa 1784
 tcaagagata caaaaatgct tcctgtaagg gttttagatt ctctgagagg agttaaaatc 1844
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 gattaaaatt cattgacat gattcttaga tttggaatat agaaattttg tttttgggct 1964
 ggagagatgg cttagcagtt aagaacacca actgcttttc cgaaggatcat gagttcaaat 2024
 cccagcaacc acgtgatggc tcacaacat ccgtagtgag atctgatgcc ctcttctgag 2084
 atgtctgaag acagctacag tgtacttaca tataataaat aaataaataa ataaataaat 2144
 aaataaatct ttgggaaaaa aattagaaat tttgttttca gctattaaat gtgatatatg 2204
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<210> 76

<211> 409

<212> PRT

<213> Mus musculus

<400> 76

Met Lys Pro Ser His Ser Ser Cys Glu Ala Ala Pro Leu Leu Pro Asn

1 5 10 15

Met Ala Glu Thr His Tyr Ala Pro Leu Ser Ser Ala Phe Pro Phe Val

20 25 30

Thr Ser Tyr Gln Thr Gly Ser Ser Arg Leu Pro Glu Val Ser Arg Ser

274/617

35 40 45
Thr Glu Arg Ala Leu Arg Glu Gly Lys Leu Leu Glu Leu Val Tyr Gly
50 55 60
Ile Lys Glu Thr Val Ala Thr Leu Ser Gln Ile Pro Val Ser Ile Phe
65 70 75 80
Val Thr Gly Asp Ser Gly Asn Gly Met Ser Ser Phe Ile Asn Ala Leu
85 90 95
Arg Val Ile Gly His Asp Glu Asp Ala Ser Ala Pro Thr Gly Val Val
100 105 110
Arg Thr Thr Lys Thr Arg Thr Glu Tyr Ser Ser Ser His Phe Pro Asn
115 120 125
Val Val Leu Trp Asp Leu Pro Gly Leu Gly Ala Thr Ala Gln Thr Val
130 135 140
Glu Asp Tyr Val Glu Glu Met Lys Phe Ser Thr Cys Asp Leu Phe Ile
145 150 155 160
Ile Ile Ala Ser Glu Gln Phe Ser Ser Asn His Val Lys Leu Ser Lys
165 170 175
Ile Ile Gln Ser Met Gly Lys Arg Phe Tyr Ile Val Trp Thr Lys Leu
180 185 190
Asp Arg Asp Leu Ser Thr Ser Val Leu Ser Glu Val Arg Leu Leu Gln
195 200 205
Asn Ile Gln Glu Asn Ile Arg Glu Asn Leu Gln Lys Glu Lys Val Lys
210 215 220
Tyr Pro Pro Val Phe Leu Val Ser Ser Leu Asp Pro Leu Leu Tyr Asp
225 230 235 240
Phe Pro Lys Leu Arg Asp Thr Leu His Lys Asp Leu Ser Asn Ile Arg
245 250 255

275/617

Cys Cys Glu Pro Leu Lys Thr Leu Tyr Gly Thr Tyr Glu Lys Ile Val

260 265 270

Gly Asp Lys Val Ala Val Trp Lys Gln Arg Ile Ala Asn Glu Ser Leu

275 280 285

Lys Asn Ser Leu Gly Val Arg Asp Asp Asp Asn Met Gly Glu Cys Leu

290 295 300

Lys Val Tyr Arg Leu Ile Phe Gly Val Asp Asp Glu Ser Val Gln Gln

305 310 315 320

Val Ala Gln Ser Met Gly Thr Val Val Met Glu Tyr Lys Asp Asn Met

325 330 335

Lys Ser Gln Asn Phe Tyr Thr Leu Arg Arg Glu Asp Trp Lys Leu Arg

340 345 350

Leu Met Thr Cys Ala Ile Val Asn Ala Phe Phe Arg Leu Leu Arg Phe

355 360 365

Leu Pro Cys Val Cys Cys Cys Leu Arg Arg Leu Arg His Lys Arg Met

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Arg Asp Ser Ile Phe Pro Pro Gln Ile

405

<210> 77

<211> 1832

<212> DNA

<213> Mus musculus

<220>

<221> CDS

276/617

<222> (77).. (1630)

<400> 77

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gcgcgcgtgc gcggac atg gct tca aac gac tat acc caa caa gca act caa   112
      Met Ala Ser Asn Asp Tyr Thr Gln Gln Ala Thr Gln
              1              5              10
agc tac ggg gcc tat cct acc cag cct ggg cag ggc tac tcc caa cag   160
Ser Tyr Gly Ala Tyr Pro Thr Gln Pro Gly Gln Gly Tyr Ser Gln Gln
      15              20              25
agc agt cag ccc tat ggc caa cag agt tac agt ggt tat ggc cag tca   208
Ser Ser Gln Pro Tyr Gly Gln Gln Ser Tyr Ser Gly Tyr Gly Gln Ser
      30              35              40
gct gac act tca gga tac ggc cag agc agc tat ggt tct tct tat gga   256
Ala Asp Thr Ser Gly Tyr Gly Gln Ser Ser Tyr Gly Ser Ser Tyr Gly
      45              50              55              60
cag acc caa aac aca ggc tat gga act cag tca gct ccc cag gga tat   304
Gln Thr Gln Asn Thr Gly Tyr Gly Thr Gln Ser Ala Pro Gln Gly Tyr
      65              70              75
ggt tcc act gga ggc tat ggc agc agc caa agt tca caa tct tct tat   352
Gly Ser Thr Gly Gly Tyr Gly Ser Ser Gln Ser Ser Gln Ser Ser Tyr
      80              85              90
ggg cag cag tcc tcc tac cct ggc tat ggc caa cag cca gct cct agc   400
Gly Gln Gln Ser Ser Tyr Pro Gly Tyr Gly Gln Gln Pro Ala Pro Ser
      95              100              105
agc acc tca gga agt tat ggt ggc agt tct cag agc agc agc tat ggg   448
Ser Thr Ser Gly Ser Tyr Gly Gly Ser Ser Gln Ser Ser Ser Tyr Gly
      110              115              120

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277/617

caa ccc cag agt gga ggt tat ggt caa cag tct ggc tat ggt gga cag 496
 Gln Pro Gln Ser Gly Gly Tyr Gly Gln Gln Ser Gly Tyr Gly Gly Gln
 125 130 135 140
 caa caa agc tac gga caa caa caa agc tcc tat aac cca cct cag ggt 544
 Gln Gln Ser Tyr Gly Gln Gln Gln Ser Ser Tyr Asn Pro Pro Gln Gly
 145 150 155
 tat gga caa cag aac cag tac aac agt agc agt gga ggt ggt gga ggg 592
 Tyr Gly Gln Gln Asn Gln Tyr Asn Ser Ser Ser Gly Gly Gly Gly Gly
 160 165 170
 ggt ggt gga ggc aac tat ggc caa gat cag tcc tct atg agt ggt ggc 640
 Gly Gly Gly Gly Asn Tyr Gly Gln Asp Gln Ser Ser Met Ser Gly Gly
 175 180 185
 ggt ggc ggt ggt ggt tat ggc aat cag gac cag agt ggt ggc ggc ggc 688
 Gly Gly Gly Gly Gly Tyr Gly Asn Gln Asp Gln Ser Gly Gly Gly Gly
 190 195 200
 ggc ggc tac ggg gga ggc caa cag gat cgt ggg ggc cga ggc agg ggc 736
 Gly Gly Tyr Gly Gly Gly Gln Gln Asp Arg Gly Gly Arg Gly Arg Gly
 205 210 215 220
 ggt gga ggt ggt tac aac cga agc agt ggt ggc tat gaa ccc aga ggc 784
 Gly Gly Gly Gly Tyr Asn Arg Ser Ser Gly Gly Tyr Glu Pro Arg Gly
 225 230 235
 cgt gga ggt ggc cga gga ggc aga ggc ggc atg ggc gga agt gac cgc 832
 Arg Gly Gly Gly Arg Gly Gly Arg Gly Gly Met Gly Gly Ser Asp Arg
 240 245 250
 ggt ggc ttc aat aaa ttt ggt ggt cct cgg gat caa gga tct cgt cat 880
 Gly Gly Phe Asn Lys Phe Gly Gly Pro Arg Asp Gln Gly Ser Arg His
 255 260 265

gat tct gaa cag gat aat tca gac aac aat acc atc ttc gtg caa ggc 928
Asp Ser Glu Gln Asp Asn Ser Asp Asn Asn Thr Ile Phe Val Gln Gly
270 275 280
cta ggc gag aat gtt aca att gaa tct gtg gct gat tac ttc aag cag 976
Leu Gly Glu Asn Val Thr Ile Glu Ser Val Ala Asp Tyr Phe Lys Gln
285 290 295 300
att gga att att aag aca aac aag aaa act gga cag cct atg att aat 1024
Ile Gly Ile Ile Lys Thr Asn Lys Lys Thr Gly Gln Pro Met Ile Asn
305 310 315
ttg tac aca gac agg gaa act ggc aag ttg aag ggt gag gca aca gtt 1072
Leu Tyr Thr Asp Arg Glu Thr Gly Lys Leu Lys Gly Glu Ala Thr Val
320 325 330
tca ttt gat gac cca cct tct gct aaa gca gct atc gac tgg ttt gat 1120
Ser Phe Asp Asp Pro Pro Ser Ala Lys Ala Ala Ile Asp Trp Phe Asp
335 340 345
ggg aaa gaa ttc tct ggg aat cct att aaa gtt tca ttt gct acc cgc 1168
Gly Lys Glu Phe Ser Gly Asn Pro Ile Lys Val Ser Phe Ala Thr Arg
350 355 360
cga gct gac ttc aat cgg ggt ggt gga aat ggt cgc gga ggc cga ggg 1216
Arg Ala Asp Phe Asn Arg Gly Gly Gly Asn Gly Arg Gly Gly Arg Gly
365 370 375 380
cga gga gga ccc atg ggc cgt gga ggc tat gga gga ggt ggc agt ggt 1264
Arg Gly Gly Pro Met Gly Arg Gly Gly Tyr Gly Gly Gly Gly Ser Gly
385 390 395
ggg ggt ggc cgg gga gga ttc ccc agt gga ggt ggt gga ggt gga gga 1312
Gly Gly Gly Arg Gly Gly Phe Pro Ser Gly Gly Gly Gly Gly Gly Gly
400 405 410

cag caa cga gct gga gac tgg aag tgt cct aat cct aca tgt gag aac 1360
 Gln Gln Arg Ala Gly Asp Trp Lys Cys Pro Asn Pro Thr Cys Glu Asn
 415 420 425
 atg aac ttc tct tgg aga aat gaa tgc aac cag tgt aag gca cct aag 1408
 Met Asn Phe Ser Trp Arg Asn Glu Cys Asn Gln Cys Lys Ala Pro Lys
 430 435 440
 cca gat ggc cca gga ggg gga cca gga ggc tct cat atg ggg gga aac 1456
 Pro Asp Gly Pro Gly Gly Gly Pro Gly Gly Ser His Met Gly Gly Asn
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 tat gga gat gat cga cgt ggc aga gga gga tat gac cgg ggc ggc tac 1504
 Tyr Gly Asp Asp Arg Arg Gly Arg Gly Gly Tyr Asp Arg Gly Gly Tyr
 465 470 475
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 Arg Gly Arg Gly Gly Asp Arg Gly Gly Phe Arg Gly Gly Arg Gly Gly
 480 485 490
 ggg gac aga ggc ggt ttt ggc cct ggc aag atg gac tcc agg ggc gag 1600
 Gly Asp Arg Gly Gly Phe Gly Pro Gly Lys Met Asp Ser Arg Gly Glu
 495 500 505
 cac aga cag gat cgc agg gag agg cca tat tagcctggct cctgaagttc 1650
 His Arg Gln Asp Arg Arg Glu Arg Pro Tyr
 510 515
 tggaactctt cctgtacca gtgttaccct tgttattttg taaacttaca attcaggatc 1710
 gctcatggat attttttttt ggggggggtg gggcggttgt gtgtgtatgt gtgtgtgtgt 1770
 gtgtcagact accctaattg taaccatata tctggttccc attaaaaaac atcatttttag 1830
 tt 1832

<210> 78

280/617

<211> 518

<212> PRT

<213> Mus musculus

<400> 78

Met Ala Ser Asn Asp Tyr Thr Gln Gln Ala Thr Gln Ser Tyr Gly Ala
 1 5 10 15
 Tyr Pro Thr Gln Pro Gly Gln Gly Tyr Ser Gln Gln Ser Ser Gln Pro
 20 25 30
 Tyr Gly Gln Gln Ser Tyr Ser Gly Tyr Gly Gln Ser Ala Asp Thr Ser
 35 40 45
 Gly Tyr Gly Gln Ser Ser Tyr Gly Ser Ser Tyr Gly Gln Thr Gln Asn
 50 55 60
 Thr Gly Tyr Gly Thr Gln Ser Ala Pro Gln Gly Tyr Gly Ser Thr Gly
 65 70 75 80
 Gly Tyr Gly Ser Ser Gln Ser Ser Gln Ser Ser Tyr Gly Gln Gln Ser
 85 90 95
 Ser Tyr Pro Gly Tyr Gly Gln Gln Pro Ala Pro Ser Ser Thr Ser Gly
 100 105 110
 Ser Tyr Gly Gly Ser Ser Gln Ser Ser Ser Tyr Gly Gln Pro Gln Ser
 115 120 125
 Gly Gly Tyr Gly Gln Gln Ser Gly Tyr Gly Gly Gln Gln Gln Ser Tyr
 130 135 140
 Gly Gln Gln Gln Ser Ser Tyr Asn Pro Pro Gln Gly Tyr Gly Gln Gln
 145 150 155 160
 Asn Gln Tyr Asn Ser Ser Ser Gly Gly Gly Gly Gly Gly Gly Gly
 165 170 175
 Asn Tyr Gly Gln Asp Gln Ser Ser Met Ser Gly Gly Gly Gly Gly Gly

281/617

180	185	190	
Gly Tyr Gly Asn Gln Asp Gln Ser Gly Gly Gly Gly Gly Gly Tyr Gly			
195	200	205	
Gly Gly Gln Gln Asp Arg Gly Gly Arg Gly Arg Gly Gly Gly Gly Gly			
210	215	220	
Tyr Asn Arg Ser Ser Gly Gly Tyr Glu Pro Arg Gly Arg Gly Gly Gly			
225	230	235	240
Arg Gly Gly Arg Gly Gly Met Gly Gly Ser Asp Arg Gly Gly Phe Asn			
245	250	255	
Lys Phe Gly Gly Pro Arg Asp Gln Gly Ser Arg His Asp Ser Glu Gln			
260	265	270	
Asp Asn Ser Asp Asn Asn Thr Ile Phe Val Gln Gly Leu Gly Glu Asn			
275	280	285	
Val Thr Ile Glu Ser Val Ala Asp Tyr Phe Lys Gln Ile Gly Ile Ile			
290	295	300	
Lys Thr Asn Lys Lys Thr Gly Gln Pro Met Ile Asn Leu Tyr Thr Asp			
305	310	315	320
Arg Glu Thr Gly Lys Leu Lys Gly Glu Ala Thr Val Ser Phe Asp Asp			
325	330	335	
Pro Pro Ser Ala Lys Ala Ala Ile Asp Trp Phe Asp Gly Lys Glu Phe			
340	345	350	
Ser Gly Asn Pro Ile Lys Val Ser Phe Ala Thr Arg Arg Ala Asp Phe			
355	360	365	
Asn Arg Gly Gly Gly Asn Gly Arg Gly Gly Arg Gly Arg Gly Gly Pro			
370	375	380	
Met Gly Arg Gly Gly Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Arg			
385	390	395	400

Gly Gly Phe Pro Ser Gly Gly Gly Gly Gly Gly Gln Gln Arg Ala

405

410

415

Gly Asp Trp Lys Cys Pro Asn Pro Thr Cys Glu Asn Met Asn Phe Ser

420

425

430

Trp Arg Asn Glu Cys Asn Gln Cys Lys Ala Pro Lys Pro Asp Gly Pro

435

440

445

Gly Gly Gly Pro Gly Gly Ser His Met Gly Gly Asn Tyr Gly Asp Asp

450

455

460

Arg Arg Gly Arg Gly Gly Tyr Asp Arg Gly Gly Tyr Arg Gly Arg Gly

465

470

475

480

Gly Asp Arg Gly Gly Phe Arg Gly Gly Arg Gly Gly Gly Asp Arg Gly

485

490

495

Gly Phe Gly Pro Gly Lys Met Asp Ser Arg Gly Glu His Arg Gln Asp

500

505

510

Arg Arg Glu Arg Pro Tyr

515

<210> 79

<211> 1116

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (70)..(909)

<400> 79

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tgcgcggaac atg gct tca aac gac tat acc caa caa gca act caa agc tac 111

Met Ala Ser Asn Asp Tyr Thr Gln Gln Ala Thr Gln Ser Tyr

1 5 10

ggg gcc tat cct acc cag cct ggg cag ggc tac tcc caa cag agc agt 159

Gly Ala Tyr Pro Thr Gln Pro Gly Gln Gly Tyr Ser Gln Gln Ser Ser

15 20 25 30

cag ccc tat ggc caa cag agt tac agt ggt tat ggc cag tca gct gac 207

Gln Pro Tyr Gly Gln Gln Ser Tyr Ser Gly Tyr Gly Gln Ser Ala Asp

35 40 45

acc tca gga tac ggc cag agc agc tat ggt tct tct tat gga cag acc 255

Thr Ser Gly Tyr Gly Gln Ser Ser Tyr Gly Ser Ser Tyr Gly Gln Thr

50 55 60

caa aac aca ggc tat gga act cag tca gct ccc cag gga tat ggt tcc 303

Gln Asn Thr Gly Tyr Gly Thr Gln Ser Ala Pro Gln Gly Tyr Gly Ser

65 70 75

act gga ggc tat ggc agc agc caa agt tcc caa tct tct tat ggg cag 351

Thr Gly Gly Tyr Gly Ser Ser Gln Ser Ser Gln Ser Ser Tyr Gly Gln

80 85 90

cag tcc tcc tac cct ggc tat ggc caa cag cca gct cct agc agc acc 399

Gln Ser Ser Tyr Pro Gly Tyr Gly Gln Gln Pro Ala Pro Ser Ser Thr

95 100 105 110

tca gga agt tat ggt ggc agt tct cag agc agc agc tat ggg caa ccc 447

Ser Gly Ser Tyr Gly Gly Ser Ser Gln Ser Ser Ser Tyr Gly Gln Pro

115 120 125

cag agt gga ggt tat ggt caa cag tct ggc tat ggt gga cag caa caa 495

Gln Ser Gly Gly Tyr Gly Gln Gln Ser Gly Tyr Gly Gly Gln Gln Gln

130 135 140

agc tac gga caa caa caa agc tcc tat aac cca cct cag ggt tat gga 543

Ser Tyr Gly Gln Gln Gln Ser Ser Tyr Asn Pro Pro Gln Gly Tyr Gly
 145 150 155
 caa cag aac cag tac aac agt agc agt gga ggt ggt gga ggt gga gga 591
 Gln Gln Asn Gln Tyr Asn Ser Ser Ser Gly Gly Gly Gly Gly Gly Gly
 160 165 170
 cag caa cga gct gga gac tgg aag tgt cct aat cct aca tgt gag aac 639
 Gln Gln Arg Ala Gly Asp Trp Lys Cys Pro Asn Pro Thr Cys Glu Asn
 175 180 185 190
 atg aac ttc tct tgg aga aat gaa tgc aac cag tgt aag gca cct aag 687
 Met Asn Phe Ser Trp Arg Asn Glu Cys Asn Gln Cys Lys Ala Pro Lys
 195 200 205
 cca gat ggc cca gga ggg gga cca gga ggc tct cat atg ggg gga aac 735
 Pro Asp Gly Pro Gly Gly Gly Pro Gly Gly Ser His Met Gly Gly Asn
 210 215 220
 tat gga gat gat cga cgt ggc aga gga gga tat gac cgg ggc ggc tac 783
 Tyr Gly Asp Asp Arg Arg Gly Arg Gly Gly Tyr Asp Arg Gly Gly Tyr
 225 230 235
 cgg ggc cga gga ggg gac cgt ggg ggc ttc aga ggg ggc cgg ggt ggt 831
 Arg Gly Arg Gly Gly Asp Arg Gly Gly Phe Arg Gly Gly Arg Gly Gly
 240 245 250
 ggg gac aga ggc ggt ttt ggc cct ggc aag atg gac tcc agg ggc gag 879
 Gly Asp Arg Gly Gly Phe Gly Pro Gly Lys Met Asp Ser Arg Gly Glu
 255 260 265 270
 cac aga cag gat cgc agg gag agg cca tat tagcctggct cctgaagttc 929
 His Arg Gln Asp Arg Arg Glu Arg Pro Tyr
 275 280
 tggaactctt cctgtacca gtgtaccct tggtattttg taaacttaca attcaggatc 989

285/617

gciccatggat attttttttg gggggggtgg ggcggttgtg tgtgtatgtg tgtgtgtgtg 1049
 tgtgtgtgtc agactaccct aattgtaacc atatctctgg ttcccatata aaaacatcat 1109
 ttttagtt 1116

<210> 80

<211> 280

<212> PRT

<213> Mus musculus

<400> 80

Met Ala Ser Asn Asp Tyr Thr Gln Gln Ala Thr Gln Ser Tyr Gly Ala
 1 5 10 15
 Tyr Pro Thr Gln Pro Gly Gln Gly Tyr Ser Gln Gln Ser Ser Gln Pro
 20 25 30
 Tyr Gly Gln Gln Ser Tyr Ser Gly Tyr Gly Gln Ser Ala Asp Thr Ser
 35 40 45
 Gly Tyr Gly Gln Ser Ser Tyr Gly Ser Ser Tyr Gly Gln Thr Gln Asn
 50 55 60
 Thr Gly Tyr Gly Thr Gln Ser Ala Pro Gln Gly Tyr Gly Ser Thr Gly
 65 70 75 80
 Gly Tyr Gly Ser Ser Gln Ser Ser Gln Ser Ser Tyr Gly Gln Gln Ser
 85 90 95
 Ser Tyr Pro Gly Tyr Gly Gln Gln Pro Ala Pro Ser Ser Thr Ser Gly
 100 105 110
 Ser Tyr Gly Gly Ser Ser Gln Ser Ser Ser Tyr Gly Gln Pro Gln Ser
 115 120 125
 Gly Gly Tyr Gly Gln Gln Ser Gly Tyr Gly Gly Gln Gln Gln Ser Tyr
 130 135 140

286/617

Gly Gln Gln Gln Ser Ser Tyr Asn Pro Pro Gln Gly Tyr Gly Gln Gln
145 150 155 160
Asn Gln Tyr Asn Ser Ser Ser Gly Gly Gly Gly Gly Gly Gly Gln Gln
165 170 175
Arg Ala Gly Asp Trp Lys Cys Pro Asn Pro Thr Cys Glu Asn Met Asn
180 185 190
Phe Ser Trp Arg Asn Glu Cys Asn Gln Cys Lys Ala Pro Lys Pro Asp
195 200 205
Gly Pro Gly Gly Gly Pro Gly Gly Ser His Met Gly Gly Asn Tyr Gly
210 215 220
Asp Asp Arg Arg Gly Arg Gly Gly Tyr Asp Arg Gly Gly Tyr Arg Gly
225 230 235 240
Arg Gly Gly Asp Arg Gly Gly Phe Arg Gly Gly Arg Gly Gly Gly Asp
245 250 255
Arg Gly Gly Phe Gly Pro Gly Lys Met Asp Ser Arg Gly Glu His Arg
260 265 270
Gln Asp Arg Arg Glu Arg Pro Tyr
275 280

<210> 81

<211> 1824

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (79).. (1656)

<400> 81

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 gtgcgcgcgt gcgcggac atg gcc tca aac gat tat acc caa caa gca acc 111
 Met Ala Ser Asn Asp Tyr Thr Gln Gln Ala Thr
 1 5 10
 caa agc tat ggg gcc tac ccc acc cag ccc ggg cag ggc tat tcc cag 159
 Gln Ser Tyr Gly Ala Tyr Pro Thr Gln Pro Gly Gln Gly Tyr Ser Gln
 15 20 25
 cag agc agt cag ccc tac gga cag cag agt tac agt ggt tat agc cag 207
 Gln Ser Ser Gln Pro Tyr Gly Gln Gln Ser Tyr Ser Gly Tyr Ser Gln
 30 35 40
 tcc acg gac act tca ggc tat ggc cag agc agc tat tct tct tat ggc 255
 Ser Thr Asp Thr Ser Gly Tyr Gly Gln Ser Ser Tyr Ser Ser Tyr Gly
 45 50 55
 cag agc cag aac aca ggc tat gga act cag tca act ccc cag gga tat 303
 Gln Ser Gln Asn Thr Gly Tyr Gly Thr Gln Ser Thr Pro Gln Gly Tyr
 60 65 70 75
 ggc tcg act ggc ggc tat ggc agt agc cag agc tcc caa tcg tct tac 351
 Gly Ser Thr Gly Gly Tyr Gly Ser Ser Gln Ser Ser Gln Ser Ser Tyr
 80 85 90
 ggg cag cag tcc tcc tac cct ggc tat ggc cag cag cca gct ccc agc 399
 Gly Gln Gln Ser Ser Tyr Pro Gly Tyr Gly Gln Gln Pro Ala Pro Ser
 95 100 105
 agc acc tcg gga agt tac ggt agc agt tct cag agc agc agc tat ggg 447
 Ser Thr Ser Gly Ser Tyr Gly Ser Ser Ser Gln Ser Ser Ser Tyr Gly
 110 115 120
 cag ccc cag agt ggg agc tac agc cag cag cct agc tat ggt gga cag 495
 Gln Pro Gln Ser Gly Ser Tyr Ser Gln Gln Pro Ser Tyr Gly Gly Gln

125	130	135	
cag caa agc tat gga cag cag caa agc tat aat ccc cct cag ggc tat			543
Gln Gln Ser Tyr Gly Gln Gln Gln Ser Tyr Asn Pro Pro Gln Gly Tyr			
140	145	150	155
gga cag cag aac cag tac aac agc agc agt ggt ggt gga ggt gga ggt			591
Gly Gln Gln Asn Gln Tyr Asn Ser Ser Ser Gly Gly Gly Gly Gly Gly			
160	165	170	
gga ggt gga ggt aac tat ggc caa gat caa tcc tcc atg agt agt ggt			639
Gly Gly Gly Gly Asn Tyr Gly Gln Asp Gln Ser Ser Met Ser Ser Gly			
175	180	185	
ggt ggc agt ggt ggc ggt tat ggc aat caa gac cag agt ggt gga ggt			687
Gly Gly Ser Gly Gly Gly Tyr Gly Asn Gln Asp Gln Ser Gly Gly Gly			
190	195	200	
ggc agc ggt ggc tat gga cag cag gac cgt gga ggc cgc ggc agg ggt			735
Gly Ser Gly Gly Tyr Gly Gln Gln Asp Arg Gly Gly Arg Gly Arg Gly			
205	210	215	
ggc agt ggt ggc ggc ggc ggc ggc ggc ggt ggt ggt tac aac cgc agc			783
Gly Ser Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Tyr Asn Arg Ser			
220	225	230	235
agt ggt ggc tat gaa ccc aga ggt cgt gga ggt ggc cgt gga ggc aga			831
Ser Gly Gly Tyr Glu Pro Arg Gly Arg Gly Gly Gly Arg Gly Gly Arg			
240	245	250	
ggt ggc atg ggc gga agt gac cgt ggt ggc ttc aat aaa ttt ggt ggc			879
Gly Gly Met Gly Gly Ser Asp Arg Gly Gly Phe Asn Lys Phe Gly Gly			
255	260	265	
cct cgg gac caa gga tca cgt cat gac tcc gaa cag gat aat tca gac			927
Pro Arg Asp Gln Gly Ser Arg His Asp Ser Glu Gln Asp Asn Ser Asp			

289/617

270	275	280	
aac aac acc atc ttt gtg caa ggc ctg ggt gag aat gtt aca att gag			975
Asn Asn Thr Ile Phe Val Gln Gly Leu Gly Glu Asn Val Thr Ile Glu			
285	290	295	
tct gtg gct gat tac ttc aag cag att ggt att att aag aca aac aag			1023
Ser Val Ala Asp Tyr Phe Lys Gln Ile Gly Ile Ile Lys Thr Asn Lys			
300	305	310	315
aaa acg gga cag ccc atg att aat ttg tac aca gac agg gaa act ggc			1071
Lys Thr Gly Gln Pro Met Ile Asn Leu Tyr Thr Asp Arg Glu Thr Gly			
320	325	330	
aag ctg aag gga gag gca acg gtc tct ttt gat gac cca cct tca gct			1119
Lys Leu Lys Gly Glu Ala Thr Val Ser Phe Asp Asp Pro Pro Ser Ala			
335	340	345	
aaa gca gct att gac tgg ttt gat ggt aaa gaa ttc tcc gga aat cct			1167
Lys Ala Ala Ile Asp Trp Phe Asp Gly Lys Glu Phe Ser Gly Asn Pro			
350	355	360	
atc aag gtc tca ttt gct act cgc cgg gca gac ttt aat cgg ggt ggt			1215
Ile Lys Val Ser Phe Ala Thr Arg Arg Ala Asp Phe Asn Arg Gly Gly			
365	370	375	
ggc aat ggt cgt gga ggc cga ggg cga gga gga ccc atg ggc cgt gga			1263
Gly Asn Gly Arg Gly Gly Arg Gly Arg Gly Gly Pro Met Gly Arg Gly			
380	385	390	395
ggc tat gga ggt ggt ggc agt ggt ggt ggt ggc cga gga gga ttt ccc			1311
Gly Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Arg Gly Gly Phe Pro			
400	405	410	
agt gga ggt ggt ggc ggt gga gga cag cag cga gct ggt gac tgg aag			1359
Ser Gly Gly Gly Gly Gly Gly Gly Gln Gln Arg Ala Gly Asp Trp Lys			

415	420	425	
tgt cct aat ccc acc tgt gag aat atg aac ttc tct tgg agg aat gaa			1407
Cys Pro Asn Pro Thr Cys Glu Asn Met Asn Phe Ser Trp Arg Asn Glu			
430	435	440	
tgc aac cag tgt aag gcc cct aaa cca gat ggc cca gga ggg gga cca			1455
Cys Asn Gln Cys Lys Ala Pro Lys Pro Asp Gly Pro Gly Gly Gly Pro			
445	450	455	
ggg ggc tct cac atg ggg ggt aac tac ggg gat gat cgt cgt ggt ggc			1503
Gly Gly Ser His Met Gly Gly Asn Tyr Gly Asp Asp Arg Arg Gly Gly			
460	465	470	475
aga gga ggc tat gat cga ggc ggc tac cgg ggc cgc ggc ggg gac cgt			1551
Arg Gly Gly Tyr Asp Arg Gly Gly Tyr Arg Gly Arg Gly Gly Asp Arg			
480	485	490	
gga ggc ttc cga ggg ggc cgg ggt ggt ggg gac aga ggt ggc ttt ggc			1599
Gly Gly Phe Arg Gly Gly Arg Gly Gly Gly Asp Arg Gly Gly Phe Gly			
495	500	505	
cct ggc aag atg gat tcc agg ggt gag cac aga cag gat cgc agg gag			1647
Pro Gly Lys Met Asp Ser Arg Gly Glu His Arg Gln Asp Arg Arg Glu			
510	515	520	
agg ccg tat taattagcct ggctccccag gttctggaac agctttttgt			1696
Arg Pro Tyr			
525			
cctgtaccca gtgttaccct cggtattttg taaccttcca attcctgac acccaagggt			1756
tttttttgtg tcggactatg taattgtaac tatacctctg gttcccatta aaagtgacca			1816
tttttagtt			1824

<210> 82

291/617

<211> 526

<212> PRT

<213> Homo sapiens

<400> 82

Met Ala Ser Asn Asp Tyr Thr Gln Gln Ala Thr Gln Ser Tyr Gly Ala

1 5 10 15

Tyr Pro Thr Gln Pro Gly Gln Gly Tyr Ser Gln Gln Ser Ser Gln Pro

20 25 30

Tyr Gly Gln Gln Ser Tyr Ser Gly Tyr Ser Gln Ser Thr Asp Thr Ser

35 40 45

Gly Tyr Gly Gln Ser Ser Tyr Ser Ser Tyr Gly Gln Ser Gln Asn Thr

50 55 60

Gly Tyr Gly Thr Gln Ser Thr Pro Gln Gly Tyr Gly Ser Thr Gly Gly

65 70 75 80

Tyr Gly Ser Ser Gln Ser Ser Gln Ser Ser Tyr Gly Gln Gln Ser Ser

85 90 95

Tyr Pro Gly Tyr Gly Gln Gln Pro Ala Pro Ser Ser Thr Ser Gly Ser

100 105 110

Tyr Gly Ser Ser Ser Gln Ser Ser Ser Tyr Gly Gln Pro Gln Ser Gly

115 120 125

Ser Tyr Ser Gln Gln Pro Ser Tyr Gly Gly Gln Gln Gln Ser Tyr Gly

130 135 140

Gln Gln Gln Ser Tyr Asn Pro Pro Gln Gly Tyr Gly Gln Gln Asn Gln

145 150 155 160

Tyr Asn Ser Ser Ser Gly Gly Gly Gly Gly Gly Gly Gly Gly Asn

165 170 175

Tyr Gly Gln Asp Gln Ser Ser Met Ser Ser Gly Gly Gly Ser Gly Gly

292/617

180	185	190	
Gly Tyr Gly Asn Gln Asp Gln Ser Gly Gly Gly Gly Ser Gly Gly Tyr			
195	200	205	
Gly Gln Gln Asp Arg Gly Gly Arg Gly Arg Gly Gly Ser Gly Gly Gly			
210	215	220	
Gly Gly Gly Gly Gly Gly Gly Tyr Asn Arg Ser Ser Gly Gly Tyr Glu			
225	230	235	240
Pro Arg Gly Arg Gly Gly Gly Arg Gly Gly Arg Gly Gly Met Gly Gly			
245	250	255	
Ser Asp Arg Gly Gly Phe Asn Lys Phe Gly Gly Pro Arg Asp Gln Gly			
260	265	270	
Ser Arg His Asp Ser Glu Gln Asp Asn Ser Asp Asn Asn Thr Ile Phe			
275	280	285	
Val Gln Gly Leu Gly Glu Asn Val Thr Ile Glu Ser Val Ala Asp Tyr			
290	295	300	
Phe Lys Gln Ile Gly Ile Ile Lys Thr Asn Lys Lys Thr Gly Gln Pro			
305	310	315	320
Met Ile Asn Leu Tyr Thr Asp Arg Glu Thr Gly Lys Leu Lys Gly Glu			
325	330	335	
Ala Thr Val Ser Phe Asp Asp Pro Pro Ser Ala Lys Ala Ala Ile Asp			
340	345	350	
Trp Phe Asp Gly Lys Glu Phe Ser Gly Asn Pro Ile Lys Val Ser Phe			
355	360	365	
Ala Thr Arg Arg Ala Asp Phe Asn Arg Gly Gly Gly Asn Gly Arg Gly			
370	375	380	
Gly Arg Gly Arg Gly Gly Pro Met Gly Arg Gly Gly Tyr Gly Gly Gly			
385	390	395	400

Gly Ser Gly Gly Gly Gly Arg Gly Gly Phe Pro Ser Gly Gly Gly Gly

405

410

415

Gly Gly Gly Gln Gln Arg Ala Gly Asp Trp Lys Cys Pro Asn Pro Thr

420

425

430

Cys Glu Asn Met Asn Phe Ser Trp Arg Asn Glu Cys Asn Gln Cys Lys

435

440

445

Ala Pro Lys Pro Asp Gly Pro Gly Gly Gly Pro Gly Gly Ser His Met

450

455

460

Gly Gly Asn Tyr Gly Asp Asp Arg Arg Gly Gly Arg Gly Gly Tyr Asp

465

470

475

480

Arg Gly Gly Tyr Arg Gly Arg Gly Gly Asp Arg Gly Gly Phe Arg Gly

485

490

495

Gly Arg Gly Gly Gly Asp Arg Gly Gly Phe Gly Pro Gly Lys Met Asp

500

505

510

Ser Arg Gly Glu His Arg Gln Asp Arg Arg Glu Arg Pro Tyr

515

520

525

<210> 83

<211> 1133

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (151).. (1041)

<400> 11

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ggtgtcgagg gcgggttgcc tcgcgtgac cttcccgcc ctccttctcg tcacacacca 120

ggccccgcg gaagccgcgg tgctggcgcc atg gcg gag ctg acg gct ctt gag 174
 Met Ala Glu Leu Thr Ala Leu Glu
 1 5
 agt ctc atc gag atg ggc ttc ccc agg gga cgc gcg gag aag gct ctg 222
 Ser Leu Ile Glu Met Gly Phe Pro Arg Gly Arg Ala Glu Lys Ala Leu
 10 15 20
 gcc ctc aca ggg aac cag ggc atc gag gct gcg atg gac tgg ctg atg 270
 Ala Leu Thr Gly Asn Gln Gly Ile Glu Ala Ala Met Asp Trp Leu Met
 25 30 35 40
 gag cac gaa gac gac ccc gat gtg gac gag cct tta gag act ccc ctt 318
 Glu His Glu Asp Asp Pro Asp Val Asp Glu Pro Leu Glu Thr Pro Leu
 45 50 55
 gga cat atc ctg gga cgg gag ccc act tcc tca gag caa ggc ggc ctt 366
 Gly His Ile Leu Gly Arg Glu Pro Thr Ser Ser Glu Gln Gly Gly Leu
 60 65 70
 gaa gga tct ggt tct gct gcc gga gaa ggc aaa ccc gct ttg agt gaa 414
 Glu Gly Ser Gly Ser Ala Ala Gly Glu Gly Lys Pro Ala Leu Ser Glu
 75 80 85
 gag gaa aga cag gaa caa act aag agg atg ttg gag ctg gtg gcc cag 462
 Glu Glu Arg Gln Glu Gln Thr Lys Arg Met Leu Glu Leu Val Ala Gln
 90 95 100
 aag cag cgg gag cgt gaa gaa aga gag gaa cgg gag gca ttg gaa cgg 510
 Lys Gln Arg Glu Arg Glu Glu Arg Glu Glu Arg Glu Ala Leu Glu Arg
 105 110 115 120
 gaa cgg cag cgc agg aga caa ggg caa gag ttg tca gca gca cga cag 558
 Glu Arg Gln Arg Arg Arg Gln Gly Gln Glu Leu Ser Ala Ala Arg Gln
 125 130 135

295/617

cgg cta cag gaa gat gag atg cgc cgg gct gct gag gag agg cgg agg 606
 Arg Leu Gln Glu Asp Glu Met Arg Arg Ala Ala Glu Glu Arg Arg Arg
 140 145 150
 gaa aag gcc gag gag tta gca gcc aga caa aga gtt aga gaa aag atc 654
 Glu Lys Ala Glu Glu Leu Ala Ala Arg Gln Arg Val Arg Glu Lys Ile
 155 160 165
 gag agg gac aaa gca gag aga gcc aag aag tat ggt ggc agt gtg ggc 702
 Glu Arg Asp Lys Ala Glu Arg Ala Lys Lys Tyr Gly Gly Ser Val Gly
 170 175 180
 tct cag cca ccc cca gtg gca cca gag cca ggt cct gtt ccc tct tcc 750
 Ser Gln Pro Pro Pro Val Ala Pro Glu Pro Gly Pro Val Pro Ser Ser
 185 190 195 200
 ccc agc cag gag cct ccc acc aag cgg gtg tat ggc cag tgt cgc ata 798
 Pro Ser Gln Glu Pro Pro Thr Lys Arg Val Tyr Gly Gln Cys Arg Ile
 205 210 215
 cag gtc agg ctg cca gat ggg acc tca ctg acc cag acg ttc cga gcc 846
 Gln Val Arg Leu Pro Asp Gly Thr Ser Leu Thr Gln Thr Phe Arg Ala
 220 225 230
 cgg gaa cag ctg gca gct gtg agg ctc tat gtg gag ctc cac cgt ggg 894
 Arg Glu Gln Leu Ala Ala Val Arg Leu Tyr Val Glu Leu His Arg Gly
 235 240 245
 gag gaa cta ggt ggg ggc cag gac cct gtg caa ttg ctc agt ggc ttc 942
 Glu Glu Leu Gly Gly Gly Gln Asp Pro Val Gln Leu Leu Ser Gly Phe
 250 255 260
 ccc aga cgg gcc ttc tca gaa gct gac atg gag cgg cct ctg cag gag 990
 Pro Arg Arg Ala Phe Ser Glu Ala Asp Met Glu Arg Pro Leu Gln Glu
 265 270 275 280

ctg gga ctc gtg cct tct gct gtt ctc att gtg gcc aag aaa tgt ccc 1038

Leu Gly Leu Val Pro Ser Ala Val Leu Ile Val Ala Lys Lys Cys Pro

285

290

295

agc tgagggcctt tgtccattg tccctctgtg accccttcat ctttgataaa 1091

Ser

gcactgacat ctccttccta ataaatagac cctgagttct gt 1133

<210> 84

<211> 297

<212> PRT

<213> Homo sapiens

<400> 84

Met Ala Glu Leu Thr Ala Leu Glu Ser Leu Ile Glu Met Gly Phe Pro

1

5

10

15

Arg Gly Arg Ala Glu Lys Ala Leu Ala Leu Thr Gly Asn Gln Gly Ile

20

25

30

Glu Ala Ala Met Asp Trp Leu Met Glu His Glu Asp Asp Pro Asp Val

35

40

45

Asp Glu Pro Leu Glu Thr Pro Leu Gly His Ile Leu Gly Arg Glu Pro

50

55

60

Thr Ser Ser Glu Gln Gly Gly Leu Glu Gly Ser Gly Ser Ala Ala Gly

65

70

75

80

Glu Gly Lys Pro Ala Leu Ser Glu Glu Glu Arg Gln Glu Gln Thr Lys

85

90

95

Arg Met Leu Glu Leu Val Ala Gln Lys Gln Arg Glu Arg Glu Glu Arg

100

105

110

Glu Glu Arg Glu Ala Leu Glu Arg Glu Arg Gln Arg Arg Arg Gln Gly

297/617

115 120 125
Gln Glu Leu Ser Ala Ala Arg Gln Arg Leu Gln Glu Asp Glu Met Arg
130 135 140
Arg Ala Ala Glu Glu Arg Arg Arg Glu Lys Ala Glu Glu Leu Ala Ala
145 150 155 160
Arg Gln Arg Val Arg Glu Lys Ile Glu Arg Asp Lys Ala Glu Arg Ala
165 170 175
Lys Lys Tyr Gly Gly Ser Val Gly Ser Gln Pro Pro Pro Val Ala Pro
180 185 190
Glu Pro Gly Pro Val Pro Ser Ser Pro Ser Gln Glu Pro Pro Thr Lys
195 200 205
Arg Val Tyr Gly Gln Cys Arg Ile Gln Val Arg Leu Pro Asp Gly Thr
210 215 220
Ser Leu Thr Gln Thr Phe Arg Ala Arg Glu Gln Leu Ala Ala Val Arg
225 230 235 240
Leu Tyr Val Glu Leu His Arg Gly Glu Glu Leu Gly Gly Gly Gln Asp
245 250 255
Pro Val Gln Leu Leu Ser Gly Phe Pro Arg Arg Ala Phe Ser Glu Ala
260 265 270
Asp Met Glu Arg Pro Leu Gln Glu Leu Gly Leu Val Pro Ser Ala Val
275 280 285
Leu Ile Val Ala Lys Lys Cys Pro Ser
290 295

<210> 85

<211> 1133

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (151)..(1041)

<400> 85

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 ggtgtcgagg gcgggttgcc tcgcgtgac ccttcccgcc ctccttctcg tcacacacca 120
 ggtccccgag gaagccggg tgcggcgcc atg gcg gag ctg acg gct ctt gag 174

Met Ala Glu Leu Thr Ala Leu Glu

1

5

agt ctc atc gag atg ggc ttc ccc agg gga cgc gcg gag aag gct ctg 222
 Ser Leu Ile Glu Met Gly Phe Pro Arg Gly Arg Ala Glu Lys Ala Leu

10

15

20

gcc ctc aca ggg aac cag ggc atc gag gct gcg atg gac tgg ctg atg 270
 Ala Leu Thr Gly Asn Gln Gly Ile Glu Ala Ala Met Asp Trp Leu Met

25

30

35

40

gag cac gaa gac gac ccc gat gtg gac gag cct tta gag act ccc ctt 318
 Glu His Glu Asp Asp Pro Asp Val Asp Glu Pro Leu Glu Thr Pro Leu

45

50

55

gga cat atc ctg gga cgg gag ccc act tcc tca gag caa ggc ggc ctt 366
 Gly His Ile Leu Gly Arg Glu Pro Thr Ser Ser Glu Gln Gly Gly Leu

60

65

70

gaa gga tct ggt tct gct gcc gga gaa ggc aaa ccc gct ttg agt gaa 414
 Glu Gly Ser Gly Ser Ala Ala Gly Glu Gly Lys Pro Ala Leu Ser Glu

75

80

85

gag gaa aga cag gaa caa act aag agg atg ttg gag ctg gtg gcc cag 462
 Glu Glu Arg Gln Glu Gln Thr Lys Arg Met Leu Glu Leu Val Ala Gln

299/617

90	95	100	
aag cag cgg gag cgt gaa gaa aga gag gaa cgg gag gca ttg gaa cgg			510
Lys Gln Arg Glu Arg Glu Glu Arg Glu Glu Arg Glu Ala Leu Glu Arg			
105	110	115	120
gaa cgg cag cgc agg aga caa ggg caa gag ttg tca gca gca cga cag			558
Glu Arg Gln Arg Arg Arg Gln Gly Gln Glu Leu Ser Ala Ala Arg Gln			
125	130	135	
cgg cta cag gaa gat gag atg cgc cgg gct gct gag gag agg cgg agg			606
Arg Leu Gln Glu Asp Glu Met Arg Arg Ala Ala Glu Glu Arg Arg Arg			
140	145	150	
gaa aag gcc gag gag tta gca gcc aga caa aga gtt aga gaa aag atc			654
Glu Lys Ala Glu Glu Leu Ala Ala Arg Gln Arg Val Arg Glu Lys Ile			
155	160	165	
gag agg gac aaa gca gag aga gcc aag aag tat ggt ggc agt gtg ggc			702
Glu Arg Asp Lys Ala Glu Arg Ala Lys Lys Tyr Gly Gly Ser Val Gly			
170	175	180	
tct cag cca ccc cca gtg gca cca gag cca ggt cct gtt ccc tct tcc			750
Ser Gln Pro Pro Pro Val Ala Pro Glu Pro Gly Pro Val Pro Ser Ser			
185	190	195	200
ccc agc cag gag cct ccc acc aag cgg gag tat gac cag tgt cgc ata			798
Pro Ser Gln Glu Pro Pro Thr Lys Arg Glu Tyr Asp Gln Cys Arg Ile			
205	210	215	
cag gtc agg ctg cca gat ggg acc tca ctg acc cag acg ttc cga gcc			846
Gln Val Arg Leu Pro Asp Gly Thr Ser Leu Thr Gln Thr Phe Arg Ala			
220	225	230	
cgg gaa cag ctg gca gct gtg agg ctc tat gtg gag ctc cac cgt ggg			894
Arg Glu Gln Leu Ala Ala Val Arg Leu Tyr Val Glu Leu His Arg Gly			

235 240 245
 gag gaa cta ggt ggg ggc cag gac cct gtg caa ttg ctc agt ggc ttc 942
 Glu Glu Leu Gly Gly Gly Gln Asp Pro Val Gln Leu Leu Ser Gly Phe
 250 255 260
 ccc aga cgg gcc ttc tca gaa gct gac atg gag cgg cct ctg cag gag 990
 Pro Arg Arg Ala Phe Ser Glu Ala Asp Met Glu Arg Pro Leu Gln Glu
 265 270 275 280
 ctg gga ctc gtg cct tct gct gtt ctc att gtg gcc aag aaa tgt ccc 1038
 Leu Gly Leu Val Pro Ser Ala Val Leu Ile Val Ala Lys Lys Cys Pro
 285 290 295
 agc tgagggcctt tgcccattg tccctctgtg accccttcat ctttgataaa 1091
 Ser
 gcactgacat ctccttccta ataaatagac cctgagttct gt 1133

<210> 86

<211> 297

<212> PRT

<213> Homo sapiens

<400> 86

Met Ala Glu Leu Thr Ala Leu Glu Ser Leu Ile Glu Met Gly Phe Pro
 1 5 10 15
 Arg Gly Arg Ala Glu Lys Ala Leu Ala Leu Thr Gly Asn Gln Gly Ile
 20 25 30
 Glu Ala Ala Met Asp Trp Leu Met Glu His Glu Asp Asp Pro Asp Val
 35 40 45
 Asp Glu Pro Leu Glu Thr Pro Leu Gly His Ile Leu Gly Arg Glu Pro
 50 55 60

301/617

302/617

275 280 285
 Leu Ile Val Ala Lys Lys Cys Pro Ser

290 295

<210> 87

<211> 1297

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (142).. (1077)

<400> 87

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ggcgggttgc ctcgcgtga ccctcccgc cctccttctc gtcacacacc agtccccgc 120
ggaagccgcg gtgtcggcgc c atg gcg gag ctg acg gct ctt gag agt ctc 171
                Met Ala Glu Leu Thr Ala Leu Glu Ser Leu
                        1             5             10
atc gag atg ggc ttc ccc agg gga cgc gcg gag aag gct ctg gcc ctc 219
Ile Glu Met Gly Phe Pro Arg Gly Arg Ala Glu Lys Ala Leu Ala Leu
                15             20             25
aca ggg aac cag ggc atc gag gct gcg atg gac tgg ctg atg gag cac 267
Thr Gly Asn Gln Gly Ile Glu Ala Ala Met Asp Trp Leu Met Glu His
                30             35             40
gaa gac gac ccc gat gtg gac gag cct tta gag act ccc ctt gga cat 315
Glu Asp Asp Pro Asp Val Asp Glu Pro Leu Glu Thr Pro Leu Gly His
                45             50             55
atc ctg gga cgg gag ccc act tcc tca gag caa ggc ggc ctt gaa gga 363

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303/617

Ile Leu Gly Arg Glu Pro Thr Ser Ser Glu Gln Gly Gly Leu Glu Gly
 60 65 70
 tct ggt tct gct gcc gga gaa ggc aaa ccc gct ttg agt gaa gag gaa 411
 Ser Gly Ser Ala Ala Gly Glu Gly Lys Pro Ala Leu Ser Glu Glu Glu
 75 80 85 90
 aga cag gaa caa act aag agg atg ttg gag ctg gtg gcc cag aag cag 459
 Arg Gln Glu Gln Thr Lys Arg Met Leu Glu Leu Val Ala Gln Lys Gln
 95 100 105
 cgg gag cgt gaa gaa aga gag gaa cgg gag gca ttg gaa cgg gaa cgg 507
 Arg Glu Arg Glu Glu Arg Glu Glu Arg Glu Ala Leu Glu Arg Glu Arg
 110 115 120
 cag cgc agg aga caa ggg caa gag ttg tca gca gca cga cag cgg cta 555
 Gln Arg Arg Arg Gln Gly Gln Glu Leu Ser Ala Ala Arg Gln Arg Leu
 125 130 135
 cag gaa gat gag atg cgc cgg gct gct gag gag agg cgg agg gaa aag 603
 Gln Glu Asp Glu Met Arg Arg Ala Ala Glu Glu Arg Arg Arg Glu Lys
 140 145 150
 gcc gag gag tta gca gcc aga caa aga gtt aga gaa aag atc gag agg 651
 Ala Glu Glu Leu Ala Ala Arg Gln Arg Val Arg Glu Lys Ile Glu Arg
 155 160 165 170
 gac aaa gca gag aga gcc aag aag tat ggt ggc agt gtg ggc tct cag 699
 Asp Lys Ala Glu Arg Ala Lys Lys Tyr Gly Gly Ser Val Gly Ser Gln
 175 180 185
 cca ccc cca gtg gca cca gag cca ggt cct gtt ccc tct tct ccc agc 747
 Pro Pro Pro Val Ala Pro Glu Pro Gly Pro Val Pro Ser Ser Pro Ser
 190 195 200
 cag gag cct ccc acc aag cgg gag tat gac cag tgt cgc ata cag gtc 795

Gln Glu Pro Pro Thr Lys Arg Glu Tyr Asp Gln Cys Arg Ile Gln Val
 205 210 215
 agg ctg cca gat ggg acc tca ctg acc cag acg ttc cgg gcc cgg gaa 843
 Arg Leu Pro Asp Gly Thr Ser Leu Thr Gln Thr Phe Arg Ala Arg Glu
 220 225 230
 cag ctg gca gct gtg agg ctc tat gtg gag ctc cac cgt ggg gag gaa 891
 Gln Leu Ala Ala Val Arg Leu Tyr Val Glu Leu His Arg Gly Glu Glu
 235 240 245 250
 cta ggt ggg ggc cag gac cct gtg caa ttg ctc agt ggc ttc ccc aga 939
 Leu Gly Gly Gly Gln Asp Pro Val Gln Leu Leu Ser Gly Phe Pro Arg
 255 260 265
 cgg gcc ttc tca gaa gct gac atg gag cgg cct ctg cag gag ctg ggt 987
 Arg Ala Phe Ser Glu Ala Asp Met Glu Arg Pro Leu Gln Glu Leu Gly
 270 275 280
 atg gct gca aga cta gaa acc agg act aga aac tgg ggg agt agg gag 1035
 Met Ala Ala Arg Leu Glu Thr Arg Thr Arg Asn Trp Gly Ser Arg Glu
 285 290 295
 gca tgc cta gga aaa gga ggg atg caa aga gaa ggg gct ttg 1077
 Ala Cys Leu Gly Lys Gly Gly Met Gln Arg Glu Gly Ala Leu
 300 305 310
 tgaacatggt gcaaggccag gaattttggg agcaaaaacc aagtatcctt gtggttcaag 1137
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<210> 88

<211> 312

305/617

<212> PRT

<213> Homo sapiens

<400> 88

Met Ala Glu Leu Thr Ala Leu Glu Ser Leu Ile Glu Met Gly Phe Pro
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Arg Gly Arg Ala Glu Lys Ala Leu Ala Leu Thr Gly Asn Gln Gly Ile
20 25 30

Glu Ala Ala Met Asp Trp Leu Met Glu His Glu Asp Asp Pro Asp Val
35 40 45

Asp Glu Pro Leu Glu Thr Pro Leu Gly His Ile Leu Gly Arg Glu Pro
50 55 60

Thr Ser Ser Glu Gln Gly Gly Leu Glu Gly Ser Gly Ser Ala Ala Gly
65 70 75 80

Glu Gly Lys Pro Ala Leu Ser Glu Glu Glu Arg Gln Glu Gln Thr Lys
85 90 95

Arg Met Leu Glu Leu Val Ala Gln Lys Gln Arg Glu Arg Glu Glu Arg
100 105 110

Glu Glu Arg Glu Ala Leu Glu Arg Glu Arg Gln Arg Arg Arg Gln Gly
115 120 125

Gln Glu Leu Ser Ala Ala Arg Gln Arg Leu Gln Glu Asp Glu Met Arg
130 135 140

Arg Ala Ala Glu Glu Arg Arg Arg Glu Lys Ala Glu Glu Leu Ala Ala
145 150 155 160

Arg Gln Arg Val Arg Glu Lys Ile Glu Arg Asp Lys Ala Glu Arg Ala
165 170 175

Lys Lys Tyr Gly Gly Ser Val Gly Ser Gln Pro Pro Pro Val Ala Pro
180 185 190

306/617

Glu Pro Gly Pro Val Pro Ser Ser Pro Ser Gln Glu Pro Pro Thr Lys
 195 200 205
 Arg Glu Tyr Asp Gln Cys Arg Ile Gln Val Arg Leu Pro Asp Gly Thr
 210 215 220
 Ser Leu Thr Gln Thr Phe Arg Ala Arg Glu Gln Leu Ala Ala Val Arg
 225 230 235 240
 Leu Tyr Val Glu Leu His Arg Gly Glu Glu Leu Gly Gly Gly Gln Asp
 245 250 255
 Pro Val Gln Leu Leu Ser Gly Phe Pro Arg Arg Ala Phe Ser Glu Ala
 260 265 270
 Asp Met Glu Arg Pro Leu Gln Glu Leu Gly Met Ala Ala Arg Leu Glu
 275 280 285
 Thr Arg Thr Arg Asn Trp Gly Ser Arg Glu Ala Cys Leu Gly Lys Gly
 290 295 300
 Gly Met Gln Arg Glu Gly Ala Leu
 305 310

<210> 89
 <211> 2206
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (226).. (1152)
 <400> 89

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gaccaggtga acggcgtgct ggtgctgagc ctcttgaca aaatcatcgg ggccgtagac 180
 cagatccagc tgactcaagc acagctggag gagcggcagg cggag atg gag ggc gca 237

Met Glu Gly Ala

1

gtg cag agc atc cag ggc gag ctg agc aag ctg ggc aag gcg cac gcc 285
 Val Gln Ser Ile Gln Gly Glu Leu Ser Lys Leu Gly Lys Ala His Ala

5 10 15 20

acc acg agc aat acg gtg agc aag ctg ctg gag aag gtg cgc aag gtc 333
 Thr Thr Ser Asn Thr Val Ser Lys Leu Leu Glu Lys Val Arg Lys Val

25 30 35

agc gtc aac gtg aag acc gtg cgc ggc agc ctg gag cgc cgg gcg ggg 381
 Ser Val Asn Val Lys Thr Val Arg Gly Ser Leu Glu Arg Arg Ala Gly

40 45 50

cag atc aag aag ctg gag gtc aac gag gcc gag ctg ctg cgg cgc cgc 429
 Gln Ile Lys Lys Leu Glu Val Asn Glu Ala Glu Leu Leu Arg Arg Arg

55 60 65

aac ttt aaa gtc atg atc tac cag gat gaa gtg aag ctg ccg gcc aaa 477
 Asn Phe Lys Val Met Ile Tyr Gln Asp Glu Val Lys Leu Pro Ala Lys

70 75 80

ctg agc atc agc aaa tcg ctg aaa gag tcg gag gcg ctg cca gag aag 525
 Leu Ser Ile Ser Lys Ser Leu Lys Glu Ser Glu Ala Leu Pro Glu Lys

85 90 95 100

gag ggc gag gag ctg ggc gag ggc gag cgg ccc gag gag gac gca gcg 573
 Glu Gly Glu Glu Leu Gly Glu Gly Glu Arg Pro Glu Glu Asp Ala Ala

105 110 115

gcg ctg gag ctt tcg tcg gac gag gcg gtg gag gtt gag gag gtt att 621
 Ala Leu Glu Leu Ser Ser Asp Glu Ala Val Glu Val Glu Glu Val Ile

308/617

120	125	130	
gag gag tcc cgc gca gag cgt atc aag cgc agc ggc ctg cgg cgc gtg			669
Glu Glu Ser Arg Ala Glu Arg Ile Lys Arg Ser Gly Leu Arg Arg Val			
135	140	145	
gac gac ttc aag gag gcc ttc tcc aag gag aag atg gag aag acc aag			717
Asp Asp Phe Lys Glu Ala Phe Ser Lys Glu Lys Met Glu Lys Thr Lys			
150	155	160	
gtg cgt acc cgc gag aac ctg gag aag acg cgc ctc aag acc aag gaa			765
Val Arg Thr Arg Glu Asn Leu Glu Lys Thr Arg Leu Lys Thr Lys Glu			
165	170	175	180
aac ctg gag aag acg cgg cac acc ctg gag aag cgc atg aac aag ctg			813
Asn Leu Glu Lys Thr Arg His Thr Leu Glu Lys Arg Met Asn Lys Leu			
185	190	195	
ggc acg cgc ctg gtg ccc gcc gag cgg cgc gag aaa ctg aag acg tcg			861
Gly Thr Arg Leu Val Pro Ala Glu Arg Arg Glu Lys Leu Lys Thr Ser			
200	205	210	
cgg gac aag ttg cgc aaa tcc ttc acg ccc gac cac gtg gtg tac gcg			909
Arg Asp Lys Leu Arg Lys Ser Phe Thr Pro Asp His Val Val Tyr Ala			
215	220	225	
cgc tcc aag acc gcg gtc tac aag gtg cca ccc ttc acc tcc cac gtc			957
Arg Ser Lys Thr Ala Val Tyr Lys Val Pro Pro Phe Thr Ser His Val			
230	235	240	
aag aag atc cgc gag ggc cag gtg gaa gtg ctc aag gcc acc gag atg			1005
Lys Lys Ile Arg Glu Gly Gln Val Glu Val Leu Lys Ala Thr Glu Met			
245	250	255	260
gtg gag gtg ggc gcc gac gac gag ggc ggc gcg gag cgc ggg gag			1053
Val Glu Val Gly Ala Asp Asp Asp Glu Gly Gly Ala Glu Arg Gly Glu			

265	270	275	
gcc tgc gac ctg cgg cgc ggg agc agc ccc gac gtg cac gcg ctg ctg			1101
Ala Cys Asp Leu Arg Arg Gly Ser Ser Pro Asp Val His Ala Leu Leu			
280	285	290	
gag atc acc gag gag tcg gac gcc gtg ctg gtg gac aag agc gac agc			1149
Glu Ile Thr Glu Glu Ser Asp Ala Val Leu Val Asp Lys Ser Asp Ser			
295	300	305	
gac tgagccgccc ccgtgccac ccacccatt cctcgctcct tccgaacttc			1202
Asp			
ctctttcgca ttctctctcg gctcgagctg gctgagattt ttctaaattg aaaacacgcc			1262
ccccccccca cactccagg aactccactc ccagtcttag agctgttagg acccgatggg			1322
gaggcagccc ccgcagtgga cagccccgc ttggacacag tccgagtgga atgggaaggg			1382
aatggtcaat ccctgtcctg gttgtccaag tcgggatctc agaggaaatt gcagtgattc			1442
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cagctgctgt cattccgctc actgagctct tcttcattct caccctgac cctgggggac			1562
tcaaagccaa aactgccccaa agaggaaaga ttgaatccta aaggggatcc ttgccccat			1622
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aaaaattagc tgggcatggt tgcgcatgcc tgtaatccca gctacttttg aggtgaggt			2102
ggggagaatt gcttgaacct gggaggtgga gtttcagtg ggccaagtc gcgacactgc			2162
actccagcct gggtagacaga gtgagactcc atctcaacag aagg			2206

<210> 90

<211> 309

<212> PRT

<213> Homo sapiens

<400> 90

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 Lys Ala His Ala Thr Thr Ser Asn Thr Val Ser Lys Leu Leu Glu Lys
 20 25 30
 Val Arg Lys Val Ser Val Asn Val Lys Thr Val Arg Gly Ser Leu Glu
 35 40 45
 Arg Arg Ala Gly Gln Ile Lys Lys Leu Glu Val Asn Glu Ala Glu Leu
 50 55 60
 Leu Arg Arg Arg Asn Phe Lys Val Met Ile Tyr Gln Asp Glu Val Lys
 65 70 75 80
 Leu Pro Ala Lys Leu Ser Ile Ser Lys Ser Leu Lys Glu Ser Glu Ala
 85 90 95
 Leu Pro Glu Lys Glu Gly Glu Glu Leu Gly Glu Gly Glu Arg Pro Glu
 100 105 110
 Glu Asp Ala Ala Ala Leu Glu Leu Ser Ser Asp Glu Ala Val Glu Val
 115 120 125
 Glu Glu Val Ile Glu Glu Ser Arg Ala Glu Arg Ile Lys Arg Ser Gly
 130 135 140
 Leu Arg Arg Val Asp Asp Phe Lys Glu Ala Phe Ser Lys Glu Lys Met
 145 150 155 160
 Glu Lys Thr Lys Val Arg Thr Arg Glu Asn Leu Glu Lys Thr Arg Leu
 165 170 175

311/617

Lys Thr Lys Glu Asn Leu Glu Lys Thr Arg His Thr Leu Glu Lys Arg
 180 185 190
 Met Asn Lys Leu Gly Thr Arg Leu Val Pro Ala Glu Arg Arg Glu Lys
 195 200 205
 Leu Lys Thr Ser Arg Asp Lys Leu Arg Lys Ser Phe Thr Pro Asp His
 210 215 220
 Val Val Tyr Ala Arg Ser Lys Thr Ala Val Tyr Lys Val Pro Pro Phe
 225 230 235 240
 Thr Ser His Val Lys Lys Ile Arg Glu Gly Gln Val Glu Val Leu Lys
 245 250 255
 Ala Thr Glu Met Val Glu Val Gly Ala Asp Asp Asp Glu Gly Gly Ala
 260 265 270
 Glu Arg Gly Glu Ala Cys Asp Leu Arg Arg Gly Ser Ser Pro Asp Val
 275 280 285
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 290 295 300
 Lys Ser Asp Ser Asp
 305

<210> 91

<211> 2206

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (226).. (1152)

<400> 91

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 gaccaggtga acggcgtgct ggtgctgagc ctctggaca aaatcatcgg ggccgtagac 180
 cagatccagc tgactcaagc acagctggag gagcggcagg cggag atg gag ggc gca 237

Met Glu Gly Ala

1

gtg cag agc atc cag ggc gag ctg agc aag ctg ggc aag gcg cac gcc 285
 Val Gln Ser Ile Gln Gly Glu Leu Ser Lys Leu Gly Lys Ala His Ala
 5 10 15 20
 acc acg agc aat acg gtg agc aag ctg ctg gag aag gtg cgc aag gtc 333
 Thr Thr Ser Asn Thr Val Ser Lys Leu Leu Glu Lys Val Arg Lys Val
 25 30 35
 agc gtc aac gtg aag acc gtg cgc ggc agc ctg gag cgc cag gcg ggg 381
 Ser Val Asn Val Lys Thr Val Arg Gly Ser Leu Glu Arg Gln Ala Gly
 40 45 50
 cag atc aag aag ctg gag gtc aac gag gcc gag ctg ctg cgg cgc cgc 429
 Gln Ile Lys Lys Leu Glu Val Asn Glu Ala Glu Leu Leu Arg Arg Arg
 55 60 65
 aac ttt aaa gtc atg atc tac cag gat gaa gtg aag ctg ccg gcc aaa 477
 Asn Phe Lys Val Met Ile Tyr Gln Asp Glu Val Lys Leu Pro Ala Lys
 70 75 80
 ctg agc atc agc aaa tcg ctg aaa gag tcg gag gcg ctg cca gag aag 525
 Leu Ser Ile Ser Lys Ser Leu Lys Glu Ser Glu Ala Leu Pro Glu Lys
 85 90 95 100
 gag ggc gag gag ctg ggc gag ggc gag cgg ccc gag gag gac gca gcg 573
 Glu Gly Glu Glu Leu Gly Glu Gly Glu Arg Pro Glu Glu Asp Ala Ala
 105 110 115

313/617

gcg ctg gag ctt tcg tcg gac gag gcg gtg gag gtt gag gag gtt att 621
 Ala Leu Glu Leu Ser Ser Asp Glu Ala Val Glu Val Glu Glu Val Ile
 120 125 130
 gag gag tcc cgc gca gag cgt atc aag cgc agc ggc ctg cgg cgc gtg 669
 Glu Glu Ser Arg Ala Glu Arg Ile Lys Arg Ser Gly Leu Arg Arg Val
 135 140 145
 gac gac ttc aag aag gcc ttc tcc aag gag aag atg gag aag acc aag 717
 Asp Asp Phe Lys Lys Ala Phe Ser Lys Glu Lys Met Glu Lys Thr Lys
 150 155 160
 gtg cgt acc cgc gag aac ctg gag aag acg cgc ctc aag acc aag gaa 765
 Val Arg Thr Arg Glu Asn Leu Glu Lys Thr Arg Leu Lys Thr Lys Glu
 165 170 175 180
 aac ctg gag aag acg cgg cac acc ctg gag aag cgc atg aac aag ctg 813
 Asn Leu Glu Lys Thr Arg His Thr Leu Glu Lys Arg Met Asn Lys Leu
 185 190 195
 ggc acg cgc ctg gtg ccc gcc gag cgg cgc gag aaa ctg aag acg tcg 861
 Gly Thr Arg Leu Val Pro Ala Glu Arg Arg Glu Lys Leu Lys Thr Ser
 200 205 210
 cgg gac aag ttg cgc aaa tcc ttc acg ccc gac cac gtg gtg tac gcg 909
 Arg Asp Lys Leu Arg Lys Ser Phe Thr Pro Asp His Val Val Tyr Ala
 215 220 225
 cgc tcc aag acc gcg gtc tac aag gtg cca ccc ttc acc ttc cac gtc 957
 Arg Ser Lys Thr Ala Val Tyr Lys Val Pro Pro Phe Thr Phe His Val
 230 235 240
 aag aag atc cgc gag ggc cag gtg gaa gtg ctc aag gcc acc gag atg 1005
 Lys Lys Ile Arg Glu Gly Gln Val Glu Val Leu Lys Ala Thr Glu Met
 245 250 255 260

gtg gag gtg ggc gcc gac gac gag ggc ggc gcg gag cgc ggg gag 1053
Val Glu Val Gly Ala Asp Asp Asp Glu Gly Gly Ala Glu Arg Gly Glu
265 270 275
gcc tgc gac ctg cgg cgc ggg agc agc ccc gac gtg cac gcg ctg ctg 1101
Ala Cys Asp Leu Arg Arg Gly Ser Ser Pro Asp Val His Ala Leu Leu
280 285 290
gag atc acc gag gag tcg gac gcc gtg ctg gtg gac aag agc gac agc 1149
Glu Ile Thr Glu Glu Ser Asp Ala Val Leu Val Asp Lys Ser Asp Ser
295 300 305
gac tgagccgccc ccgtgccac ccacccatt cctcgtcct tccgaacttc 1202
Asp
ctcttttcgca ttctctctcg gctcgagctg gctgagattt ttctaaattg aaaacacgcc 1262
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aaaaattagc tgggcatggt tgcgcatgcc tgtaatccca gctactttgg aggetgaggt 2102
ggggagaatt gcttgaacct gggaggtgga ggttgacgtg ggccaaggtc gcgacactgc 2162

actccagcct gggtgacaga gtgagactcc atctcaacag aagg

2206

<210> 92

<211> 309

<212> PRT

<213> Homo sapiens

<400> 92

Met Glu Gly Ala Val Gln Ser Ile Gln Gly Glu Leu Ser Lys Leu Gly
1 5 10 15
Lys Ala His Ala Thr Thr Ser Asn Thr Val Ser Lys Leu Leu Glu Lys
20 25 30
Val Arg Lys Val Ser Val Asn Val Lys Thr Val Arg Gly Ser Leu Glu
35 40 45
Arg Gln Ala Gly Gln Ile Lys Lys Leu Glu Val Asn Glu Ala Glu Leu
50 55 60
Leu Arg Arg Arg Asn Phe Lys Val Met Ile Tyr Gln Asp Glu Val Lys
65 70 75 80
Leu Pro Ala Lys Leu Ser Ile Ser Lys Ser Leu Lys Glu Ser Glu Ala
85 90 95
Leu Pro Glu Lys Glu Gly Glu Glu Leu Gly Glu Gly Glu Arg Pro Glu
100 105 110
Glu Asp Ala Ala Ala Leu Glu Leu Ser Ser Asp Glu Ala Val Glu Val
115 120 125
Glu Glu Val Ile Glu Glu Ser Arg Ala Glu Arg Ile Lys Arg Ser Gly
130 135 140
Leu Arg Arg Val Asp Asp Phe Lys Lys Ala Phe Ser Lys Glu Lys Met
145 150 155 160

316/617

Glu Lys Thr Lys Val Arg Thr Arg Glu Asn Leu Glu Lys Thr Arg Leu
 165 170 175
 Lys Thr Lys Glu Asn Leu Glu Lys Thr Arg His Thr Leu Glu Lys Arg
 180 185 190
 Met Asn Lys Leu Gly Thr Arg Leu Val Pro Ala Glu Arg Arg Glu Lys
 195 200 205
 Leu Lys Thr Ser Arg Asp Lys Leu Arg Lys Ser Phe Thr Pro Asp His
 210 215 220
 Val Val Tyr Ala Arg Ser Lys Thr Ala Val Tyr Lys Val Pro Pro Phe
 225 230 235 240
 Thr Phe His Val Lys Lys Ile Arg Glu Gly Gln Val Glu Val Leu Lys
 245 250 255
 Ala Thr Glu Met Val Glu Val Gly Ala Asp Asp Asp Glu Gly Gly Ala
 260 265 270
 Glu Arg Gly Glu Ala Cys Asp Leu Arg Arg Gly Ser Ser Pro Asp Val
 275 280 285
 His Ala Leu Leu Glu Ile Thr Glu Glu Ser Asp Ala Val Leu Val Asp
 290 295 300
 Lys Ser Asp Ser Asp
 305

<210> 93

<211> 2333

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (110).. (1279)

<400> 93

ctctccgctc tcgcccgcta gctctcctcc cttccgctcc tgcttctctc cgggtctccc 60
 gctccagctc cagccccacc cggccggtcc cgcacggctc cgggtagcc atg gag gac 118

Met Glu Asp

1

ccc acg ctc tat att gtc gag cgg ccg ctt ccc ggg tac ccc gac gcc 166
 Pro Thr Leu Tyr Ile Val Glu Arg Pro Leu Pro Gly Tyr Pro Asp Ala

5

10

15

gag gcc ccg gag cct tcc tcc gct ggg gct cag gca gcg gag gag ccg 214
 Glu Ala Pro Glu Pro Ser Ser Ala Gly Ala Gln Ala Ala Glu Glu Pro

20

25

30

35

tcg ggg gcc ggc tca gaa gag ctg atc aag tcg gac cag gtg aac ggc 262
 Ser Gly Ala Gly Ser Glu Glu Leu Ile Lys Ser Asp Gln Val Asn Gly

40

45

50

gtg ctg gtg ctg agc ctc ctg gac aaa atc atc ggg gcc gta gac cag 310
 Val Leu Val Leu Ser Leu Leu Asp Lys Ile Ile Gly Ala Val Asp Gln

55

60

65

atc cag ctg act caa gca cag ctg gag gag cgg cag gcg gag atg gag 358
 Ile Gln Leu Thr Gln Ala Gln Leu Glu Glu Arg Gln Ala Glu Met Glu

70

75

80

ggc gca gtg cag agc atc cag ggc gag ctg agc aag ctg ggc aag gcg 406
 Gly Ala Val Gln Ser Ile Gln Gly Glu Leu Ser Lys Leu Gly Lys Ala

85

90

95

cac gcc acc acg agc aat acg gtg agc aag ctg ctg gag aag gtg cgc 454
 His Ala Thr Thr Ser Asn Thr Val Ser Lys Leu Leu Glu Lys Val Arg

100

105

110

115

318/617

aag gtc agc gtc aac gtg aag acc gtg cgc ggc agc ctg gag cgc cag	502
Lys Val Ser Val Asn Val Lys Thr Val Arg Gly Ser Leu Glu Arg Gln	
120 125 130	
gcg ggg cag atc aag aag ctg gag gtc aac gag gcc gag ctg ctg cgg	550
Ala Gly Gln Ile Lys Lys Leu Glu Val Asn Glu Ala Glu Leu Leu Arg	
135 140 145	
cgc cgc aac ttt aaa gtc atg atc tac cag gat gaa gtg aag ctg ccg	598
Arg Arg Asn Phe Lys Val Met Ile Tyr Gln Asp Glu Val Lys Leu Pro	
150 155 160	
gcc aaa ctg agc atc agc aaa tcg ctg aaa gag tcg gag gcg ctg cca	646
Ala Lys Leu Ser Ile Ser Lys Ser Leu Lys Glu Ser Glu Ala Leu Pro	
165 170 175	
gag aag gag ggc gag gag ctg ggc gag ggc gag cgg ccc gag gag gac	694
Glu Lys Glu Gly Glu Glu Leu Gly Glu Gly Glu Arg Pro Glu Glu Asp	
180 185 190 195	
gca gcg gcg ctg gag ctt tcg tcg gac gag gcg gtg gag gtt gag gag	742
Ala Ala Ala Leu Glu Leu Ser Ser Asp Glu Ala Val Glu Val Glu Glu	
200 205 210	
gtt att gag gag tcc cgc gca gag cgt atc aag cgc agc ggc ctg cgg	790
Val Ile Glu Glu Ser Arg Ala Glu Arg Ile Lys Arg Ser Gly Leu Arg	
215 220 225	
cgc gtg gac gac ttc aag aag gcc ttc tcc aag gag aag atg gag aag	838
Arg Val Asp Asp Phe Lys Lys Ala Phe Ser Lys Glu Lys Met Glu Lys	
230 235 240	
acc aag gtg cgt acc cgc gag aac ctg gag aag acg cgc ctc aag acc	886
Thr Lys Val Arg Thr Arg Glu Asn Leu Glu Lys Thr Arg Leu Lys Thr	
245 250 255	

aag gaa aac ctg gag aag acg cgg cac acc ctg gag aag cgc atg aac 934
 Lys Glu Asn Leu Glu Lys Thr Arg His Thr Leu Glu Lys Arg Met Asn
 260 265 270 275
 aag ctg ggc acg cgc ctg gtg ccc gcc gag cgg cgc gag aaa ctg aag 982
 Lys Leu Gly Thr Arg Leu Val Pro Ala Glu Arg Arg Glu Lys Leu Lys
 280 285 290
 acg tcg cgg gac aag ttg cgc aaa tcc ttc acg ccc gac cac gtg gtg 1030
 Thr Ser Arg Asp Lys Leu Arg Lys Ser Phe Thr Pro Asp His Val Val
 295 300 305
 tac gcg cgc tcc aag acc gcg gtc tac aag gtg cca ccc ttc acc ttc 1078
 Tyr Ala Arg Ser Lys Thr Ala Val Tyr Lys Val Pro Pro Phe Thr Phe
 310 315 320
 cac gtc aag aag atc cgc gag ggc cag gtg gaa gtg ctc aag gcc acc 1126
 His Val Lys Lys Ile Arg Glu Gly Gln Val Glu Val Leu Lys Ala Thr
 325 330 335
 gag atg gtg gag gtg ggc gcc gac gac gac gag ggc ggc gcg gag cgc 1174
 Glu Met Val Glu Val Gly Ala Asp Asp Asp Glu Gly Gly Ala Glu Arg
 340 345 350 355
 ggg gag gcc tgc gac ctg cgg cgc ggg agc agc ccc gac gtg cac gcg 1222
 Gly Glu Ala Cys Asp Leu Arg Arg Gly Ser Ser Pro Asp Val His Ala
 360 365 370
 ctg ctg gag atc acc gag gag tcg gac gcc gtg ctg gtg gac aag agc 1270
 Leu Leu Glu Ile Thr Glu Glu Ser Asp Ala Val Leu Val Asp Lys Ser
 375 380 385
 gac agc gac tgagccgccc ccgctgccac ccacccatt cctcgtcct 1319
 Asp Ser Asp
 390

tccgaacttc ctctttcgca ttctctctcg gctcgagctg gctgagattt ttctaaattg 1379
 aaaacacgcc cccctcccca cacctccagg aactccactc ccagtcttag agctgttagg 1439
 acccgatggg gaggcagccc ccgcagtgga cagccccgc ttggacacag tccgagtgga 1499
 atgggaaggg aatggtaaat ccctgtcctg gttgtccaag tcgggatctc agaggaaatt 1559
 gcagtgattc cacggttagg cccccctggg ggggtgcct tccccacgc ctctccccac 1619
 accaccacc cagctgctgt cattccgctc actgagctct tcttcattct caccctgac 1679
 cctgggggac tcaaagccaa aactgccaa agaggaaaga ttgaatccta aaggggatcc 1739
 ttgccccat gggaggcccc ctactagaag gacgtgaaag cagcttttgg gggaaactga 1799
 ggcagtgggg aagacagagc agaatgagcc ctcaccctgg ctgggggtcc agcacaggct 1859
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 gcgcatggcc atggcttgg aaaggagaat ggaaaaatag aagaaggctg gccgggcttg 2039
 gtggcttaag cctgtaacc cagcactttg ggaggccgag gtgggcggat cacctgaggt 2099
 caggagtctg ggaccagcct ggcaaacacc ccattctctac taagcgaaaa cccattctta 2159
 ctaaaattac aaaaattagc tgggcatggt tgcgcatgcc tgtaatccca gctactttgg 2219
 aggtgaggt ggggagaatt gcttgaacct gggaggtgga ggttgagtg ggccaaggct 2279
 gcgacactgc actccagcct gggtgacaga gtgagactcc atctcaacag aagg 2333

<210> 94

<211> 390

<212> PRT

<213> Homo sapiens

<400> 94

Met	Glu	Asp	Pro	Thr	Leu	Tyr	Ile	Val	Glu	Arg	Pro	Leu	Pro	Gly	Tyr
1				5					10					15	
Pro	Asp	Ala	Glu	Ala	Pro	Glu	Pro	Ser	Ser	Ala	Gly	Ala	Gln	Ala	Ala
			20						25					30	

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Glu Glu Pro Ser Gly Ala Gly Ser Glu Glu Leu Ile Lys Ser Asp Gln
35 40 45
Val Asn Gly Val Leu Val Leu Ser Leu Leu Asp Lys Ile Ile Gly Ala
50 55 60
Val Asp Gln Ile Gln Leu Thr Gln Ala Gln Leu Glu Glu Arg Gln Ala
65 70 75 80
Glu Met Glu Gly Ala Val Gln Ser Ile Gln Gly Glu Leu Ser Lys Leu
85 90 95
Gly Lys Ala His Ala Thr Thr Ser Asn Thr Val Ser Lys Leu Leu Glu
100 105 110
Lys Val Arg Lys Val Ser Val Asn Val Lys Thr Val Arg Gly Ser Leu
115 120 125
Glu Arg Gln Ala Gly Gln Ile Lys Lys Leu Glu Val Asn Glu Ala Glu
130 135 140
Leu Leu Arg Arg Arg Asn Phe Lys Val Met Ile Tyr Gln Asp Glu Val
145 150 155 160
Lys Leu Pro Ala Lys Leu Ser Ile Ser Lys Ser Leu Lys Glu Ser Glu
165 170 175
Ala Leu Pro Glu Lys Glu Gly Glu Glu Leu Gly Glu Gly Glu Arg Pro
180 185 190
Glu Glu Asp Ala Ala Ala Leu Glu Leu Ser Ser Asp Glu Ala Val Glu
195 200 205
Val Glu Glu Val Ile Glu Glu Ser Arg Ala Glu Arg Ile Lys Arg Ser
210 215 220
Gly Leu Arg Arg Val Asp Asp Phe Lys Lys Ala Phe Ser Lys Glu Lys
225 230 235 240
Met Glu Lys Thr Lys Val Arg Thr Arg Glu Asn Leu Glu Lys Thr Arg

245 250 255
 Leu Lys Thr Lys Glu Asn Leu Glu Lys Thr Arg His Thr Leu Glu Lys
 260 265 270
 Arg Met Asn Lys Leu Gly Thr Arg Leu Val Pro Ala Glu Arg Arg Glu
 275 280 285
 Lys Leu Lys Thr Ser Arg Asp Lys Leu Arg Lys Ser Phe Thr Pro Asp
 290 295 300
 His Val Val Tyr Ala Arg Ser Lys Thr Ala Val Tyr Lys Val Pro Pro
 305 310 315 320
 Phe Thr Phe His Val Lys Lys Ile Arg Glu Gly Gln Val Glu Val Leu
 325 330 335
 Lys Ala Thr Glu Met Val Glu Val Gly Ala Asp Asp Asp Glu Gly Gly
 340 345 350
 Ala Glu Arg Gly Glu Ala Cys Asp Leu Arg Arg Gly Ser Ser Pro Asp
 355 360 365
 Val His Ala Leu Leu Glu Ile Thr Glu Glu Ser Asp Ala Val Leu Val
 370 375 380
 Asp Lys Ser Asp Ser Asp
 385 390

<210> 95

<211> 1523

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (87).. (545)

<400> 95

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 ctccagagaa gcatggtggc cgcacc atg gtg cag ttg ttt gaa aag ggc tat 113

Met Val Gln Leu Phe Glu Lys Gly Tyr

1

5

ggc aag gat gct gct ggc att gcc atg gaa gcc att gct ttt gca cgt 161
 Gly Lys Asp Ala Ala Gly Ile Ala Met Glu Ala Ile Ala Phe Ala Arg

10 15 20 25

aac caa ggc ttt gac gtg gtg ctg gtg gac acg gca ggc cgc atg caa 209
 Asn Gln Gly Phe Asp Val Val Leu Val Asp Thr Ala Gly Arg Met Gln

30 35 40

gac aat gcc cct ctg atg act gcc ctg gcc aaa ctc att act gtc aat 257
 Asp Asn Ala Pro Leu Met Thr Ala Leu Ala Lys Leu Ile Thr Val Asn

45 50 55

aca cct gat ttg gtg ctg ttt gta gga gaa gcc tta gta ggc aat gaa 305
 Thr Pro Asp Leu Val Leu Phe Val Gly Glu Ala Leu Val Gly Asn Glu

60 65 70

gcc gtg gac cag ctg gtc aag ttc aac aga gcc ttg gct gac cat tct 353
 Ala Val Asp Gln Leu Val Lys Phe Asn Arg Ala Leu Ala Asp His Ser

75 80 85

atg gct cag aca cct cgg ctc att gat ggc att gtt ctt acc aaa ttt 401
 Met Ala Gln Thr Pro Arg Leu Ile Asp Gly Ile Val Leu Thr Lys Phe

90 95 100 105

gat acc att gat gac aag gtg gga gct gct att tct atg acg tac atc 449
 Asp Thr Ile Asp Asp Lys Val Gly Ala Ala Ile Ser Met Thr Tyr Ile

110 115 120

aca agc aaa ccc atc gtc ttt gtg ggc acc ggc cag acc tac tgt gac 497

324/617

Thr Ser Lys Pro Ile Val Phe Val Gly Thr Gly Gln Thr Tyr Cys Asp
 125 130 135
 cta cgc agc ctc aat gcc aag gct gtg gtg gct gcc ctc atg aag gct 545
 Leu Arg Ser Leu Asn Ala Lys Ala Val Val Ala Ala Leu Met Lys Ala
 140 145 150
 taacgtggct ctgcccatt accaaatcgc cgctttcccc acaagccctt ctctctgtat 605
 caagaatgtg ctttagagta tgtgagcaac ctgtcttcag ttagtagaca aggagagtg 665
 agggggcttg tggctccttc caatcccact cccgcttcag cacagccgcc atctgcaagg 725
 aaggcctaata catgttaca tcaactgccc ctgacctct cccagcgggc ctcccccttc 785
 ctactcaggc acccccttca ctctgcctac agactcagtc ttattacagc ttgaccaat 845
 ggttggaacc caacaccaga gctttgctaa taattagtgt ggtcaagagc cgtctgagcc 905
 taatgagtcc cagctgcatt aggttaagag actcttcag agccagcgc aggtcttgaa 965
 tggcacctct cctaggata cacagcctgc aggtccccag gacctggatg acaccgcct 1025
 cactgtggca gtgtattgcc tgttaattgc tgctaattct aattctgatg atgactccta 1085
 ctccattgtt taccctaaag catcagctag gctggagtga ttgtttaca atgagcaaaa 1145
 gatgagtcct tgcttcctc agaaataaaa ggagctcagc tgcagcgttg cattgggctt 1205
 ctggcctcc caactcttc cactcccaga atccagaagt aagctctgca tgttccccctt 1265
 cctgggagga aaccaattgt cagaaggatg tatgatgacc cctccccctc ccatccttca 1325
 cctcctaagc agtcctggct tttctcctc actccccctc acagtgcctg gtagacaagt 1385
 gctacattga agaacacaaa cctcttgta agacttgtcc ttagcttga tattacagat 1445
 gtgctattag tgcaataagg tgaaggctgt ctgcccagag aaataagtaa tttatataag 1505
 aaataaatt tcataaat 1523.

<210> 96

<211> 153

<212> PRT

<213> Homo sapiens

<400> 96

Met Val Gln Leu Phe Glu Lys Gly Tyr Gly Lys Asp Ala Ala Gly Ile
1 5 10 15
Ala Met Glu Ala Ile Ala Phe Ala Arg Asn Gln Gly Phe Asp Val Val
20 25 30
Leu Val Asp Thr Ala Gly Arg Met Gln Asp Asn Ala Pro Leu Met Thr
35 40 45
Ala Leu Ala Lys Leu Ile Thr Val Asn Thr Pro Asp Leu Val Leu Phe
50 55 60
Val Gly Glu Ala Leu Val Gly Asn Glu Ala Val Asp Gln Leu Val Lys
65 70 75 80
Phe Asn Arg Ala Leu Ala Asp His Ser Met Ala Gln Thr Pro Arg Leu
85 90 95
Ile Asp Gly Ile Val Leu Thr Lys Phe Asp Thr Ile Asp Asp Lys Val
100 105 110
Gly Ala Ala Ile Ser Met Thr Tyr Ile Thr Ser Lys Pro Ile Val Phe
115 120 125
Val Gly Thr Gly Gln Thr Tyr Cys Asp Leu Arg Ser Leu Asn Ala Lys
130 135 140
Ala Val Val Ala Ala Leu Met Lys Ala
145 150

<210> 97

<211> 2976

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (85).. (1998) .

<400> 97

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cccagctcct ctgccgtgc cgcc atg ctc gac ttc ttc acc att ttc tcc 111

Met Leu Asp Phe Phe Thr Ile Phe Ser

1

5

aag ggc ggg ctt gtg ctc tgg tgc ttc cag ggc gtt agc gac tca tgc 159

Lys Gly Gly Leu Val Leu Trp Cys Phe Gln Gly Val Ser Asp Ser Cys

10

15

20

25

acc gga ccc gtt aac gcg ttg att cgt tcc gtg ctg ctg cag gaa cgg 207

Thr Gly Pro Val Asn Ala Leu Ile Arg Ser Val Leu Leu Gln Glu Arg

30

35

40

gga ggt aac aac tcc ttc acc cat gag gca ctc aca ctc aag tat aaa 255

Gly Gly Asn Asn Ser Phe Thr His Glu Ala Leu Thr Leu Lys Tyr Lys

45

50

55

ctg gac aac cag ttt gag ctg gtg ttt gtg gtt ggt ttt cag aag atc 303

Leu Asp Asn Gln Phe Glu Leu Val Phe Val Val Gly Phe Gln Lys Ile

60

65

70

ctg aca ctg aca tat gta gac aaa ttg ata gat gac gtg cat cgg ctg 351

Leu Thr Leu Thr Tyr Val Asp Lys Leu Ile Asp Asp Val His Arg Leu

75

80

85

ttt cgg gac aag tac cgc aca gag atc caa cag caa agt gct tta agt 399

Phe Arg Asp Lys Tyr Arg Thr Glu Ile Gln Gln Gln Ser Ala Leu Ser

90

95

100

105

tta tta aat ggc act ttt gat ttc caa aat gac ttc ctg cgg ctc ctt 447

Leu Leu Asn Gly Thr Phe Asp Phe Gln Asn Asp Phe Leu Arg Leu Leu

327/617

110	115	120	
cgt gaa gca gag gag agc agt aag atc cgt gct ccc act acc atg aag			495
Arg Glu Ala Glu Glu Ser Ser Lys Ile Arg Ala Pro Thr Thr Met Lys			
125	130	135	
aaa ttt gaa gat tct gaa aag gcc aag aaa cct gtg agg tcc atg att			543
Lys Phe Glu Asp Ser Glu Lys Ala Lys Lys Pro Val Arg Ser Met Ile			
140	145	150	
gag aca cgg ggg gaa aag ccc aag gaa aaa gca aag aat agc aaa aaa			591
Glu Thr Arg Gly Glu Lys Pro Lys Glu Lys Ala Lys Asn Ser Lys Lys			
155	160	165	
aag ggg gcc aag aag gaa ggt tct gat ggt cct ttg gct acc agc aaa			639
Lys Gly Ala Lys Lys Glu Gly Ser Asp Gly Pro Leu Ala Thr Ser Lys			
170	175	180	185
cca gtc cct gca gaa aag tca ggt ctt cca gtg ggt cct gag aac gga			687
Pro Val Pro Ala Glu Lys Ser Gly Leu Pro Val Gly Pro Glu Asn Gly			
190	195	200	
gta gaa ctt tcc aaa gag gag ctg atc cgc agg aag cgc gag gag ttc			735
Val Glu Leu Ser Lys Glu Glu Leu Ile Arg Arg Lys Arg Glu Glu Phe			
205	210	215	
att cag aag cat ggg agg ggt atg gag aag tcc aac aag tcc acg aag			783
Ile Gln Lys His Gly Arg Gly Met Glu Lys Ser Asn Lys Ser Thr Lys			
220	225	230	
tca gat gct cca aag gag aag ggc aaa aaa gca ccc cgg gtg tgg gaa			831
Ser Asp Ala Pro Lys Glu Lys Gly Lys Lys Ala Pro Arg Val Trp Glu			
235	240	245	
ctg ggt ggc tgt gct aac aaa gaa gtg ttg gat tac agt act ccc acc			879
Leu Gly Gly Cys Ala Asn Lys Glu Val Leu Asp Tyr Ser Thr Pro Thr			

250	255	260	265	
acc aat gga acc cct gag gct gcc ttg tct gag gac atc aac ctg att				927
Thr Asn Gly Thr Pro Glu Ala Ala Leu Ser Glu Asp Ile Asn Leu Ile				
270	275	280		
cga ggg act ggg tct ggg ggg cag ctt cag gat ctg gac tgc agc agc				975
Arg Gly Thr Gly Ser Gly Gly Gln Leu Gln Asp Leu Asp Cys Ser Ser				
285	290	295		
tct gat gac gaa ggg gct gct caa aac tct acc aaa cct agt gcg acc				1023
Ser Asp Asp Glu Gly Ala Ala Gln Asn Ser Thr Lys Pro Ser Ala Thr				
300	305	310		
aag gga aca ctg ggt ggc atg ttt ggt atg ctg aag ggc ctt gtg ggt				1071
Lys Gly Thr Leu Gly Gly Met Phe Gly Met Leu Lys Gly Leu Val Gly				
315	320	325		
tca aag agc ttg agt cgt gaa gac atg gaa tct gtg ctg gac aag atg				1119
Ser Lys Ser Leu Ser Arg Glu Asp Met Glu Ser Val Leu Asp Lys Met				
330	335	340	345	
cgt gat cat ctc att gct aag aac gtg gct gca gac att gcc gtc cag				1167
Arg Asp His Leu Ile Ala Lys Asn Val Ala Ala Asp Ile Ala Val Gln				
350	355	360		
ctc tgt gaa tct gtt gcc aac aag ttg gaa ggg aag gtg atg ggg acg				1215
Leu Cys Glu Ser Val Ala Asn Lys Leu Glu Gly Lys Val Met Gly Thr				
365	370	375		
ttc agc acg gtg act tcc aca gta aag caa gcc cta cag gag tcc ctg				1263
Phe Ser Thr Val Thr Ser Thr Val Lys Gln Ala Leu Gln Glu Ser Leu				
380	385	390		
gtg cag att ctg cag cca cag cgt cgt gta gac atg ctc cgg gac atc				1311
Val Gln Ile Leu Gln Pro Gln Arg Arg Val Asp Met Leu Arg Asp Ile				

329/617

395	400	405	
atg gat gcc cag cgt cgc cag cgc cct tat gtc gtc acc ttc tgc ggc	1359		
Met Asp Ala Gln Arg Arg Gln Arg Pro Tyr Val Val Thr Phe Cys Gly			
410	415	420	425
gtt aat gga gtg ggg aaa tct act aat ctt gcc aag att tcc ttc tgg	1407		
Val Asn Gly Val Gly Lys Ser Thr Asn Leu Ala Lys Ile Ser Phe Trp			
430	435	440	
ttg tta gag aat ggc ttc agt gtc ctc att gct gcc tgt gat aca ttt	1455		
Leu Leu Glu Asn Gly Phe Ser Val Leu Ile Ala Ala Cys Asp Thr Phe			
445	450	455	
cgt gct ggg gcc gtg gag cag ctg cgt aca cac acc cgg cgt ttg agt	1503		
Arg Ala Gly Ala Val Glu Gln Leu Arg Thr His Thr Arg Arg Leu Ser			
460	465	470	
gcc cta cac cct cca gag aag cat ggt ggc cgc acc atg gtg cag ttg	1551		
Ala Leu His Pro Pro Glu Lys His Gly Gly Arg Thr Met Val Gln Leu			
475	480	485	
ttt gaa aag ggc tat ggc aag gat gct gct ggc att gcc atg gaa gcc	1599		
Phe Glu Lys Gly Tyr Gly Lys Asp Ala Ala Gly Ile Ala Met Glu Ala			
490	495	500	505
att gct ttt gca cgt aac caa ggc ttt gac gtg gtg ctg gtg gac acg	1647		
Ile Ala Phe Ala Arg Asn Gln Gly Phe Asp Val Val Leu Val Asp Thr			
510	515	520	
gca ggc cgc atg caa gac aat gcc cct ctg atg act gcc ctg gcc aaa	1695		
Ala Gly Arg Met Gln Asp Asn Ala Pro Leu Met Thr Ala Leu Ala Lys			
525	530	535	
ctc att act gtc aat aca cct gat ttg gtg ctg ttt gta gga gaa gcc	1743		
Leu Ile Thr Val Asn Thr Pro Asp Leu Val Leu Phe Val Gly Glu Ala			

540	545	550	
tta gta ggc aat gaa gcc gtg gac cag ctg gtc aag ttc aac aga gcc			1791
Leu Val Gly Asn Glu Ala Val Asp Gln Leu Val Lys Phe Asn Arg Ala			
555	560	565	
ttg gct gac cat tct atg gct cag aca cct cgg ctc att gat ggc att			1839
Leu Ala Asp His Ser Met Ala Gln Thr Pro Arg Leu Ile Asp Gly Ile			
570	575	580	585
gtt ctt acc aaa ttt gat acc att gat gac aag gtg gga gct gct att			1887
Val Leu Thr Lys Phe Asp Thr Ile Asp Asp Lys Val Gly Ala Ala Ile			
	590	595	600
tct atg acg tac atc aca agc aaa ccc atc gtc ttt gtg ggc acc ggc			1935
Ser Met Thr Tyr Ile Thr Ser Lys Pro Ile Val Phe Val Gly Thr Gly			
	605	610	615
cag acc tac tgt gac cta cgc agc ctc aat gcc aag gct gtg gtg gct			1983
Gln Thr Tyr Cys Asp Leu Arg Ser Leu Asn Ala Lys Ala Val Val Ala			
	620	625	630
gcc ctc atg aag gct taacgtggct cttgccaat accaaatcgc cgttttcccc			2038
Ala Leu Met Lys Ala			
635			
acaagccctt cttcctgtat caagaatgtg ctttagagta tgtgagcaac ctgtcttcag			2098
tgtagtacaa aggcagagtg agggggcttg tggctccttc caacccact ccccgttcag			2158
cacagccgcc atttgcaagg aaggcctaata catgttacaa tcaactgcca ctgacctct			2218
cccagcgggc ctcccccttc ctactcaggc acccccttca ctctgcctac agactcagtc			2278
ttattacagc tttagaccaat gggttgaacc caacaccaga gctttgctaa taattagtgt			2338
ggtcaagagc cgtctgagcc taatgagtcc cagctgcatt aggttaagag actcttccag			2398
agccagcgc aggtcttgaa tggcacctct ccctaggata cacagcctgc aggtccccag			2458
gacctggatg acaccgcct cactgtggca gtgtattgcc tgtaattgc tgctaattct			2518

aattctgatg atgactccta ctccattgtt taccccaaag catcagctag gctggagtga 2578
tttgttacaa atgagcaaaa gatgagtcct tgcttcctc agaaataaaa gtagctcagc 2638
tgcagcgttg cattgggctt ctgggcctcc caactcttcc cactcccaga atccagaagt 2698
aagctctgca tgttccccctt cctgggagga aaccaattgt cagaaggatg tatgatgacc 2758
ccctcccctc ccatccttca cctcctaagc agtcctggct tttcctcacc actcccctct 2818
acagtgcctg gtagacaagt gctacattga agaacacaaa cctcttggtta agacttgctc 2878
tgtagcttga tattacagat gtgctattag tgcaataagg tgaaggctgt ctgccagag 2938
aaataagtaa tttatataag aaaataaatt tcataaat 2976

<210> 98

<211> 638

<212> PRT

<213> Homo sapiens

<400> 98

Met Leu Asp Phe Phe Thr Ile Phe Ser Lys Gly Gly Leu Val Leu Trp
1 5 10 15
Cys Phe Gln Gly Val Ser Asp Ser Cys Thr Gly Pro Val Asn Ala Leu
20 25 30
Ile Arg Ser Val Leu Leu Gln Glu Arg Gly Gly Asn Asn Ser Phe Thr
35 40 45
His Glu Ala Leu Thr Leu Lys Tyr Lys Leu Asp Asn Gln Phe Glu Leu
50 55 60
Val Phe Val Val Gly Phe Gln Lys Ile Leu Thr Leu Thr Tyr Val Asp
65 70 75 80
Lys Leu Ile Asp Asp Val His Arg Leu Phe Arg Asp Lys Tyr Arg Thr
85 90 95
Glu Ile Gln Gln Gln Ser Ala Leu Ser Leu Leu Asn Gly Thr Phe Asp

100 105 110
 Phe Gln Asn Asp Phe Leu Arg Leu Leu Arg Glu Ala Glu Glu Ser Ser
 115 120 125
 Lys Ile Arg Ala Pro Thr Thr Met Lys Lys Phe Glu Asp Ser Glu Lys
 130 135 140
 Ala Lys Lys Pro Val Arg Ser Met Ile Glu Thr Arg Gly Glu Lys Pro
 145 150 155 160
 Lys Glu Lys Ala Lys Asn Ser Lys Lys Lys Gly Ala Lys Lys Glu Gly
 165 170 175
 Ser Asp Gly Pro Leu Ala Thr Ser Lys Pro Val Pro Ala Glu Lys Ser
 180 185 190
 Gly Leu Pro Val Gly Pro Glu Asn Gly Val Glu Leu Ser Lys Glu Glu
 195 200 205
 Leu Ile Arg Arg Lys Arg Glu Glu Phe Ile Gln Lys His Gly Arg Gly
 210 215 220
 Met Glu Lys Ser Asn Lys Ser Thr Lys Ser Asp Ala Pro Lys Glu Lys
 225 230 235 240
 Gly Lys Lys Ala Pro Arg Val Trp Glu Leu Gly Gly Cys Ala Asn Lys
 245 250 255
 Glu Val Leu Asp Tyr Ser Thr Pro Thr Thr Asn Gly Thr Pro Glu Ala
 260 265 270
 Ala Leu Ser Glu Asp Ile Asn Leu Ile Arg Gly Thr Gly Ser Gly Gly
 275 280 285
 Gln Leu Gln Asp Leu Asp Cys Ser Ser Ser Asp Asp Glu Gly Ala Ala
 290 295 300
 Gln Asn Ser Thr Lys Pro Ser Ala Thr Lys Gly Thr Leu Gly Gly Met
 305 310 315 320

333/617

Phe Gly Met Leu Lys Gly Leu Val Gly Ser Lys Ser Leu Ser Arg Glu
325 330 335
Asp Met Glu Ser Val Leu Asp Lys Met Arg Asp His Leu Ile Ala Lys
340 345 350
Asn Val Ala Ala Asp Ile Ala Val Gln Leu Cys Glu Ser Val Ala Asn
355 360 365
Lys Leu Glu Gly Lys Val Met Gly Thr Phe Ser Thr Val Thr Ser Thr
370 375 380
Val Lys Gln Ala Leu Gln Glu Ser Leu Val Gln Ile Leu Gln Pro Gln
385 390 395 400
Arg Arg Val Asp Met Leu Arg Asp Ile Met Asp Ala Gln Arg Arg Gln
405 410 415
Arg Pro Tyr Val Val Thr Phe Cys Gly Val Asn Gly Val Gly Lys Ser
420 425 430
Thr Asn Leu Ala Lys Ile Ser Phe Trp Leu Leu Glu Asn Gly Phe Ser
435 440 445
Val Leu Ile Ala Ala Cys Asp Thr Phe Arg Ala Gly Ala Val Glu Gln
450 455 460
Leu Arg Thr His Thr Arg Arg Leu Ser Ala Leu His Pro Pro Glu Lys
465 470 475 480
His Gly Gly Arg Thr Met Val Gln Leu Phe Glu Lys Gly Tyr Gly Lys
485 490 495
Asp Ala Ala Gly Ile Ala Met Glu Ala Ile Ala Phe Ala Arg Asn Gln
500 505 510
Gly Phe Asp Val Val Leu Val Asp Thr Ala Gly Arg Met Gln Asp Asn
515 520 525
Ala Pro Leu Met Thr Ala Leu Ala Lys Leu Ile Thr Val Asn Thr Pro

530 535 540
 Asp Leu Val Leu Phe Val Gly Glu Ala Leu Val Gly Asn Glu Ala Val
 545 550 555 560
 Asp Gln Leu Val Lys Phe Asn Arg Ala Leu Ala Asp His Ser Met Ala
 565 570 575
 Gln Thr Pro Arg Leu Ile Asp Gly Ile Val Leu Thr Lys Phe Asp Thr
 580 585 590
 Ile Asp Asp Lys Val Gly Ala Ala Ile Ser Met Thr Tyr Ile Thr Ser
 595 600 605
 Lys Pro Ile Val Phe Val Gly Thr Gly Gln Thr Tyr Cys Asp Leu Arg
 610 615 620
 Ser Leu Asn Ala Lys Ala Val Val Ala Ala Leu Met Lys Ala
 625 630 635

 <210> 99
 <211> 1176
 <212> DNA
 <213> Mus musculus
 <220>
 <221> CDS
 <222> (69).. (848)
 <400> 99

 gcgagaatca gcgcgtcctt ctgactgagc ggctgcggct ggagcggagc agttcggcta 60
 gctgttgg atg gcg cgg ggc gga gct ggg cgg gca gtg gcc ctg ggc ctg 110
 Met Ala Arg Gly Gly Ala Gly Arg Ala Val Ala Leu Gly Leu
 1 5 10
 gtg ctg cgg ctc ctc ttt ggt ctc aga aca ggc cta gag gcc gct ccg 158

Val	Leu	Arg	Leu	Leu	Phe	Gly	Leu	Arg	Thr	Gly	Leu	Glu	Ala	Ala	Pro				
15					20					25					30				
gct ccg gcc cat acc cgg gtc caa gtc tcc ggc tct aga gct gac tcc																206			
Ala	Pro	Ala	His	Thr	Arg	Val	Gln	Val	Ser	Gly	Ser	Arg	Ala	Asp	Ser				
				35						40					45				
tgc ccg aca gac acc ttc cag tgt ctt acc agt ggc tat tgt gtg ccc																254			
Cys	Pro	Thr	Asp	Thr	Phe	Gln	Cys	Leu	Thr	Ser	Gly	Tyr	Cys	Val	Pro				
				50						55					60				
ctt tcc tgg cgc tgt gat ggg gac cag gac tgc tct gat ggc agt gac																302			
Leu	Ser	Trp	Arg	Cys	Asp	Gly	Asp	Gln	Asp	Cys	Ser	Asp	Gly	Ser	Asp				
				65						70					75				
gag gaa gac tgt agg att gag tca tgt gct cag aat ggg cag tgc caa																350			
Glu	Glu	Asp	Cys	Arg	Ile	Glu	Ser	Cys	Ala	Gln	Asn	Gly	Gln	Cys	Gln				
				80						85					90				
cca cag tct gcc ctt cct tgc tcc tgt gac aac atc agt ggt tgc tct																398			
Pro	Gln	Ser	Ala	Leu	Pro	Cys	Ser	Cys	Asp	Asn	Ile	Ser	Gly	Cys	Ser				
				95						100					105				110
gat gtc tct gac aag aac ctc aac tgc agc cgc cca ccc tgt cag gag																446			
Asp	Val	Ser	Asp	Lys	Asn	Leu	Asn	Cys	Ser	Arg	Pro	Pro	Cys	Gln	Glu				
										115					120				125
agt gag ctg cat tgc ata ctg gat gat gtc tgt att cca cac acg tgg																494			
Ser	Glu	Leu	His	Cys	Ile	Leu	Asp	Asp	Val	Cys	Ile	Pro	His	Thr	Trp				
										130					135				140
cgc tgt gat ggc cac cca gac tgt ctt gac tcc agt gat gag ctc agc																542			
Arg	Cys	Asp	Gly	His	Pro	Asp	Cys	Leu	Asp	Ser	Ser	Asp	Glu	Leu	Ser				
										145					150				155
tgt gac act gac aca gaa att gat aag ata ttc cag gag gag aat gcc																590			

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Cys Asp Thr Asp Thr Glu Ile Asp Lys Ile Phe Gln Glu Glu Asn Ala
 160 165 170
 aca act aca agg att tct acg acc atg gag aat gag acc tct ttc agg 638
 Thr Thr Thr Arg Ile Ser Thr Thr Met Glu Asn Glu Thr Ser Phe Arg
 175 180 185 190
 aat gta aca ttt acc tct gct ggg gac tca tcc cga aac cca agt gcc 686
 Asn Val Thr Phe Thr Ser Ala Gly Asp Ser Ser Arg Asn Pro Ser Ala
 195 200 205
 tat ggg gtt att gca gct gct ggg gtg ttg agt gcc atc ctg gtt tcg 734
 Tyr Gly Val Ile Ala Ala Ala Gly Val Leu Ser Ala Ile Leu Val Ser
 210 215 220
 gcc acc ctt ctc ata ttg cta cgc ctc cga ggt cag ggt tat ctg ccc 782
 Ala Thr Leu Leu Ile Leu Leu Arg Leu Arg Gly Gln Gly Tyr Leu Pro
 225 230 235
 cca cca ggg ctg ttg gtg gct gtg aag gag tcg ctg ctg ctg tca gaa 830
 Pro Pro Gly Leu Leu Val Ala Val Lys Glu Ser Leu Leu Leu Ser Glu
 240 245 250
 agg aaa acc tct ctg atc tgaggacaca tggttaccac ctggccctga 878
 Arg Lys Thr Ser Leu Ile
 255 260
 gtgcagtcag actgggacaa aggagccgtg aaacacgcaa ggagcttctg gcttctcagc 938
 tttgagacct gggctctttg gagcacagag aactttgatt tttaagcttc tacagatatg 998
 gtccatagaga ctggggtcct cagacactcc cgctgtatgt ggtgagcttg gctggaaact 1058
 tgccatagcc aggactgagg ggctggcccc aggacgctct caagaaatgg ggctactgtg 1118
 gtttagacac tctgtctgct cacattgatg ggtggctatt aaagtttctt caccctc 1176

<210> 100

337/617

<211> 260

<212> PRT

<213> Mus musculus

<400> 100

Met Ala Arg Gly Gly Ala Gly Arg Ala Val Ala Leu Gly Leu Val Leu
1 5 10 15
Arg Leu Leu Phe Gly Leu Arg Thr Gly Leu Glu Ala Ala Pro Ala Pro
20 25 30
Ala His Thr Arg Val Gln Val Ser Gly Ser Arg Ala Asp Ser Cys Pro
35 40 45
Thr Asp Thr Phe Gln Cys Leu Thr Ser Gly Tyr Cys Val Pro Leu Ser
50 55 60
Trp Arg Cys Asp Gly Asp Gln Asp Cys Ser Asp Gly Ser Asp Glu Glu
65 70 75 80
Asp Cys Arg Ile Glu Ser Cys Ala Gln Asn Gly Gln Cys Gln Pro Gln
85 90 95
Ser Ala Leu Pro Cys Ser Cys Asp Asn Ile Ser Gly Cys Ser Asp Val
100 105 110
Ser Asp Lys Asn Leu Asn Cys Ser Arg Pro Pro Cys Gln Glu Ser Glu
115 120 125
Leu His Cys Ile Leu Asp Asp Val Cys Ile Pro His Thr Trp Arg Cys
130 135 140
Asp Gly His Pro Asp Cys Leu Asp Ser Ser Asp Glu Leu Ser Cys Asp
145 150 155 160
Thr Asp Thr Glu Ile Asp Lys Ile Phe Gln Glu Glu Asn Ala Thr Thr
165 170 175
Thr Arg Ile Ser Thr Thr Met Glu Asn Glu Thr Ser Phe Arg Asn Val

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180 185 190
 Thr Phe Thr Ser Ala Gly Asp Ser Ser Arg Asn Pro Ser Ala Tyr Gly
 195 200 205
 Val Ile Ala Ala Ala Gly Val Leu Ser Ala Ile Leu Val Ser Ala Thr
 210 215 220
 Leu Leu Ile Leu Leu Arg Leu Arg Gly Gln Gly Tyr Leu Pro Pro Pro
 225 230 235 240
 Gly Leu Leu Val Ala Val Lys Glu Ser Leu Leu Leu Ser Glu Arg Lys
 245 250 255
 Thr Ser Leu Ile
 260

<210> 101

<211> 1176

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (271).. (642)

<400> 101

gcgagaatca gcgcgtcctt ctgactgagc ggctgcggct ggagcggagc agttcggcta 60
 gctgttggat ggcgcggggc ggagctgggc gggcagtggc cctgggcctg gtgctgcggc 120
 tcctcttttg tctcagaaca ggcctagagg ccgctccggc tccggcccat acccgggtcc 180
 aagtctccgg ctctagagct gactcctgcc cgacagacac cttccagtgt cttaccagtg 240
 gctattgtgt gcccctttcc tggcgctgtg atg ggg acc agg act gct ctg atg 294

Met Gly Thr Arg Thr Ala Leu Met

1

5

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gca gtg acg agg aag act gta gga ttg agt cat gtg ctc aga atg ggc 342
 Ala Val Thr Arg Lys Thr Val Gly Leu Ser His Val Leu Arg Met Gly
 10 15 20
 agt gcc aac cac agt ctg ccc ttc ctt gct cct gtg aca aca tca gtg 390
 Ser Ala Asn His Ser Leu Pro Phe Leu Ala Pro Val Thr Thr Ser Val
 25 30 35 40
 gtt gct ctg atg tct ctg aca aga acc tca act gca gcc gcc cac cct 438
 Val Ala Leu Met Ser Leu Thr Arg Thr Ser Thr Ala Ala Ala His Pro
 45 50 55
 gtc agg aga gtg agc tgc att gca tac tgg atg atg tct gta ttc cac 486
 Val Arg Arg Val Ser Cys Ile Ala Tyr Trp Met Met Ser Val Phe His
 60 65 70
 aca cgt gcc gct gtg atg gcc acc cag act gtc ttg act cca gtg atg 534
 Thr Arg Gly Ala Val Met Ala Thr Gln Thr Val Leu Thr Pro Val Met
 75 80 85
 agc tca gct gtg aca ctg aca cag aaa ttg ata aga tat tcc agg agg 582
 Ser Ser Ala Val Thr Leu Thr Gln Lys Leu Ile Arg Tyr Ser Arg Arg
 90 95 100
 aga atg cca caa cta caa gga ttt cta cga cca tgg aga atg aga cct 630
 Arg Met Pro Gln Leu Gln Gly Phe Leu Arg Pro Trp Arg Met Arg Pro
 105 110 115 120
 ctt tca gga atg taacatttac ctctgctggg gactcatccc gaaaccaag 682
 Leu Ser Gly Met
 tgcctatggg gttattgcag ctgctggggt gttgagtgcc atcctggttt cggccaccct 742
 tctcatattg ctacgcctcc gaggtcaggg ttatctgccc ccaccagggc tgttggtggc 802
 tgtgaaggag tcgctgctgc tgtcagaaag gaaaacctct ctgatctgag gacacatggt 862
 taccacctgg cctgagtgc agtcagactg ggacaaagga gccgtgaaac acgcaaggag 922

cttctggctt ctcagctttg agacctgggc tctttggagc acagagaact ttgattttta 982
 agcttctaca gatatgggtcc tagagactgg ggtcctcaga cactcccgt gtatgtggtg 1042
 agcttggctg gaaacttgcc atagccagga ctgaggggct ggccccagga cgctctcaag 1102
 aaatggggct actgtggttt agacactcct gctgctcaca ttgatgggtg gctattaaag 1162
 tttcttcacc cctc 1176

<210> 102

<211> 124

<212> PRT

<213> Mus musculus

<400> 102

Met Gly Thr Arg Thr Ala Leu Met Ala Val Thr Arg Lys Thr Val Gly
 1 5 10 15
 Leu Ser His Val Leu Arg Met Gly Ser Ala Asn His Ser Leu Pro Phe
 20 25 30
 Leu Ala Pro Val Thr Thr Ser Val Val Ala Leu Met Ser Leu Thr Arg
 35 40 45
 Thr Ser Thr Ala Ala Ala His Pro Val Arg Arg Val Ser Cys Ile Ala
 50 55 60
 Tyr Trp Met Met Ser Val Phe His Thr Arg Gly Ala Val Met Ala Thr
 65 70 75 80
 Gln Thr Val Leu Thr Pro Val Met Ser Ser Ala Val Thr Leu Thr Gln
 85 90 95
 Lys Leu Ile Arg Tyr Ser Arg Arg Arg Met Pro Gln Leu Gln Gly Phe
 100 105 110
 Leu Arg Pro Trp Arg Met Arg Pro Leu Ser Gly Met
 115 120

341/617

<210> 103

<211> 1205

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (21).. (866)

<400> 103

ggcgccgctg tggggacagc atg agc ggc ggt tgg atg gcg cag gtt gga gcg 53

Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala

1

5

10

tgg cga aca ggg gct ctg ggc ctg gcg ctg ctg ctg ctc ggc ctc 101

Trp Arg Thr Gly Ala Leu Gly Leu Ala Leu Leu Leu Leu Gly Leu

15

20

25

gga cta ggc ctg gag gcc gcc gcg agc ccg ctt tcc acc ccg acc tct 149

Gly Leu Gly Leu Glu Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser

30

35

40

gcc cag gcc gca ggc ccc agc tca ggc tgc tgc cca ccc acc aag ttc 197

Ala Gln Ala Ala Gly Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe

45

50

55

cag tgc cgc acc agt ggc tta tgc gtg ccc ctc acc tgg cgc tgc gac 245

Gln Cys Arg Thr Ser Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp

60

65

70

75

agg gac ttg gac tgc agc gat ggc agc gat gag gag gag tgc agg att 293

Arg Asp Leu Asp Cys Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile

80

85

90

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gag cca tgt acc cag aaa ggg caa tgc cca ccg ccc cct ggc ctc ccc	341
Glu Pro Cys Thr Gln Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro	
95 100 105	
tgc ccc tgc acc ggc gtc agt gac tgc tct ggg gga act gac aag aaa	389
Cys Pro Cys Thr Gly Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys	
110 115 120	
ctg cgc aac tgc agc cgc ctg gcc tgc cta gca ggc gag ctc cgt tgc	437
Leu Arg Asn Cys Ser Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys	
125 130 135	
acg ctg agc gat gac tgc att cca ctc acg tgg cgc tgc gac ggc cac	485
Thr Leu Ser Asp Asp Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His	
140 145 150 155	
cca gac tgt ccc gac tcc agc gac gag ctc ggc tgt gga acc aat gag	533
Pro Asp Cys Pro Asp Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu	
160 165 170	
atc ctc ccg gaa ggg gat gcc aca acc atg ggg ccc cct gtg acc ctg	581
Ile Leu Pro Glu Gly Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu	
175 180 185	
gag agt gtc acc tct ctc agg aat gcc aca acc atg ggg ccc cct gtg	629
Glu Ser Val Thr Ser Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val	
190 195 200	
acc ctg gag agt gtc ccc tct gtc ggg aat gcc aca tcc tcc tct gcc	677
Thr Leu Glu Ser Val Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala	
205 210 215	
gga gac cag tct gga agc cca act gcc tat ggg gtt att gca gct gct	725
Gly Asp Gln Ser Gly Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala	
220 225 230 235	

gcg gtg ctc agt gca agc ctg gtc acc gcc acc ctc ctc ctt ttg tcc 773
 Ala Val Leu Ser Ala Ser Leu Val Thr Ala Thr Leu Leu Leu Leu Ser
 240 245 250
 tgg ctc cga gcc cag gag cgc ctc cgc cca ctg ggg tta ctg gtg gcc 821
 Trp Leu Arg Ala Gln Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala
 255 260 265
 atg aag gag tcc ctg ctg ctg tca gaa cag aag acc tcg ctg ccc 866
 Met Lys Glu Ser Leu Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro
 270 275 280
 tgaggacaag cacttgccac caccgtcact cagccctggg cgtagccgga caggaggaga 926
 gcagtgatgc ggatgggtac ccgggcacac cagccctcag agacctgagc tcttctggcc 986
 acgtggaacc tcgaaccga gtcctgcag aagtggccct ggagattgag ggtccctgga 1046
 cactccctat ggagatccgg ggagctagga tggggaacct gccacagcca gaactgaggg 1106
 gctggcccca ggcagctccc agggggtaga acggccctgt gcttaagaca ctctgctgc 1166
 cccgtctgag ggtggcgatt aaagttgctt cacatcctt 1205

<210> 104

<211> 282

<212> PRT

<213> Homo sapiens

<400> 104

Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala
 1 5 10 15
 Leu Gly Leu Ala Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu
 20 25 30
 Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly
 35 40 45

Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser
 50 55 60
 Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys
 65 70 75 80
 Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln
 85 90 95
 Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly
 100 105 110
 Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser
 115 120 125
 Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp
 130 135 140
 Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp
 145 150 155 160
 Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly
 165 170 175
 Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser
 180 185 190
 Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val
 195 200 205
 Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly
 210 215 220
 Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Val Leu Ser Ala
 225 230 235 240
 Ser Leu Val Thr Ala Thr Leu Leu Leu Leu Ser Trp Leu Arg Ala Gln
 245 250 255
 Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu

345/617

260 265 270
 Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro
 275 280

 <210> 105
 <211> 1881
 <212> DNA
 <213> Mus musculus
 <220>
 <221> CDS
 <222> (90).. (1532)
 <400> 105

 attttgtcgg tgtctgtcgc agcggctgga gaggaacgac ggcggtttgg cgacatttct 60
 cggccaaaag gccgcttgct tttgcggag atg cgg cat tcc aaa cga act cac 113

 Met Arg His Ser Lys Arg Thr His
 1 5

 tgt cct gat tgg gat agt aga gaa agc tgg ggc cat gaa agc tac agt 161
 Cys Pro Asp Trp Asp Ser Arg Glu Ser Trp Gly His Glu Ser Tyr Ser
 10 15 20

 gga agt cac aaa cgc aag aga agg tct cac agc agt act cag gag aac 209
 Gly Ser His Lys Arg Lys Arg Arg Ser His Ser Ser Thr Gln Glu Asn
 25 30 35 40

 agg cac tgt aaa cca cat cat cag ttt aaa gac tcg gat tgt cac tat 257
 Arg His Cys Lys Pro His His Gln Phe Lys Asp Ser Asp Cys His Tyr
 45 50 55

 tta gaa gca aga tgc ttg aat gag aga gat tat cgg gac cgg aga tac 305
 Leu Glu Ala Arg Cys Leu Asn Glu Arg Asp Tyr Arg Asp Arg Arg Tyr

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60	65	70	
att gat gaa tac aga aat gac tac tgc gaa gga tat gtt cca aga cat			353
Ile Asp Glu Tyr Arg Asn Asp Tyr Cys Glu Gly Tyr Val Pro Arg His			
75	80	85	
tac cat aga gac gtt gaa agc act tac cgg atc cat tgc agt aaa tcc			401
Tyr His Arg Asp Val Glu Ser Thr Tyr Arg Ile His Cys Ser Lys Ser			
90	95	100	
tca gtc agg agc agg aga agc agc cct aag aga aag cgt aat aga ccc			449
Ser Val Arg Ser Arg Arg Ser Ser Pro Lys Arg Lys Arg Asn Arg Pro			
105	110	115	120
tgt gca agt cat cag tcg cat tcg aag agc cac cga agg aaa aga tcc			497
Cys Ala Ser His Gln Ser His Ser Lys Ser His Arg Arg Lys Arg Ser			
125	130	135	
agg agt ata gag gat gat gag gag ggt cac ctg atc tgt caa agt gga			545
Arg Ser Ile Glu Asp Asp Glu Glu Gly His Leu Ile Cys Gln Ser Gly			
140	145	150	
gac gtt cta aga gca aga tat gaa atc gtg gac act tta ggt gaa gga			593
Asp Val Leu Arg Ala Arg Tyr Glu Ile Val Asp Thr Leu Gly Glu Gly			
155	160	165	
gcc ttt ggc aaa gtt gta gag tgc att gat cac ggc atg gat ggc tta			641
Ala Phe Gly Lys Val Val Glu Cys Ile Asp His Gly Met Asp Gly Leu			
170	175	180	
cat gta gca gtg aaa att gta aaa aat gta ggc cgt tac cgg gag gca			689
His Val Ala Val Lys Ile Val Lys Asn Val Gly Arg Tyr Arg Glu Ala			
185	190	195	200
gct cgt tct gaa atc caa gta ttg gag cac ttg aac agc act gac ccc			737
Ala Arg Ser Glu Ile Gln Val Leu Glu His Leu Asn Ser Thr Asp Pro			

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205	210	215	
aac agt gtc ttc cga tgc gtc cag atg cta gag tgg ttt gat cat cat			785
Asn Ser Val Phe Arg Cys Val Gln Met Leu Glu Trp Phe Asp His His			
220	225	230	
ggt cat gtt tgt att gtg ttt gag ctg ctg gga ctt agt acc tat gat			833
Gly His Val Cys Ile Val Phe Glu Leu Leu Gly Leu Ser Thr Tyr Asp			
235	240	245	
ttt att aaa gaa aat agt ttt ctg cca ttt caa att gat cac atc agg			881
Phe Ile Lys Glu Asn Ser Phe Leu Pro Phe Gln Ile Asp His Ile Arg			
250	255	260	
caa atg gct tat cag atc tgc cag tct ata aat ttt tta cat cat aat			929
Gln Met Ala Tyr Gln Ile Cys Gln Ser Ile Asn Phe Leu His His Asn			
265	270	275	280
aaa tta aca cac acg gac cta aaa cct gaa aat att tta ttt gtg aag			977
Lys Leu Thr His Thr Asp Leu Lys Pro Glu Asn Ile Leu Phe Val Lys			
285	290	295	
tct gac tat gta gtc aaa tac aat tct aaa atg aaa cga gat gag cgc			1025
Ser Asp Tyr Val Val Lys Tyr Asn Ser Lys Met Lys Arg Asp Glu Arg			
300	305	310	
aca ttg aaa aac aca gat atc aaa gtt gtt gat ttt gga agt gca aca			1073
Thr Leu Lys Asn Thr Asp Ile Lys Val Val Asp Phe Gly Ser Ala Thr			
315	320	325	
tat gac gac gaa cat cat agt act ttg gtg tcc aca agg cac tac agg			1121
Tyr Asp Asp Glu His His Ser Thr Leu Val Ser Thr Arg His Tyr Arg			
330	335	340	
gct cca gag gtc att ttg gct cta ggt tgg tct cag cct tgt gat gtt			1169
Ala Pro Glu Val Ile Leu Ala Leu Gly Trp Ser Gln Pro Cys Asp Val			

345	350	355	360	
tgg agc ata ggc tgc att ctt att gag tac tac ctt ggg ttc aca gtc				1217
Trp Ser Ile Gly Cys Ile Leu Ile Glu Tyr Tyr Leu Gly Phe Thr Val				
365	370	375		
ttt cag acc cac gat agt aaa gag cac ctg gca atg atg gag cgg atc				1265
Phe Gln Thr His Asp Ser Lys Glu His Leu Ala Met Met Glu Arg Ile				
380	385	390		
tta gga ccc atc cca gca cat atg atc cag aag aca agg aaa cgc aag				1313
Leu Gly Pro Ile Pro Ala His Met Ile Gln Lys Thr Arg Lys Arg Lys				
395	400	405		
tat ttc cac cat aac cag cta gat tgg gac gag cat agt tca gct ggg				1361
Tyr Phe His His Asn Gln Leu Asp Trp Asp Glu His Ser Ser Ala Gly				
410	415	420		
aga tat gtt agg aga cgc tgc aag ccg tta aag gaa ttt atg ctg tgt				1409
Arg Tyr Val Arg Arg Arg Cys Lys Pro Leu Lys Glu Phe Met Leu Cys				
425	430	435	440	
cat gac gaa gag cat gag aag ctg ttt gac ctg gtt cga aga atg ttg				1457
His Asp Glu Glu His Glu Lys Leu Phe Asp Leu Val Arg Arg Met Leu				
445	450	455		
gag tat gac cca gcg aga agg atc acc ttg gat gaa gca ttg cag cac				1505
Glu Tyr Asp Pro Ala Arg Arg Ile Thr Leu Asp Glu Ala Leu Gln His				
460	465	470		
cct ttc ttt gac tta tta aaa agg aaa tgagtgggag tcaggggtct				1552
Pro Phe Phe Asp Leu Leu Lys Arg Lys				
475	480			
tctgtgtact tctctaggag cagttacttc cagactgtgt cagtcaacta aaccttctaa				1612
tatttttgta aacattaaat tattttgtac agttaagtgt aaatactgta tgttttgtat				1672

caatagcata actaccttgt taagtatggt gttgataatg aatgcaatac aagagttaca 1732
 atgaattttc cttttgatgt taattgccac tttaaaggct tttagaatgc cctttgtgtc 1792
 cagtataaaa cgtgattggt cccatctttt gtacatgaag gttgactctg aagtgatttt 1852
 tttttttcct caagtaaaag gaaatcttg 1881

<210> 106

<211> 481

<212> PRT

<213> Mus musculus

<400> 106

Met Arg His Ser Lys Arg Thr His Cys Pro Asp Trp Asp Ser Arg Glu
 1 5 10 15
 Ser Trp Gly His Glu Ser Tyr Ser Gly Ser His Lys Arg Lys Arg Arg
 20 25 30
 Ser His Ser Ser Thr Gln Glu Asn Arg His Cys Lys Pro His His Gln
 35 40 45
 Phe Lys Asp Ser Asp Cys His Tyr Leu Glu Ala Arg Cys Leu Asn Glu
 50 55 60
 Arg Asp Tyr Arg Asp Arg Arg Tyr Ile Asp Glu Tyr Arg Asn Asp Tyr
 65 70 75 80
 Cys Glu Gly Tyr Val Pro Arg His Tyr His Arg Asp Val Glu Ser Thr
 85 90 95
 Tyr Arg Ile His Cys Ser Lys Ser Ser Val Arg Ser Arg Arg Ser Ser
 100 105 110
 Pro Lys Arg Lys Arg Asn Arg Pro Cys Ala Ser His Gln Ser His Ser
 115 120 125
 Lys Ser His Arg Arg Lys Arg Ser Arg Ser Ile Glu Asp Asp Glu Glu

130 135 140
Gly His Leu Ile Cys Gln Ser Gly Asp Val Leu Arg Ala Arg Tyr Glu
145 150 155 160
Ile Val Asp Thr Leu Gly Glu Gly Ala Phe Gly Lys Val Val Glu Cys
165 170 175
Ile Asp His Gly Met Asp Gly Leu His Val Ala Val Lys Ile Val Lys
180 185 190
Asn Val Gly Arg Tyr Arg Glu Ala Ala Arg Ser Glu Ile Gln Val Leu
195 200 205
Glu His Leu Asn Ser Thr Asp Pro Asn Ser Val Phe Arg Cys Val Gln
210 215 220
Met Leu Glu Trp Phe Asp His His Gly His Val Cys Ile Val Phe Glu
225 230 235 240
Leu Leu Gly Leu Ser Thr Tyr Asp Phe Ile Lys Glu Asn Ser Phe Leu
245 250 255
Pro Phe Gln Ile Asp His Ile Arg Gln Met Ala Tyr Gln Ile Cys Gln
260 265 270
Ser Ile Asn Phe Leu His His Asn Lys Leu Thr His Thr Asp Leu Lys
275 280 285
Pro Glu Asn Ile Leu Phe Val Lys Ser Asp Tyr Val Val Lys Tyr Asn
290 295 300
Ser Lys Met Lys Arg Asp Glu Arg Thr Leu Lys Asn Thr Asp Ile Lys
305 310 315 320
Val Val Asp Phe Gly Ser Ala Thr Tyr Asp Asp Glu His His Ser Thr
325 330 335
Leu Val Ser Thr Arg His Tyr Arg Ala Pro Glu Val Ile Leu Ala Leu
340 345 350

351/617

Gly Trp Ser Gln Pro Cys Asp Val Trp Ser Ile Gly Cys Ile Leu Ile
 355 360 365
 Glu Tyr Tyr Leu Gly Phe Thr Val Phe Gln Thr His Asp Ser Lys Glu
 370 375 380
 His Leu Ala Met Met Glu Arg Ile Leu Gly Pro Ile Pro Ala His Met
 385 390 395 400
 Ile Gln Lys Thr Arg Lys Arg Lys Tyr Phe His His Asn Gln Leu Asp
 405 410 415
 Trp Asp Glu His Ser Ser Ala Gly Arg Tyr Val Arg Arg Arg Cys Lys
 420 425 430
 Pro Leu Lys Glu Phe Met Leu Cys His Asp Glu Glu His Glu Lys Leu
 435 440 445
 Phe Asp Leu Val Arg Arg Met Leu Glu Tyr Asp Pro Ala Arg Arg Ile
 450 455 460
 Thr Leu Asp Glu Ala Leu Gln His Pro Phe Phe Asp Leu Leu Lys Arg
 465 470 475 480
 Lys

<210> 107

<211> 1792

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1443)

<400> 107

atg cgg cat tcc aaa aga act cac tgt cct gat tgg gat agc aga gaa

48

352/617

Met Arg His Ser Lys Arg Thr His Cys Pro Asp Trp Asp Ser Arg Glu
 1 5 10 15
 agc tgg gga cat gaa agc tat cgt gga agt cac aag cgg aag agg aga 96
 Ser Trp Gly His Glu Ser Tyr Arg Gly Ser His Lys Arg Lys Arg Arg
 20 25 30
 tct cat agt agc aca caa gag aac agg cat tgt aaa cca cat cac cag 144
 Ser His Ser Ser Thr Gln Glu Asn Arg His Cys Lys Pro His His Gln
 35 40 45
 ttt aaa gaa tct gat tgt cat tat tta gaa gca agg tcc ttg aat gag 192
 Phe Lys Glu Ser Asp Cys His Tyr Leu Glu Ala Arg Ser Leu Asn Glu
 50 55 60
 cga gat tat cgg gac cgg aga tac gtt gac gaa tac agg aat gac tac 240
 Arg Asp Tyr Arg Asp Arg Arg Tyr Val Asp Glu Tyr Arg Asn Asp Tyr
 65 70 75 80
 tgt gaa gga tat gtt cct aga cat tat cac aga gac att gaa agc ggg 288
 Cys Glu Gly Tyr Val Pro Arg His Tyr His Arg Asp Ile Glu Ser Gly
 85 90 95
 tat cga atc cac tgc agt aaa tct tca gtc cgc agc agg aga agc agt 336
 Tyr Arg Ile His Cys Ser Lys Ser Ser Val Arg Ser Arg Arg Ser Ser
 100 105 110
 cct aaa agg aag cgc aat aga cac tgt tca agt cat cag tca cgt tcg 384
 Pro Lys Arg Lys Arg Asn Arg His Cys Ser Ser His Gln Ser Arg Ser
 115 120 125
 aag agc cac cga agg aaa aga tcc agg agt ata gag gat gat gag gag 432
 Lys Ser His Arg Arg Lys Arg Ser Arg Ser Ile Glu Asp Asp Glu Glu
 130 135 140
 ggt cac ctg atc tgt caa agt gga gac gtt cta aga gca aga tat gaa 480

353/617

Gly His Leu Ile Cys Gln Ser Gly Asp Val Leu Arg Ala Arg Tyr Glu
 145 150 155 160
 atc gtg gac act ttg ggt gaa gga gcc ttt ggc aaa gtt gta gag tgc 528
 Ile Val Asp Thr Leu Gly Glu Gly Ala Phe Gly Lys Val Val Glu Cys
 165 170 175
 att gat cat ggc atg gat ggc atg cat gta gca gtg aaa atc gta aaa 576
 Ile Asp His Gly Met Asp Gly Met His Val Ala Val Lys Ile Val Lys
 180 185 190
 aat gta ggc cgt tac cgt gaa gca gct cgt tca gaa atc caa gta tta 624
 Asn Val Gly Arg Tyr Arg Glu Ala Ala Arg Ser Glu Ile Gln Val Leu
 195 200 205
 gag cac tta aat agt act gat ccc aat agt gtc ttc cga tgt gtc cag 672
 Glu His Leu Asn Ser Thr Asp Pro Asn Ser Val Phe Arg Cys Val Gln
 210 215 220
 atg cta gaa tgg ttt gat cat cat ggt cat gtt tgt att gtg ttt gaa 720
 Met Leu Glu Trp Phe Asp His His Gly His Val Cys Ile Val Phe Glu
 225 230 235 240
 cta ctg gga ctt agt act tac gat ttc att aaa gaa aac agc ttt ctg 768
 Leu Leu Gly Leu Ser Thr Tyr Asp Phe Ile Lys Glu Asn Ser Phe Leu
 245 250 255
 cca ttt caa att gac cac atc agg cag atg gcg tat cag atc tgc cag 816
 Pro Phe Gln Ile Asp His Ile Arg Gln Met Ala Tyr Gln Ile Cys Gln
 260 265 270
 tca ata aat ttt tta cat cat aat aaa tta acc cat aca gat ctg aag 864
 Ser Ile Asn Phe Leu His His Asn Lys Leu Thr His Thr Asp Leu Lys
 275 280 285
 cct gaa aat att ttg ttt gtg aag tct gac tat gta gtc aaa tat aat 912

Pro Glu Asn Ile Leu Phe Val Lys Ser Asp Tyr Val Val Lys Tyr Asn
 290 295 300
 tct aaa atg aaa cgt gat gaa cgc aca ctg aaa aac aca gat atc aaa 960
 Ser Lys Met Lys Arg Asp Glu Arg Thr Leu Lys Asn Thr Asp Ile Lys
 305 310 315 320
 gtt gtt gac ttt gga agt gca acg tat gat gat gaa cat cac agt act 1008
 Val Val Asp Phe Gly Ser Ala Thr Tyr Asp Asp Glu His His Ser Thr
 325 330 335
 ttg gtg tct acc cgg cac tac aga gct ccc gag gtc att ttg gct tta 1056
 Leu Val Ser Thr Arg His Tyr Arg Ala Pro Glu Val Ile Leu Ala Leu
 340 345 350
 ggt tgg tct cag cct tgt gat gtt tgg agc ata ggt tgc att ctt att 1104
 Gly Trp Ser Gln Pro Cys Asp Val Trp Ser Ile Gly Cys Ile Leu Ile
 355 360 365
 gaa tat tac ctt ggt ttc aca gtc ttt cag act cat gat agt aaa gag 1152
 Glu Tyr Tyr Leu Gly Phe Thr Val Phe Gln Thr His Asp Ser Lys Glu
 370 375 380
 cac ctg gca atg atg gaa cga ata tta gga ccc ata cca caa cac atg 1200
 His Leu Ala Met Met Glu Arg Ile Leu Gly Pro Ile Pro Gln His Met
 385 390 395 400
 att cag aaa aca aga aaa cgc aag tat ttt cac cat aac cag cta gat 1248
 Ile Gln Lys Thr Arg Lys Arg Lys Tyr Phe His His Asn Gln Leu Asp
 405 410 415
 tgg gat gaa cac agt tct gct ggt aga tat gtt agg aga cgc tgc aaa 1296
 Trp Asp Glu His Ser Ser Ala Gly Arg Tyr Val Arg Arg Arg Cys Lys
 420 425 430
 ccg ttg aag gaa ttt atg ctt tgt cat gat gaa gaa cat gag aaa ctg 1344

Pro Leu Lys Glu Phe Met Leu Cys His Asp Glu Glu His Glu Lys Leu

435

440

445

ttt gac ctg gtt cga aga atg tta gaa tat gat cca act caa aga att 1392

Phe Asp Leu Val Arg Arg Met Leu Glu Tyr Asp Pro Thr Gln Arg Ile

450

455

460

acc ttg gat gaa gca ttg cag cat cct ttc ttt gac tta tta aaa aag 1440

Thr Leu Asp Glu Ala Leu Gln His Pro Phe Phe Asp Leu Leu Lys Lys

465

470

475

480

aaa tgaaatggga atcagtgggc ttactatata cttctctaga agagattact 1493

Lys

taagactgtg tcagtcaact aaacattcta atatTTTTgt aaacattaaa ttatTTTTgta 1553

cagttaagng taaatattgt atgttttga tcaatagcat aattaacttg ttaagcaagt 1613

atggcttga taatgcatta gaaaaattaa aattaatttt tcttttggaa attaccattt 1673

ttaaaaacct ttgaaatata ctttgtgtcc agtgataaat gtgattgatac ttgccttttg 1733

tacatggagg tcacctctga agtgattttt ttgagtaaa aggaaatctt gactacttt 1792

<210> 108

<211> 481

<212> PRT

<213> Homo sapiens

<400> 108

Met Arg His Ser Lys Arg Thr His Cys Pro Asp Trp Asp Ser Arg Glu

1

5

10

15

Ser Trp Gly His Glu Ser Tyr Arg Gly Ser His Lys Arg Lys Arg Arg

20

25

30

Ser His Ser Ser Thr Gln Glu Asn Arg His Cys Lys Pro His His Gln

35

40

45

356/617

Phe Lys Glu Ser Asp Cys His Tyr Leu Glu Ala Arg Ser Leu Asn Glu
 50 55 60
 Arg Asp Tyr Arg Asp Arg Arg Tyr Val Asp Glu Tyr Arg Asn Asp Tyr
 65 70 75 80
 Cys Glu Gly Tyr Val Pro Arg His Tyr His Arg Asp Ile Glu Ser Gly
 85 90 95
 Tyr Arg Ile His Cys Ser Lys Ser Ser Val Arg Ser Arg Arg Ser Ser
 100 105 110
 Pro Lys Arg Lys Arg Asn Arg His Cys Ser Ser His Gln Ser Arg Ser
 115 120 125
 Lys Ser His Arg Arg Lys Arg Ser Arg Ser Ile Glu Asp Asp Glu Glu
 130 135 140
 Gly His Leu Ile Cys Gln Ser Gly Asp Val Leu Arg Ala Arg Tyr Glu
 145 150 155 160
 Ile Val Asp Thr Leu Gly Glu Gly Ala Phe Gly Lys Val Val Glu Cys
 165 170 175
 Ile Asp His Gly Met Asp Gly Met His Val Ala Val Lys Ile Val Lys
 180 185 190
 Asn Val Gly Arg Tyr Arg Glu Ala Ala Arg Ser Glu Ile Gln Val Leu
 195 200 205
 Glu His Leu Asn Ser Thr Asp Pro Asn Ser Val Phe Arg Cys Val Gln
 210 215 220
 Met Leu Glu Trp Phe Asp His His Gly His Val Cys Ile Val Phe Glu
 225 230 235 240
 Leu Leu Gly Leu Ser Thr Tyr Asp Phe Ile Lys Glu Asn Ser Phe Leu
 245 250 255
 Pro Phe Gln Ile Asp His Ile Arg Gln Met Ala Tyr Gln Ile Cys Gln

260 265 270
Ser Ile Asn Phe Leu His His Asn Lys Leu Thr His Thr Asp Leu Lys
275 280 285
Pro Glu Asn Ile Leu Phe Val Lys Ser Asp Tyr Val Val Lys Tyr Asn
290 295 300
Ser Lys Met Lys Arg Asp Glu Arg Thr Leu Lys Asn Thr Asp Ile Lys
305 310 315 320
Val Val Asp Phe Gly Ser Ala Thr Tyr Asp Asp Glu His His Ser Thr
325 330 335
Leu Val Ser Thr Arg His Tyr Arg Ala Pro Glu Val Ile Leu Ala Leu
340 345 350
Gly Trp Ser Gln Pro Cys Asp Val Trp Ser Ile Gly Cys Ile Leu Ile
355 360 365
Glu Tyr Tyr Leu Gly Phe Thr Val Phe Gln Thr His Asp Ser Lys Glu
370 375 380
His Leu Ala Met Met Glu Arg Ile Leu Gly Pro Ile Pro Gln His Met
385 390 395 400
Ile Gln Lys Thr Arg Lys Arg Lys Tyr Phe His His Asn Gln Leu Asp
405 410 415
Trp Asp Glu His Ser Ser Ala Gly Arg Tyr Val Arg Arg Arg Cys Lys
420 425 430
Pro Leu Lys Glu Phe Met Leu Cys His Asp Glu Glu His Glu Lys Leu
435 440 445
Phe Asp Leu Val Arg Arg Met Leu Glu Tyr Asp Pro Thr Gln Arg Ile
450 455 460
Thr Leu Asp Glu Ala Leu Gln His Pro Phe Phe Asp Leu Leu Lys Lys
465 470 475 480

358/617

Lys

<210> 109

<211> 1865

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (154).. (1512)

<400> 109

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atttttagat aatcattaaa gaccacagaa aatgtaacag atcctactct tcaaaataat   60
tgctattcag tattaaaacg cagtcagctg cgtgattccc gtgattgcgt tacaagcttt  120
gtctccttcg acttggagtc tttgtccagg acg atg aga cac tca aag aga act   174
                                Met Arg His Ser Lys Arg Thr
                                1             5
tac tgt cct gat tgg gat gac aag gat tgg gat tat gga aaa tgg agg   222
Tyr Cys Pro Asp Trp Asp Asp Lys Asp Trp Asp Tyr Gly Lys Trp Arg
    10             15             20
agc agc agc agt cat aaa aga agg aag aga tca cat agc agt gcc cag   270
Ser Ser Ser Ser His Lys Arg Arg Lys Arg Ser His Ser Ser Ala Gln
    25             30             35
gag aac aag cgc tgc aaa tac aat cac tct aaa atg tgt gat agc cat   318
Glu Asn Lys Arg Cys Lys Tyr Asn His Ser Lys Met Cys Asp Ser His
    40             45             50             55
tat ttg gaa agc agg tct ata aat gag aaa gat tat cat agt cga cgc   366
Tyr Leu Glu Ser Arg Ser Ile Asn Glu Lys Asp Tyr His Ser Arg Arg
    60             65             70

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359/617

tac att gat gag tac aga aat gac tac act caa gga tgt gaa cct gga	414
Tyr Ile Asp Glu Tyr Arg Asn Asp Tyr Thr Gln Gly Cys Glu Pro Gly	
75 80 85	
cat cgc caa aga gac cat gaa agc cgg tat cag aac cat agt agc aag	462
His Arg Gln Arg Asp His Glu Ser Arg Tyr Gln Asn His Ser Ser Lys	
90 95 100	
tct tct ggt aga agt gga aga agt agt tat aaa agc aaa cac agg att	510
Ser Ser Gly Arg Ser Gly Arg Ser Ser Tyr Lys Ser Lys His Arg Ile	
105 110 115	
cac cac agt act tca cat cgt cgg tca cat ggg gat gaa att gtt gat	558
His His Ser Thr Ser His Arg Arg Ser His Gly Asp Glu Ile Val Asp	
120 125 130 135	
act tta ggt gaa gga gct ttt gga aaa gtt gtg gag tgc atc gat cat	606
Thr Leu Gly Glu Gly Ala Phe Gly Lys Val Val Glu Cys Ile Asp His	
140 145 150	
aaa gcg gga ggt aga cat gta gca gta aaa ata gtt aaa aat gtg gat	654
Lys Ala Gly Gly Arg His Val Ala Val Lys Ile Val Lys Asn Val Asp	
155 160 165	
aga tac tgt gaa gct gct cgc tca gaa ata caa gtt ctg gaa cat ctg	702
Arg Tyr Cys Glu Ala Ala Arg Ser Glu Ile Gln Val Leu Glu His Leu	
170 175 180	
aat aca aca gac ccc aac agt act ttc cgc tgt gtc cag atg ttg gaa	750
Asn Thr Thr Asp Pro Asn Ser Thr Phe Arg Cys Val Gln Met Leu Glu	
185 190 195	
tgg ttt gag cat cat ggt cac att tgc att gtt ttt gaa cta ttg gga	798
Trp Phe Glu His His Gly His Ile Cys Ile Val Phe Glu Leu Leu Gly	
200 205 210 215	

ctt agt act tac gac ttc att aaa gaa aat ggt ttt cta cca ttt cga 846
 Leu Ser Thr Tyr Asp Phe Ile Lys Glu Asn Gly Phe Leu Pro Phe Arg
 220 225 230
 ctg gat cat atc aga aag atg gca tat cag ata tgc aag tct gtg aat 894
 Leu Asp His Ile Arg Lys Met Ala Tyr Gln Ile Cys Lys Ser Val Asn
 235 240 245
 ttt ttg cac agt aat aag ttg act cac aca gac tta aag cct gaa aac 942
 Phe Leu His Ser Asn Lys Leu Thr His Thr Asp Leu Lys Pro Glu Asn
 250 255 260
 atc tta ttt gtg cag tct gac tac aca gag gcg tat aat ccc aaa ata 990
 Ile Leu Phe Val Gln Ser Asp Tyr Thr Glu Ala Tyr Asn Pro Lys Ile
 265 270 275
 aaa cgt gat gaa cgc acc tta ata aat cca gat att aaa gtt gta gac 1038
 Lys Arg Asp Glu Arg Thr Leu Ile Asn Pro Asp Ile Lys Val Val Asp
 280 285 290 295
 ttt ggt agt gca aca tat gat gac gaa cat cac agt aca ttg gta tct 1086
 Phe Gly Ser Ala Thr Tyr Asp Asp Glu His His Ser Thr Leu Val Ser
 300 305 310
 aca aga cat tat aga gca cct gaa gtt att tta gcc cta ggg tgg tcc 1134
 Thr Arg His Tyr Arg Ala Pro Glu Val Ile Leu Ala Leu Gly Trp Ser
 315 320 325
 cag cct tgt gat gtt tgg agc ata ggt ggc att ctt aat gaa tat tac 1182
 Gln Pro Cys Asp Val Trp Ser Ile Gly Gly Ile Leu Asn Glu Tyr Tyr
 330 335 340
 ctt ggt ttc aca gtc ttc cag act cat gat agt aaa gag cac ctg gca 1230
 Leu Gly Phe Thr Val Phe Gln Thr His Asp Ser Lys Glu His Leu Ala
 345 350 355

361/617

atg atg gaa cga ata tta gga ccc ata cca caa cac atg att cag aaa 1278
 Met Met Glu Arg Ile Leu Gly Pro Ile Pro Gln His Met Ile Gln Lys
 360 365 370 375
 aca aga aaa cgc aag tat ttt cac cat aac cag cta gat tgg gat gaa 1326
 Thr Arg Lys Arg Lys Tyr Phe His His Asn Gln Leu Asp Trp Asp Glu
 380 385 390
 cac agt tct gct ggt aga tat gtt agg aga cgc tgc aaa ccg ttg aag 1374
 His Ser Ser Ala Gly Arg Tyr Val Arg Arg Arg Cys Lys Pro Leu Lys
 395 400 405
 gaa ttt atg ctt tgt cat gat gaa gaa cat gag aaa ctg ttt gac ctg 1422
 Glu Phe Met Leu Cys His Asp Glu Glu His Glu Lys Leu Phe Asp Leu
 410 415 420
 gtt cga aga atg tta gaa tat gat cca act caa aga att acc ttg gat 1470
 Val Arg Arg Met Leu Glu Tyr Asp Pro Thr Gln Arg Ile Thr Leu Asp
 425 430 435
 gaa gca ttg cag cat cct ttc ttt gac tta tta aaa aag aaa 1512
 Glu Ala Leu Gln His Pro Phe Phe Asp Leu Leu Lys Lys Lys
 440 445 450
 tgaatggga atcagtgggc ttactatata cttctctaga agagattact taagactgtg 1572
 tcagtcaact aaacattcta atatttttgt aaacattaaa ttattttgta cagttaagtg 1632
 taaatattgt atgttttgta tcaatagcat aattaacttg ttaagcaagt atggtcttga 1692
 taatgcatta gaaaaattaa aattaatitt tctttttgaa attaccattt ttaaatacct 1752
 ttgaaatata ctttgtgtcc agtgataaat gtgattgatc ttgccttttg tacatggagg 1812
 tcacctctga agtgatTTTT tttgagtaaa aggaaatctt gactacttta aaa 1865

<210> 110

<211> 453

<212> PRT

<213> Homo sapiens

<400> 110

Met Arg His Ser Lys Arg Thr Tyr Cys Pro Asp Trp Asp Asp Lys Asp
 1 5 10 15
 Trp Asp Tyr Gly Lys Trp Arg Ser Ser Ser Ser His Lys Arg Arg Lys
 20 25 30
 Arg Ser His Ser Ser Ala Gln Glu Asn Lys Arg Cys Lys Tyr Asn His
 35 40 45
 Ser Lys Met Cys Asp Ser His Tyr Leu Glu Ser Arg Ser Ile Asn Glu
 50 55 60
 Lys Asp Tyr His Ser Arg Arg Tyr Ile Asp Glu Tyr Arg Asn Asp Tyr
 65 70 75 80
 Thr Gln Gly Cys Glu Pro Gly His Arg Gln Arg Asp His Glu Ser Arg
 85 90 95
 Tyr Gln Asn His Ser Ser Lys Ser Ser Gly Arg Ser Gly Arg Ser Ser
 100 105 110
 Tyr Lys Ser Lys His Arg Ile His His Ser Thr Ser His Arg Arg Ser
 115 120 125
 His Gly Asp Glu Ile Val Asp Thr Leu Gly Glu Gly Ala Phe Gly Lys
 130 135 140
 Val Val Glu Cys Ile Asp His Lys Ala Gly Gly Arg His Val Ala Val
 145 150 155 160
 Lys Ile Val Lys Asn Val Asp Arg Tyr Cys Glu Ala Ala Arg Ser Glu
 165 170 175
 Ile Gln Val Leu Glu His Leu Asn Thr Thr Asp Pro Asn Ser Thr Phe
 180 185 190

363/617

Arg Cys Val Gln Met Leu Glu Trp Phe Glu His His Gly His Ile Cys
 195 200 205
 Ile Val Phe Glu Leu Leu Gly Leu Ser Thr Tyr Asp Phe Ile Lys Glu
 210 215 220
 Asn Gly Phe Leu Pro Phe Arg Leu Asp His Ile Arg Lys Met Ala Tyr
 225 230 235 240
 Gln Ile Cys Lys Ser Val Asn Phe Leu His Ser Asn Lys Leu Thr His
 245 250 255
 Thr Asp Leu Lys Pro Glu Asn Ile Leu Phe Val Gln Ser Asp Tyr Thr
 260 265 270
 Glu Ala Tyr Asn Pro Lys Ile Lys Arg Asp Glu Arg Thr Leu Ile Asn
 275 280 285
 Pro Asp Ile Lys Val Val Asp Phe Gly Ser Ala Thr Tyr Asp Asp Glu
 290 295 300
 His His Ser Thr Leu Val Ser Thr Arg His Tyr Arg Ala Pro Glu Val
 305 310 315 320
 Ile Leu Ala Leu Gly Trp Ser Gln Pro Cys Asp Val Trp Ser Ile Gly
 325 330 335
 Gly Ile Leu Asn Glu Tyr Tyr Leu Gly Phe Thr Val Phe Gln Thr His
 340 345 350
 Asp Ser Lys Glu His Leu Ala Met Met Glu Arg Ile Leu Gly Pro Ile
 355 360 365
 Pro Gln His Met Ile Gln Lys Thr Arg Lys Arg Lys Tyr Phe His His
 370 375 380
 Asn Gln Leu Asp Trp Asp Glu His Ser Ser Ala Gly Arg Tyr Val Arg
 385 390 395 400
 Arg Arg Cys Lys Pro Leu Lys Glu Phe Met Leu Cys His Asp Glu Glu

405 410 415
 His Glu Lys Leu Phe Asp Leu Val Arg Arg Met Leu Glu Tyr Asp Pro
 420 425 430
 Thr Gln Arg Ile Thr Leu Asp Glu Ala Leu Gln His Pro Phe Phe Asp
 435 440 445
 Leu Leu Lys Lys Lys
 450

<210> 111

<211> 1882

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (637).. (1317)

<400> 111

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 ttccagagct ccgcctggct gcccaccgc cgcgagccct cccgaagcct ggaggagtga 180
 gggccgccgg cgcgggctga ggagtcctga gacgggggac gcgaacggcg cggcgcccgg 240
 agcctccgcc gcttcctgct gcgggcgagc ggctcctcc ggctcctccc tcccttcgct 300
 gcggtcctt aggtccgga gcccgggggc ggctgtggc gcgaggcgcc ggctctggac 360
 cgcgtttctt cggaccttaa ggggaacatg cattcggtt ggacagtttg aaattcttag 420
 tttggggtcc ccgctcgctt gctttttcca ccccgcgat tttttttgag gattcccccc 480
 ctacactttt ttcatttttc tcccctcgag gctcttttgt gactctcccc aaccccaacc 540
 ctccgccttt atgttcgcc agacctccac ccgcttctga gtagtggggg agggtttcag 600
 cctccacgtt cccgccccac cggggccccg gcgaac atg ggg ggc aag cag agc 654

		Met Gly Gly Lys Gln Ser										
		1					5					
acg gcg gcc cgc tct cgg ggc ccc ttc ccg ggg gtc tct acg gat gac	702											
Thr Ala Ala Arg Ser Arg Gly Pro Phe Pro Gly Val Ser Thr Asp Asp												
		10			15			20				
agc gcc gtg ccg ccg ccg gga ggg gcg ccc cac ttt ggg cac tac cgg	750											
Ser Ala Val Pro Pro Pro Gly Gly Ala Pro His Phe Gly His Tyr Arg												
		25			30			35				
acg ggc gac ggg gcg atg ggg ctg cgc agc cgc tcg gtc agc tcg gtg	798											
Thr Gly Asp Gly Ala Met Gly Leu Arg Ser Arg Ser Val Ser Ser Val												
		40			45			50				
gcg ggc atg ggc atg gac ccc agc acg gcc gga ggg gtg ccc ttt agt	846											
Ala Gly Met Gly Met Asp Pro Ser Thr Ala Gly Gly Val Pro Phe Ser												
		55			60			65			70	
ctc tac acc ccc gcc tcc cgc ggg acc ggc gac tcc gag agg gcg ccg	894											
Leu Tyr Thr Pro Ala Ser Arg Gly Thr Gly Asp Ser Glu Arg Ala Pro												
		75			80			85				
ggc ggc gga ggg tcc acg tcg gac tcc acc tat gcc cac ggc aat ggt	942											
Gly Gly Gly Gly Ser Thr Ser Asp Ser Thr Tyr Ala His Gly Asn Gly												
		90			95			100				
tac caa gag acc ggc ggc ggt cac cat aga gac ggg atg ctg tac ctg	990											
Tyr Gln Glu Thr Gly Gly Gly His His Arg Asp Gly Met Leu Tyr Leu												
		105			110			115				
ggc tcc cga gcc tcg ctg gcg gat gct cta cct ctg cac atc gca ccc	1038											
Gly Ser Arg Ala Ser Leu Ala Asp Ala Leu Pro Leu His Ile Ala Pro												
		120			125			130				
agg tgg ttc agc tcg cac agt ggt ttc aag tgc ccc att tgt tcc aag	1086											

Arg Trp Phe Ser Ser His Ser Gly Phe Lys Cys Pro Ile Cys Ser Lys
 135 140 145 150
 tct gtg gct tcc gat gag atg gaa atg cac ttt ata atg tgt ctg agc 1134
 Ser Val Ala Ser Asp Glu Met Glu Met His Phe Ile Met Cys Leu Ser
 155 160 165
 aag cct cgc ctg tcc tac aat gat gat gtg ctg act aaa gat gcg ggt 1182
 Lys Pro Arg Leu Ser Tyr Asn Asp Asp Val Leu Thr Lys Asp Ala Gly
 170 175 180
 gag tgt gtg atc tgc ctg gag gag ctg ctt cag ggg gac acg ata gcc 1230
 Glu Cys Val Ile Cys Leu Glu Glu Leu Leu Gln Gly Asp Thr Ile Ala
 185 190 195
 .agg ctg cct tgc ctg tgc atc tat cac aaa agc tgc ata gac tca tgg 1278
 Arg Leu Pro Cys Leu Cys Ile Tyr His Lys Ser Cys Ile Asp Ser Trp
 200 205 210
 ttt gaa gtg aac aga tct tgt cca gag cac cct gct gac tgacctgct 1327
 Phe Glu Val Asn Arg Ser Cys Pro Glu His Pro Ala Asp
 215 220 225
 gggcctgctt gccgactcct ctcaaaggtt tattttattt attccaagcg agggagagtg 1387
 aggcagaggg actggatccc agctccagag tgcaggtcca gaatgccgcc gccggcatga 1447
 tgtttggctt ccaatgggcc tgcctggact gaaccagatg cccagccaa ccagcctggt 1507
 ctgaggggga cacaagctgc tgccaccgtg cgatggagcg gcaactctca gcaagatgaa 1567
 gcgggactga cttcttccga cccacacagg gacagccagc cctgtttcct gggaggaggc 1627
 tcctcggaca ctggacagag ctgagcttgg gacaccagag agaacagggc acccttctgc 1687
 actgacttcc agaaaatggt cctccctgag gacaccaggt ggatgagaga agaatgaatt 1747
 gacctctatc cttcccctca cctcgcacc aggagggaaa gggcattttc tttttcacct 1807
 ttgaaaggcg ttgtgggtct gtcttttaaaa agtgtttaca aacaacaaaa aattctataa 1867
 aaaagtcttg tgtcg 1882

<210> 112

<211> 227

<212> PRT

<213> Mus musculus

<400> 112

Met Gly Gly Lys Gln Ser Thr Ala Ala Arg Ser Arg Gly Pro Phe Pro
 1 5 10 15
 Gly Val Ser Thr Asp Asp Ser Ala Val Pro Pro Pro Gly Gly Ala Pro
 20 25 30
 His Phe Gly His Tyr Arg Thr Gly Asp Gly Ala Met Gly Leu Arg Ser
 35 40 45
 Arg Ser Val Ser Ser Val Ala Gly Met Gly Met Asp Pro Ser Thr Ala
 50 55 60
 Gly Gly Val Pro Phe Ser Leu Tyr Thr Pro Ala Ser Arg Gly Thr Gly
 65 70 75 80
 Asp Ser Glu Arg Ala Pro Gly Gly Gly Gly Ser Thr Ser Asp Ser Thr
 85 90 95
 Tyr Ala His Gly Asn Gly Tyr Gln Glu Thr Gly Gly Gly His His Arg
 100 105 110
 Asp Gly Met Leu Tyr Leu Gly Ser Arg Ala Ser Leu Ala Asp Ala Leu
 115 120 125
 Pro Leu His Ile Ala Pro Arg Trp Phe Ser Ser His Ser Gly Phe Lys
 130 135 140
 Cys Pro Ile Cys Ser Lys Ser Val Ala Ser Asp Glu Met Glu Met His
 145 150 155 160
 Phe Ile Met Cys Leu Ser Lys Pro Arg Leu Ser Tyr Asn Asp Asp Val

165 170 175
 Leu Thr Lys Asp Ala Gly Glu Cys Val Ile Cys Leu Glu Glu Leu Leu
 180 185 190
 Gln Gly Asp Thr Ile Ala Arg Leu Pro Cys Leu Cys Ile Tyr His Lys
 195 200 205
 Ser Cys Ile Asp Ser Trp Phe Glu Val Asn Arg Ser Cys Pro Glu His
 210 215 220
 Pro Ala Asp
 225

<210> 113

<211> 1882

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (637)..(1317)

<400> 113

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 cggctggctg gcggggccgg cggcggctgg agccggagcg cgacgccacg cgaccgcggc 120
 ttccagagct ccgcctggct gccccaccgc cgcgagccct cccgaagcct ggaggagtga 180
 gggccgccgg cgcgggctga ggagtcctga gacggggggac gcgaacggcg cggcgccccg 240
 agcctcggcc gcttctgct gcgggcgagc ggctcctcc ggctcctccc tcccttcgct 300
 gcggctcctt aggtccgga gcccgggggc ggctgtggc gcgaggcgcc ggctctggac 360
 cgcgttctt cggaccttaa ggggaacatg cattcgctt ggacagtttg aaattcttag 420
 tttgggtcc ccgtcgtt gctttttcca ccccgcgat ttttttgag gattcccccc 480
 ctcacctttt ttcatTTTTt tccctcgag gctctttgt gactctccc aacccaacc 540


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ctccgccttt atgttcgccc agacctccac ccgcttctga gtagtggggg agggtttcag 600
cctccacgtt cccgccccac cggggccccg gcgaac atg ggg ggc aag cag agc 654
Met Gly Gly Lys Gln Ser
1 5
acg gcg gcc cgc tct cgg ggc ccc ttc ccg ggg gtc tct acg gat gac 702
Thr Ala Ala Arg Ser Arg Gly Pro Phe Pro Gly Val Ser Thr Asp Asp
10 15 20
agc gcc gtg ccg ccg ccg gga ggg gcg ccc cac ttt ggg cac tac cgg 750
Ser Ala Val Pro Pro Pro Gly Gly Ala Pro His Phe Gly His Tyr Arg
25 30 35
acg ggc ggc ggg gcg atg ggg ctg cgc agc cgc tcg gtc agc tcg gtg 798
Thr Gly Gly Gly Ala Met Gly Leu Arg Ser Arg Ser Val Ser Ser Val
40 45 50
gcg ggc atg ggc atg gac ccc agc acg gcc gga ggg gtg ccc ttt agt 846
Ala Gly Met Gly Met Asp Pro Ser Thr Ala Gly Gly Val Pro Phe Ser
55 60 65 70
ctc tac acc ccc gcc tcc cgc ggg acc ggc gac tcc gag agg gcg ccg 894
Leu Tyr Thr Pro Ala Ser Arg Gly Thr Gly Asp Ser Glu Arg Ala Pro
75 80 85
ggc ggc gga ggg tcc acg tcg gac tcc acc tat gcc cac ggc aat ggt 942
Gly Gly Gly Gly Ser Thr Ser Asp Ser Thr Tyr Ala His Gly Asn Gly
90 95 100
tac caa gag acc ggc ggc ggt cac cat aga gac ggg atg ctg tac ctg 990
Tyr Gln Glu Thr Gly Gly Gly His His Arg Asp Gly Met Leu Tyr Leu
105 110 115
ggc tcc cga gcc tcg ctg gcg gat gct cta cct ctg cac atc gca ccc 1038
Gly Ser Arg Ala Ser Leu Ala Asp Ala Leu Pro Leu His Ile Ala Pro

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120	125	130	
agg tgg ttc agc tcg cac agt ggt ttc aag tgc ccc att tgt tcc aag			1086
Arg Trp Phe Ser Ser His Ser Gly Phe Lys Cys Pro Ile Cys Ser Lys			
135	140	145	150
tct gtg gct tcc gat gag atg gaa atg cac ttt ata atg tgt ctg agc			1134
Ser Val Ala Ser Asp Glu Met Glu Met His Phe Ile Met Cys Leu Ser			
155	160	165	
aag cct cgc ctg tcc tac aat gat gat gtg ctg act aaa gat gcg ggt			1182
Lys Pro Arg Leu Ser Tyr Asn Asp Asp Val Leu Thr Lys Asp Ala Gly			
170	175	180	
gag tgt gtg atc tgc ctg gag gag ctg ctt cag ggg gac acg ata gcc			1230
Glu Cys Val Ile Cys Leu Glu Glu Leu Leu Gln Gly Asp Thr Ile Ala			
185	190	195	
agg ctg cct tgc ctg tgc atc tat cac aaa agc tgc ata gac tca tgg			1278
Arg Leu Pro Cys Leu Cys Ile Tyr His Lys Ser Cys Ile Asp Ser Trp			
200	205	210	
ttt gaa gtg aac aga tct tgt cca gag cac cct gct gac tgaccctgct			1327
Phe Glu Val Asn Arg Ser Cys Pro Glu His Pro Ala Asp			
215	220	225	
gggcctgctt gccgactcct ctcaaagggtt tatittatitt attccaagcg agggagagtg			1387
aggcagaggg actggatccc agctccagag tgcaggtcca gaatgccgcc gccggcatga			1447
tgtttgctt ccaatgggcc tgccctggact gaaccagatg cccagccaa ccagcctggt			1507
ctcaggggga cacaagctgc tgccaccgtg cgatggagcg gcaactctca gcaagatgaa			1567
gcgggactga cttcttccga cccacacagg gacagccagc cctgttcct gggaggaggc			1627
tcctcgaca ctggacagag ctgagcttgg gacaccagag agaacagggc acccttctgc			1687
actgacttcc agaaaatggt cctccctgag gacacccagt ggatgagaga agaatgaatt			1747
gacctctatc cttccctca cctcgaccc aggagggaaa gggcattttc tttttcacct			1807

ttgaaaggcg ttgtgggtct gcttttaaaa agtgtttaca aacaacaaaa aattctataa 1867
 aaaagtcttg tgtcg 1882

<210> 114

<211> 227

<212> PRT

<213> Mus musculus

<400> 114

Met Gly Gly Lys Gln Ser Thr Ala Ala Arg Ser Arg Gly Pro Phe Pro
 1 5 10 15
 Gly Val Ser Thr Asp Asp Ser Ala Val Pro Pro Pro Gly Gly Ala Pro
 20 25 30
 His Phe Gly His Tyr Arg Thr Gly Gly Gly Ala Met Gly Leu Arg Ser
 35 40 45
 Arg Ser Val Ser Ser Val Ala Gly Met Gly Met Asp Pro Ser Thr Ala
 50 55 60
 Gly Gly Val Pro Phe Ser Leu Tyr Thr Pro Ala Ser Arg Gly Thr Gly
 65 70 75 80
 Asp Ser Glu Arg Ala Pro Gly Gly Gly Gly Ser Thr Ser Asp Ser Thr
 85 90 95
 Tyr Ala His Gly Asn Gly Tyr Gln Glu Thr Gly Gly Gly His His Arg
 100 105 110
 Asp Gly Met Leu Tyr Leu Gly Ser Arg Ala Ser Leu Ala Asp Ala Leu
 115 120 125
 Pro Leu His Ile Ala Pro Arg Trp Phe Ser Ser His Ser Gly Phe Lys
 130 135 140
 Cys Pro Ile Cys Ser Lys Ser Val Ala Ser Asp Glu Met Glu Met His

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145 150 155 160
 Phe Ile Met Cys Leu Ser Lys Pro Arg Leu Ser Tyr Asn Asp Asp Val
 165 170 175
 Leu Thr Lys Asp Ala Gly Glu Cys Val Ile Cys Leu Glu Glu Leu Leu
 180 185 190
 Gln Gly Asp Thr Ile Ala Arg Leu Pro Cys Leu Cys Ile Tyr His Lys
 195 200 205
 Ser Cys Ile Asp Ser Trp Phe Glu Val Asn Arg Ser Cys Pro Glu His
 210 215 220
 Pro Ala Asp
 225

<210> 115

<211> 1225

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (328).. (1008)

<400> 115

ccctgcggct cccccggcct tcggagcccg ggggcggcct gtggcgcgcg gagcccgcg 60
 cggactgcgc ctctttggac cttgagggga aacatgcgtt tgccttgat cgtttgaaat 120
 tctgagtttg ggateccccgc ccgcccgcct gcctcttcgc ccccgcggtt ttttctttt 180
 tttccttttg ctttttttcc ttttctccct ccgggtctcc tttttgactc cctccccctt 240
 tatgctgcc cagccctccc cctgctgctg agaagtggg gaggtctcg gcctccaggt 300
 tcccgcacca ccggggcccg ggcgagc atg ggg ggc aag cag agc acg gcg gcc 354

Met Gly Gly Lys Gln Ser Thr Ala Ala

373/617

	1	5	
cgc tcc cgg ggc ccc ttc ccg ggg gtc tcc acc gat gac agc gcc gtg			402
Arg Ser Arg Gly Pro Phe Pro Gly Val Ser Thr Asp Asp Ser Ala Val			
10	15	20	25
ccg ccg ccg gga ggg gcg ccc cat ttc ggg cac tac cgg acg ggc ggc			450
Pro Pro Pro Gly Gly Ala Pro His Phe Gly His Tyr Arg Thr Gly Gly			
	30	35	40
ggg gcc atg ggg ctg cgc agc cgc tcg gtc agc tcg gtg gca ggc atg			498
Gly Ala Met Gly Leu Arg Ser Arg Ser Val Ser Ser Val Ala Gly Met			
	45	50	55
ggc atg gac ccc agc acg gcc ggg ggg gtg ccc ttt ggc ctc tac acc			546
Gly Met Asp Pro Ser Thr Ala Gly Gly Val Pro Phe Gly Leu Tyr Thr			
	60	65	70
ccc gcc tcc cgg ggc acc ggc gac tcc gag agg gcg ccc ggc ggc gga			594
Pro Ala Ser Arg Gly Thr Gly Asp Ser Glu Arg Ala Pro Gly Gly Gly			
	75	80	85
ggg tct gcg tcc gac tcc acc tat gcc cat ggc aat ggt tac cag gag			642
Gly Ser Ala Ser Asp Ser Thr Tyr Ala His Gly Asn Gly Tyr Gln Glu			
90	95	100	105
acg ggc ggc ggt cac cat aga gac ggg atg ctg tac ctg ggc tcc cga			690
Thr Gly Gly Gly His His Arg Asp Gly Met Leu Tyr Leu Gly Ser Arg			
	110	115	120
gcc tcg ctg gcg gat gct cta cct ctg cac atc gca ccc agg tgg ttc			738
Ala Ser Leu Ala Asp Ala Leu Pro Leu His Ile Ala Pro Arg Trp Phe			
	125	130	135
agc tcg cat agt ggt ttc aag tgc ccc att tgc tcc aag tct gtg gct			786
Ser Ser His Ser Gly Phe Lys Cys Pro Ile Cys Ser Lys Ser Val Ala			

374/617

140 145 150
 tct gac gag atg gaa atg cac ttt ata atg tgt ttg agc aaa cct cgc 834
 Ser Asp Glu Met Glu Met His Phe Ile Met Cys Leu Ser Lys Pro Arg
 155 160 165
 ctc tcc tac aac gat gat gtg ctg act aaa gac gcg ggt gag tgt gtg 882
 Leu Ser Tyr Asn Asp Asp Val Leu Thr Lys Asp Ala Gly Glu Cys Val
 170 175 180 185
 atc tgc ctg gag gag ctg ctg cag ggg gac acg ata gcc agg ctg ccc 930
 Ile Cys Leu Glu Glu Leu Leu Gln Gly Asp Thr Ile Ala Arg Leu Pro
 190 195 200
 tgc ctg tgc atc tat cac aaa agc tgc ata gac tcg tgg ttt gaa gtg 978
 Cys Leu Cys Ile Tyr His Lys Ser Cys Ile Asp Ser Trp Phe Glu Val
 205 210 215
 aac aga tct tgt ccg gaa cac cct gcg gac tgacctgcgg gcttgcttgc 1028
 Asn Arg Ser Cys Pro Glu His Pro Ala Asp
 220 225
 tgactcctct caaagatcat gggtctccct tcctccctga ggacacccaaa ttggatgaga 1088
 gcaagtttga gagaagaatg aatcaactgc tatccttccc ctcacccctc agcccaggag 1148
 ggaaagggca ttttcttttt catctttgaa aggcattgtg ggtctgtctt taaagtgttt 1208
 acaaaaaaaaa attatat 1225

<210> 116
 <211> 227
 <212> PRT
 <213> Homo sapiens
 <400> 116

Met Gly Gly Lys Gln Ser Thr Ala Ala Arg Ser Arg Gly Pro Phe Pro

375/617

1 5 10 15
Gly Val Ser Thr Asp Asp Ser Ala Val Pro Pro Pro Gly Gly Ala Pro
20 25 30
His Phe Gly His Tyr Arg Thr Gly Gly Gly Ala Met Gly Leu Arg Ser
35 40 45
Arg Ser Val Ser Ser Val Ala Gly Met Gly Met Asp Pro Ser Thr Ala
50 55 60
Gly Gly Val Pro Phe Gly Leu Tyr Thr Pro Ala Ser Arg Gly Thr Gly
65 70 75 80
Asp Ser Glu Arg Ala Pro Gly Gly Gly Gly Ser Ala Ser Asp Ser Thr
85 90 95
Tyr Ala His Gly Asn Gly Tyr Gln Glu Thr Gly Gly Gly His His Arg
100 105 110
Asp Gly Met Leu Tyr Leu Gly Ser Arg Ala Ser Leu Ala Asp Ala Leu
115 120 125
Pro Leu His Ile Ala Pro Arg Trp Phe Ser Ser His Ser Gly Phe Lys
130 135 140
Cys Pro Ile Cys Ser Lys Ser Val Ala Ser Asp Glu Met Glu Met His
145 150 155 160
Phe Ile Met Cys Leu Ser Lys Pro Arg Leu Ser Tyr Asn Asp Asp Val
165 170 175
Leu Thr Lys Asp Ala Gly Glu Cys Val Ile Cys Leu Glu Glu Leu Leu
180 185 190
Gln Gly Asp Thr Ile Ala Arg Leu Pro Cys Leu Cys Ile Tyr His Lys
195 200 205
Ser Cys Ile Asp Ser Trp Phe Glu Val Asn Arg Ser Cys Pro Glu His
210 215 220

376/617

Pro Ala Asp

225

<210> 117

<211> 448

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (20).. (445)

<400> 117

agcgcgcccc aggggaaag atg gca gca ccg gcg aag ggc atg tgg tgc tcc 52

Met Ala Ala Pro Ala Lys Gly Met Trp Cys Ser

1

5

10

ctg gga tca ttg ctg cgg gtg gtc cag act cgg gac ctc aac gct cgg 100

Leu Gly Ser Leu Leu Arg Val Val Gln Thr Arg Asp Leu Asn Ala Arg

15

20

25

cgc tgg gtc cgg gcg ctg cgg cgt agc ccg gtg aga gtg ttg tct ccc 148

Arg Trp Val Arg Ala Leu Arg Arg Ser Pro Val Arg Val Leu Ser Pro

30

35

40

tcg gga cag gtg gag gaa cgg aag cgc gct cct gac cag cag cct cgc 196

Ser Gly Gln Val Glu Glu Arg Lys Arg Ala Pro Asp Gln Gln Pro Arg

45

50

55

aag gca gct gag gat aaa ggt gga aga ctt gag cag gga cag gag tta 244

Lys Ala Ala Glu Asp Lys Gly Gly Arg Leu Glu Gln Gly Gln Glu Leu

60

65

70

75

cca ctg aag gag cac agg aat cct cag tgg gag ggg aag ggc acc tcc 292

377/617

Pro Leu Lys Glu His Arg Asn Pro Gln Trp Glu Gly Lys Gly Thr Ser
80 85 90
agc ccc tcc tct gct agg agg ctg gcc aag gtg aca aca cag gag cca 340
Ser Pro Ser Ser Ala Arg Arg Leu Ala Lys Val Thr Thr Gln Glu Pro
95 100 105
ggg ggt agg cac tgc cac cat tgt gtg gta ctt aga aaa aaa aga gtt 388
Gly Gly Arg His Cys His His Cys Val Val Leu Arg Lys Lys Arg Val
110 115 120
tct att agt gtc tgc tgt tcc tta tta aac aac aaa ggt caa aat tct 436
Ser Ile Ser Val Cys Cys Ser Leu Leu Asn Asn Lys Gly Gln Asn Ser
125 130 135
ttt tca ttt taa 448
Phe Ser Phe
140

<210> 118

<211> 142

<212> PRT

<213> Mus musculus

<400> 118

Met Ala Ala Pro Ala Lys Gly Met Trp Cys Ser Leu Gly Ser Leu Leu
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Arg Val Val Gln Thr Arg Asp Leu Asn Ala Arg Arg Trp Val Arg Ala
20 25 30
Leu Arg Arg Ser Pro Val Arg Val Leu Ser Pro Ser Gly Gln Val Glu
35 40 45
Glu Arg Lys Arg Ala Pro Asp Gln Gln Pro Arg Lys Ala Ala Glu Asp

378/617

50 55 60
 Lys Gly Gly Arg Leu Glu Gln Gly Gln Glu Leu Pro Leu Lys Glu His
 65 70 75 80
 Arg Asn Pro Gln Trp Glu Gly Lys Gly Thr Ser Ser Pro Ser Ser Ala
 85 90 95
 Arg Arg Leu Ala Lys Val Thr Thr Gln Glu Pro Gly Gly Arg His Cys
 100 105 110
 His His Cys Val Val Leu Arg Lys Lys Arg Val Ser Ile Ser Val Cys
 115 120 125
 Cys Ser Leu Leu Asn Asn Lys Gly Gln Asn Ser Phe Ser Phe
 130 135 140

<210> 119
 <211> 1454
 <212> DNA
 <213> Mus musculus
 <220>
 <221> CDS
 <222> (4)..(1257)
 <400> 119

aag atg gca gcg ccg gcg aag ggc atg tgg tgc tcc ctg gga tca ttg 48
 Met Ala Ala Pro Ala Lys Gly Met Trp Cys Ser Leu Gly Ser Leu
 1 5 10 15
 ctg cgg gtg gtc cag act cgg gac ctc aac gct cgg cgc tgg gtc cgg 96
 Leu Arg Val Val Gln Thr Arg Asp Leu Asn Ala Arg Arg Trp Val Arg
 20 25 30
 gcg ctg cgg cgt agc ccg gtg aga gtg ttg tct ccc tcg gga cag gtg 144

Ala Leu Arg Arg Ser Pro Val Arg Val Leu Ser Pro Ser Gly Gln Val
35 40 45
gag gaa cgg aag cgc gct cct gac cag cag cct cgc aag gcg gtc cct 192
Glu Glu Arg Lys Arg Ala Pro Asp Gln Gln Pro Arg Lys Ala Val Pro
50 55 60
aag gcc agt tcc cag gga cag cga cag aaa cag cct ctt gag aca tcc 240
Lys Ala Ser Ser Gln Gly Gln Arg Gln Lys Gln Pro Leu Glu Thr Ser
65 70 75
cca tcc cag acc cct cac acc tgg gaa gag gca ggg ctt cgc tac gat 288
Pro Ser Gln Thr Pro His Thr Trp Glu Glu Ala Gly Leu Arg Tyr Asp
80 85 90 95
aag gcc ttt ccc ggg gac agg agg cta agc agt gtg atg aca ata gtt 336
Lys Ala Phe Pro Gly Asp Arg Arg Leu Ser Ser Val Met Thr Ile Val
100 105 110
aag tcc agg cct ttt cgg gaa aag caa ggg aag atc cta ctg gaa ggt 384
Lys Ser Arg Pro Phe Arg Glu Lys Gln Gly Lys Ile Leu Leu Glu Gly
115 120 125
cgc agg ctg att gca gat gct ctc aag gct gga gct gtg ccc aaa gcg 432
Arg Arg Leu Ile Ala Asp Ala Leu Lys Ala Gly Ala Val Pro Lys Ala
130 135 140
ttc ttt ttt agc cgt ctg gag tac gtc aag gag ttg ccg gta gac aag 480
Phe Phe Phe Ser Arg Leu Glu Tyr Val Lys Glu Leu Pro Val Asp Lys
145 150 155
ctg aaa gac gtc agc ctc att aag gtg aaa ttt gag gac atc aag gat 528
Leu Lys Asp Val Ser Leu Ile Lys Val Lys Phe Glu Asp Ile Lys Asp
160 165 170 175
tgg tca gac cta gta acg cca caa gga ata atg ggg att ttt gcc aaa 576

Trp Ser Asp Leu Val Thr Pro Gln Gly Ile Met Gly Ile Phe Ala Lys
 180 185 190
 cct gac cct gtt aag atg aca tat cca gag act ccg ctt cac cat aca 624
 Pro Asp Pro Val Lys Met Thr Tyr Pro Glu Thr Pro Leu His His Thr
 195 200 205
 ctg ccc cta gtg ttg att tgt gac aat ctc cgt gac cct ggg aac ctg 672
 Leu Pro Leu Val Leu Ile Cys Asp Asn Leu Arg Asp Pro Gly Asn Leu
 210 215 220
 ggg aca atc ctg aga tct gca gct gga gca ggc tgc agt aaa gtc tta 720
 Gly Thr Ile Leu Arg Ser Ala Ala Gly Ala Gly Cys Ser Lys Val Leu
 225 230 235
 ctc acc aaa ggc tgt gtg gat gcc tgg gag cct aaa gtg ctc cgg gca 768
 Leu Thr Lys Gly Cys Val Asp Ala Trp Glu Pro Lys Val Leu Arg Ala
 240 245 250 255
 ggc atg ggg gca cat ttc cag gta ccc att gtg aac aat gtg gaa tgg 816
 Gly Met Gly Ala His Phe Gln Val Pro Ile Val Asn Asn Val Glu Trp
 260 265 270
 gaa aca gtg ccc aat cac ttg cct cct gac act cga gtc tat gtg gca 864
 Glu Thr Val Pro Asn His Leu Pro Pro Asp Thr Arg Val Tyr Val Ala
 275 280 285
 gac aac tgt ggt cac tat gcc cag gtt cag atg tct gat aaa acc ggt 912
 Asp Asn Cys Gly His Tyr Ala Gln Val Gln Met Ser Asp Lys Thr Gly
 290 295 300
 gac cgt gac tgg gca tgt gat cgc cga ttc tta aag ttt cac aag tat 960
 Asp Arg Asp Trp Ala Cys Asp Arg Arg Phe Leu Lys Phe His Lys Tyr
 305 310 315
 gaa gag gac cta gac act aaa acc aga aag gac tgg ctg ccc aaa ctt 1008

381/617

Glu Glu Asp Leu Asp Thr Lys Thr Arg Lys Asp Trp Leu Pro Lys Leu
 320 325 330 335
 gag gtc cag agt tat gat ttg gac tgg aca gga gca cca gca gct gtg 1056
 Glu Val Gln Ser Tyr Asp Leu Asp Trp Thr Gly Ala Pro Ala Ala Val
 340 345 350
 gtg ata ggt ggg gag acg cat gga gtg agc ctg gaa tcc ctg caa ctg 1104
 Val Ile Gly Gly Glu Thr His Gly Val Ser Leu Glu Ser Leu Gln Leu
 355 360 365
 gcc gag agt acc ggt ggc aag aga ctg ctg atc ccc gtt gta cct ggt 1152
 Ala Glu Ser Thr Gly Gly Lys Arg Leu Leu Ile Pro Val Val Pro Gly
 370 375 380
 gtg gac agt ctg aac tca gcc atg gct gcg agc atc ctg ctc ttt gaa 1200
 Val Asp Ser Leu Asn Ser Ala Met Ala Ala Ser Ile Leu Leu Phe Glu
 385 390 395
 ggg aaa agg cag ctg agg ata aag gtg gaa gac ttg agc agg gac agg 1248
 Gly Lys Arg Gln Leu Arg Ile Lys Val Glu Asp Leu Ser Arg Asp Arg
 400 405 410 415
 agt tac cac tgaaggagca caggaatcct cagtgggagg ggaagggcac 1297
 Ser Tyr His
 ctccagcccc tctctgcta ggaggctggc caaggtgaca acacaggagc cagggggtag 1357
 gcaactgccac cattgtgtgg tacttaaaaa aaaagagttt ctattagtgt ctgctgttcc 1417
 ttattaaaca acaaaggtca aaattctttt tcatttt 1454

<210> 120

<211> 418

<212> PRT

<213> Mus musculus

<400> 120

Met Ala Ala Pro Ala Lys Gly Met Trp Cys Ser Leu Gly Ser Leu Leu
 1 5 10 15
 Arg Val Val Gln Thr Arg Asp Leu Asn Ala Arg Arg Trp Val Arg Ala
 20 25 30
 Leu Arg Arg Ser Pro Val Arg Val Leu Ser Pro Ser Gly Gln Val Glu
 35 40 45
 Glu Arg Lys Arg Ala Pro Asp Gln Gln Pro Arg Lys Ala Val Pro Lys
 50 55 60
 Ala Ser Ser Gln Gly Gln Arg Gln Lys Gln Pro Leu Glu Thr Ser Pro
 65 70 75 80
 Ser Gln Thr Pro His Thr Trp Glu Glu Ala Gly Leu Arg Tyr Asp Lys
 85 90 95
 Ala Phe Pro Gly Asp Arg Arg Leu Ser Ser Val Met Thr Ile Val Lys
 100 105 110
 Ser Arg Pro Phe Arg Glu Lys Gln Gly Lys Ile Leu Leu Glu Gly Arg
 115 120 125
 Arg Leu Ile Ala Asp Ala Leu Lys Ala Gly Ala Val Pro Lys Ala Phe
 130 135 140
 Phe Phe Ser Arg Leu Glu Tyr Val Lys Glu Leu Pro Val Asp Lys Leu
 145 150 155 160
 Lys Asp Val Ser Leu Ile Lys Val Lys Phe Glu Asp Ile Lys Asp Trp
 165 170 175
 Ser Asp Leu Val Thr Pro Gln Gly Ile Met Gly Ile Phe Ala Lys Pro
 180 185 190
 Asp Pro Val Lys Met Thr Tyr Pro Glu Thr Pro Leu His His Thr Leu
 195 200 205

383/617

Pro Leu Val Leu Ile Cys Asp Asn Leu Arg Asp Pro Gly Asn Leu Gly
210 215 220
Thr Ile Leu Arg Ser Ala Ala Gly Ala Gly Cys Ser Lys Val Leu Leu
225 230 235 240
Thr Lys Gly Cys Val Asp Ala Trp Glu Pro Lys Val Leu Arg Ala Gly
245 250 255
Met Gly Ala His Phe Gln Val Pro Ile Val Asn Asn Val Glu Trp Glu
260 265 270
Thr Val Pro Asn His Leu Pro Pro Asp Thr Arg Val Tyr Val Ala Asp
275 280 285
Asn Cys Gly His Tyr Ala Gln Val Gln Met Ser Asp Lys Thr Gly Asp
290 295 300
Arg Asp Trp Ala Cys Asp Arg Arg Phe Leu Lys Phe His Lys Tyr Glu
305 310 315 320
Glu Asp Leu Asp Thr Lys Thr Arg Lys Asp Trp Leu Pro Lys Leu Glu
325 330 335
Val Gln Ser Tyr Asp Leu Asp Trp Thr Gly Ala Pro Ala Ala Val Val
340 345 350
Ile Gly Gly Glu Thr His Gly Val Ser Leu Glu Ser Leu Gln Leu Ala
355 360 365
Glu Ser Thr Gly Gly Lys Arg Leu Leu Ile Pro Val Val Pro Gly Val
370 375 380
Asp Ser Leu Asn Ser Ala Met Ala Ala Ser Ile Leu Leu Phe Glu Gly
385 390 395 400
Lys Arg Gln Leu Arg Ile Lys Val Glu Asp Leu Ser Arg Asp Arg Ser
405 410 415
Tyr His

<210> 121

<211> 1800

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (107).. (1366)

<400> 121

gccgtcacgc gcaccgtaca gcccagtcca cgaaggcgccg caccggccgt gacgtcacta 60
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Met Ala Ala

1

ctg gtg aga ccc gcg agg ttt gtc gtg cga ccg ttg ctg cag gtg gtc 163
 Leu Val Arg Pro Ala Arg Phe Val Val Arg Pro Leu Leu Gln Val Val

5

10

15

cag gct tgg gac ctt gac gcg agg cgc tgg gtc cgg gcg ctg cgg cgg 211
 Gln Ala Trp Asp Leu Asp Ala Arg Arg Trp Val Arg Ala Leu Arg Arg

20

25

30

35

agc cca gtg aaa gtg gtg ttt cct tcc gga gag gtg gtg gaa cag aag 259
 Ser Pro Val Lys Val Val Phe Pro Ser Gly Glu Val Val Glu Gln Lys

40

45

50

cgc gct cct ggg aag cag ccc cgc aag gca cca tct gag gcc agt gcc 307
 Arg Ala Pro Gly Lys Gln Pro Arg Lys Ala Pro Ser Glu Ala Ser Ala

55

60

65

cag gag caa cga gag aaa caa ccg ctc gag gag tcc gca tcc cgc gct 355
 Gln Glu Gln Arg Glu Lys Gln Pro Leu Glu Glu Ser Ala Ser Arg Ala

385/617

70	75	80	
ccc agc acc tgg gaa gag tct ggg ctt cgc tac gat aaa gct tat ccc			403
Pro Ser Thr Trp Glu Glu Ser Gly Leu Arg Tyr Asp Lys Ala Tyr Pro			
85	90	95	
ggg gac agg agg ctg agc agt gta atg aca ata gta aag tcc agg cca			451
Gly Asp Arg Arg Leu Ser Ser Val Met Thr Ile Val Lys Ser Arg Pro			
100	105	110	115
ttt cgg gaa aaa caa ggg aag atc ctg ctg gaa ggt cgc agg ctc att			499
Phe Arg Glu Lys Gln Gly Lys Ile Leu Leu Glu Gly Arg Arg Leu Ile			
120	125	130	
tca gac gct ctc aag gct gga gct gtg cca aaa atg ttc ttc ttt agc			547
Ser Asp Ala Leu Lys Ala Gly Ala Val Pro Lys Met Phe Phe Phe Ser			
135	140	145	
cgt cta gaa tac cta aag gag ttg cca gtc gat aag ctg aaa ggt gtc			595
Arg Leu Glu Tyr Leu Lys Glu Leu Pro Val Asp Lys Leu Lys Gly Val			
150	155	160	
agc ctc att aag gtg aaa ttt gag gat atc aag gat tgg tcc gac ctc			643
Ser Leu Ile Lys Val Lys Phe Glu Asp Ile Lys Asp Trp Ser Asp Leu			
165	170	175	
gta acg cca caa gga ata atg ggg att ttt gcc aag cct gac cat gtt			691
Val Thr Pro Gln Gly Ile Met Gly Ile Phe Ala Lys Pro Asp His Val			
180	185	190	195
aag atg aca tat cca aag act cag ctt cag cat tca ctg cct tta tta			739
Lys Met Thr Tyr Pro Lys Thr Gln Leu Gln His Ser Leu Pro Leu Leu			
200	205	210	
ttg att tgt gac aat ctc cgt gac cct ggg aac ctg ggg aca att ctg			787
Leu Ile Cys Asp Asn Leu Arg Asp Pro Gly Asn Leu Gly Thr Ile Leu			

215	220	225	
aga tct gca gct ggg gca ggc tgc agc aaa gtg tta ctc acc aaa ggc			835
Arg Ser Ala Ala Gly Ala Gly Cys Ser Lys Val Leu Leu Thr Lys Gly			
230	235	240	
tgt gtg gat gcc tgg gag ccc aaa gtg ctc cgg gcg ggt atg ggc gca			883
Cys Val Asp Ala Trp Glu Pro Lys Val Leu Arg Ala Gly Met Gly Ala			
245	250	255	
cat ttc cgg atg ccc att atc aat aat ctg gaa tgg gaa acc gtg ccc			931
His Phe Arg Met Pro Ile Ile Asn Asn Leu Glu Trp Glu Thr Val Pro			
260	265	270	275
aat tac ctg ccc cct gac act cgg gtc tat gtg gct gac aac tgt ggc			979
Asn Tyr Leu Pro Pro Asp Thr Arg Val Tyr Val Ala Asp Asn Cys Gly			
280	285	290	
ctt tat gcc cag gct gag atg tct aat aaa gct agt gac cat ggc tgg			1027
Leu Tyr Ala Gln Ala Glu Met Ser Asn Lys Ala Ser Asp His Gly Trp			
295	300	305	
gtg tgt gat caa cga gtg atg aag ttt cac aag tat gag gaa gag gaa			1075
Val Cys Asp Gln Arg Val Met Lys Phe His Lys Tyr Glu Glu Glu Glu			
310	315	320	
gat gta gaa acc gga gcc agt caa gat tgg ctg cct cat gtt gag gtt			1123
Asp Val Glu Thr Gly Ala Ser Gln Asp Trp Leu Pro His Val Glu Val			
325	330	335	
cag agt tac gac tcg gac tgg aca gag gcg ccg gca gct gtg gtg att			1171
Gln Ser Tyr Asp Ser Asp Trp Thr Glu Ala Pro Ala Ala Val Val Ile			
340	345	350	355
ggc ggg gag acc tac ggc gtg agc ctg gag tcc ctg cag ctg gcc gag			1219
Gly Gly Glu Thr Tyr Gly Val Ser Leu Glu Ser Leu Gln Leu Ala Glu			

360	365	370	
agc act ggt ggc aag agg ctg ctg atc ccc gtt gtg cct ggt gtg gac			1267
Ser Thr Gly Gly Lys Arg Leu Leu Ile Pro Val Val Pro Gly Val Asp			
375	380	385	
agc ctc aac tcg gcc atg gcg gca agc atc ctg ctt ttc gaa ggg aaa			1315
Ser Leu Asn Ser Ala Met Ala Ala Ser Ile Leu Leu Phe Glu Gly Lys			
390	395	400	
aga cag ctg cgg ggg agg gcg gag gac ttg agc agg gac agg agt tac			1363
Arg Gln Leu Arg Gly Arg Ala Glu Asp Leu Ser Arg Asp Arg Ser Tyr			
405	410	415	
cac tgaggacgca gaagtgactt ctgcttgagg acgtctgcag ctctctctac			1416
His			
420			
accagcacac tgggtgggagg ctggcggagt cagtgactat ggccccacg ttcaggagga			1476
aggtgtgatg ccgtcataca gttacaggaa aaataagaac ttcttcagaa agaacaggtc			1536
cgaattcttc ctgtcgcgtc actgattttg aggttctttt ttctcttggt gacaataggt			1596
gacccacgtg gctctgtgtg tttttaaaaa ttgtccacca agaagcactt tgtgcccaga			1656
aagttctga agcatcatcc tggcagggag gcgcctgctc caccagctgg tgggtgtttg			1716
taatcgccaa gcaccagcta taggtcacag ccacatcact cacagctgat cactgggttg			1776
tggaaaataa actatgagca gcag			1800

<210> 122

<211> 420

<212> PRT

<213> Homo sapiens

<400> 122

Met Ala Ala Leu Val Arg Pro Ala Arg Phe Val Val Arg Pro Leu Leu

389/617

Thr Ile Leu Arg Ser Ala Ala Gly Ala Gly Cys Ser Lys Val Leu Leu
225 230 235 240
Thr Lys Gly Cys Val Asp Ala Trp Glu Pro Lys Val Leu Arg Ala Gly
245 250 255
Met Gly Ala His Phe Arg Met Pro Ile Ile Asn Asn Leu Glu Trp Glu
260 265 270
Thr Val Pro Asn Tyr Leu Pro Pro Asp Thr Arg Val Tyr Val Ala Asp
275 280 285
Asn Cys Gly Leu Tyr Ala Gln Ala Glu Met Ser Asn Lys Ala Ser Asp
290 295 300
His Gly Trp Val Cys Asp Gln Arg Val Met Lys Phe His Lys Tyr Glu
305 310 315 320
Glu Glu Glu Asp Val Glu Thr Gly Ala Ser Gln Asp Trp Leu Pro His
325 330 335
Val Glu Val Gln Ser Tyr Asp Ser Asp Trp Thr Glu Ala Pro Ala Ala
340 345 350
Val Val Ile Gly Gly Glu Thr Tyr Gly Val Ser Leu Glu Ser Leu Gln
355 360 365
Leu Ala Glu Ser Thr Gly Gly Lys Arg Leu Leu Ile Pro Val Val Pro
370 375 380
Gly Val Asp Ser Leu Asn Ser Ala Met Ala Ala Ser Ile Leu Leu Phe
385 390 395 400
Glu Gly Lys Arg Gln Leu Arg Gly Arg Ala Glu Asp Leu Ser Arg Asp
405 410 415
Arg Ser Tyr His
420

<210> 123

<211> 2557

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (556).. (1833)

<400> 123

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 tcctgcagcc ctggccctcc cccgcccccc ggcttggttt ttcccagccg tggaggttgg 120
 gccaggggct ggggtgagag gagagtcggc gccgcagca ggagctggga aggcgctgg 180
 actcgggtgg ccctcggagt tggtttgca ggcgcggggt gcggaggtcg ctcatccgat 240
 cctgccctga gagaggcgcc aacaaaggag ttgaggaggt gccaccacc ccagctgcgg 300
 cgggaggagg agcgccaagg cccgtgtccc gaccgcgct gcgtactcac tggagggaag 360
 ggcggggtgc cgctccggga gggggacgcc cgggtggctcg gggttagcca agttccagct 420
 tttggcgctc cctcctctgc tcccacgca ggaaagtgtg ccgtcgacgc ttgcggccgg 480
 ctgcgccccg ccgggcccag gcggtcgagt cttcggagcg ggcgctgtcc cagctccggg 540
 gaaccgcgag ccgcg atg cct ggg gcg ggc tcc cgg ggc ccc tcc gcc ggg 591

Met Pro Gly Ala Gly Ser Arg Gly Pro Ser Ala Gly

1

5

10

gac gga cgg ctg agg ttg gca agg ctg gcg cta gtg ctg ctg ggt tgg 639
 Asp Gly Arg Leu Arg Leu Ala Arg Leu Ala Leu Val Leu Leu Gly Trp

15

20

25

gtc tcc gcg tcg gcc ccc agc tct tcg gta ccc tcg tct tcc acc tcc 687
 Val Ser Ala Ser Ala Pro Ser Ser Ser Val Pro Ser Ser Ser Thr Ser

30

35

40

ccg gca gcc ttc ctg gcc tcg ggg tct gcg cag cct ccg cca gcc gag 735

391/617

Pro Ala Ala Phe Leu Ala Ser Gly Ser Ala Gln Pro Pro Pro Ala Glu
 45 50 55 60
 aga tgc ccc gcg gcg tgc gag tgc tcc gag gcg gcg cgc acg gtt aag 783
 Arg Cys Pro Ala Ala Cys Glu Cys Ser Glu Ala Ala Arg Thr Val Lys
 65 70 75
 tgc gtg aac cgc aac ctg ctg gag gtg ccg gcg gat cta ccg cct tac 831
 Cys Val Asn Arg Asn Leu Leu Glu Val Pro Ala Asp Leu Pro Pro Tyr
 80 85 90
 gtg cgc aac ctt ttc ctt acc ggc aac cag atg acc gtg ctc ccc gcg 879
 Val Arg Asn Leu Phe Leu Thr Gly Asn Gln Met Thr Val Leu Pro Ala
 95 100 105
 ggc gcc ttc gcc cgc cag ccg ccg ctc gcc gac ctg gag gcg ctc aac 927
 Gly Ala Phe Ala Arg Gln Pro Pro Leu Ala Asp Leu Glu Ala Leu Asn
 110 115 120
 ctc agc ggc aac cac ctg aag gag gtg tgt gca ggt gcc ttc gag cat 975
 Leu Ser Gly Asn His Leu Lys Glu Val Cys Ala Gly Ala Phe Glu His
 125 130 135 140
 ctg ccg ggt ctg cgc cgg ctt gac ctc agc cac aac cct ctc acc aac 1023
 Leu Pro Gly Leu Arg Arg Leu Asp Leu Ser His Asn Pro Leu Thr Asn
 145 150 155
 ctc agc gcc ttc gtc ttt gcg ggc agc aac gcc agc gtc tcg gcc ccc 1071
 Leu Ser Ala Phe Val Phe Ala Gly Ser Asn Ala Ser Val Ser Ala Pro
 160 165 170
 agc ccc ctg gag gag ctg atc ctg aat cac atc gtg ccc cct gag gat 1119
 Ser Pro Leu Glu Glu Leu Ile Leu Asn His Ile Val Pro Pro Glu Asp
 175 180 185
 cag agg cag aac ggg agc ttc gag ggt atg gtg gcc ttc gaa ggc atg 1167

Gln Arg Gln Asn Gly Ser Phe Glu Gly Met Val Ala Phe Glu Gly Met
 190 195 200
 gtg gca gca gct ctg cgc tca ggc ctt gca ctc cga ggt ctt aca cgc 1215
 Val Ala Ala Ala Leu Arg Ser Gly Leu Ala Leu Arg Gly Leu Thr Arg
 205 210 215 220
 ctg gag cta gcc agc aat cac ttt ctt ttc ctg cct cgg gac tta cta 1263
 Leu Glu Leu Ala Ser Asn His Phe Leu Phe Leu Pro Arg Asp Leu Leu
 225 230 235
 gcc caa ctg ccg agt ctc aga tac ctg gac ctc agg aac aat tcc ctg 1311
 Ala Gln Leu Pro Ser Leu Arg Tyr Leu Asp Leu Arg Asn Asn Ser Leu
 240 245 250
 gtg agc ctg acc tac gca tcc ttc cgc aac ctg aca cac ctc gaa agc 1359
 Val Ser Leu Thr Tyr Ala Ser Phe Arg Asn Leu Thr His Leu Glu Ser
 255 260 265
 ctc cac ttg gag gac aat gcc ctc aag gtc ctt cac aac tcc acc ttg 1407
 Leu His Leu Glu Asp Asn Ala Leu Lys Val Leu His Asn Ser Thr Leu
 270 275 280
 gct gag tgg caa ggc ctg gct cat gtc aag gtg ttc ctg gac aac aat 1455
 Ala Glu Trp Gln Gly Leu Ala His Val Lys Val Phe Leu Asp Asn Asn
 285 290 295 300
 ccc tgg gtt tgc gac tgc tac atg gct gac atg gtg gct tgg ctt aaa 1503
 Pro Trp Val Cys Asp Cys Tyr Met Ala Asp Met Val Ala Trp Leu Lys
 305 310 315
 gag aca gag gtg gtg cca gat aaa gcc agg ctt acc tgc gca ttc ccg 1551
 Glu Thr Glu Val Val Pro Asp Lys Ala Arg Leu Thr Cys Ala Phe Pro
 320 325 330
 gag aag atg agg aat cgt ggc ctc tta gac ctc aac agc tct gac ctg 1599

Glu Lys Met Arg Asn Arg Gly Leu Leu Asp Leu Asn Ser Ser Asp Leu
 335 340 345
 gac tgt gac gct gtc ctt ccc caa tcc ctg cag act tcc tat gtc ttc 1647
 Asp Cys Asp Ala Val Leu Pro Gln Ser Leu Gln Thr Ser Tyr Val Phe
 350 355 360
 cta ggt att gtt tta gct ctg ata ggc gct att ttc ctc ctc gtt ttg 1695
 Leu Gly Ile Val Leu Ala Leu Ile Gly Ala Ile Phe Leu Leu Val Leu
 365 370 375 380
 tat ttg aac cgt aaa ggc ata aaa aag tgg atg cat aac atc aga gat 1743
 Tyr Leu Asn Arg Lys Gly Ile Lys Lys Trp Met His Asn Ile Arg Asp
 385 390 395
 gcc tgc agg gat cac atg gaa ggg tat cat tac aga tac gaa atc aat 1791
 Ala Cys Arg Asp His Met Glu Gly Tyr His Tyr Arg Tyr Glu Ile Asn
 400 405 410
 gcg gac ccc aga tta aca aat ctt agt tcc aac tcg gat gtc 1833
 Ala Asp Pro Arg Leu Thr Asn Leu Ser Ser Asn Ser Asp Val
 415 420 425
 tgagaaacag gacccatcaa ggaggactct gcatgaggtg tagacttaag ggTTTTTTTT 1893
 ttccccTTTA ctaggcttgc tccacttcca cacttcaccg tagacactat tgactttgat 1953
 ccttgTTatg taaaatcccg gtgtgttctg ttaatgtaag gacatgaaca actgcacatg 2013
 tttatTTTcc ctattccttt cggTactcct cgatgcctgc ggagggattg tttttttttt 2073
 tctctctctc tcaagtcgca gcatggactt ggattagttc agttcaaggt gtagcacaga 2133
 taacattcaa cggaagctgc ctcaGTTTT tttttttttt ttttgagaaa agtactttat 2193
 tcataaatat gagtttcac ctcacctacc taaatgatgg aggaaatatt gcatccccc 2253
 actgcctgca gaccgtagca agctcttaca tagaactttg tagtgcatag gagcacctgc 2313
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 agataacttc tttgacaaac taaattactt tttgattgca gtttatagga aactgacctg 2433

agatttttcg gtgttttttt tttttgttt gttttggttt tgttttgttt tgttttttaa 2493
 ataaactgca ttgagatcca acaaactgga ttgttataaa aaatcaataa aagaatctta 2553
 aaag 2557

<210> 124

<211> 426

<212> PRT

<213> Mus musculus

<400> 124

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 20 25 30
 Ala Pro Ser Ser Ser Val Pro Ser Ser Ser Thr Ser Pro Ala Ala Phe
 35 40 45
 Leu Ala Ser Gly Ser Ala Gln Pro Pro Pro Ala Glu Arg Cys Pro Ala
 50 55 60
 Ala Cys Glu Cys Ser Glu Ala Ala Arg Thr Val Lys Cys Val Asn Arg
 65 70 75 80
 Asn Leu Leu Glu Val Pro Ala Asp Leu Pro Pro Tyr Val Arg Asn Leu
 85 90 95
 Phe Leu Thr Gly Asn Gln Met Thr Val Leu Pro Ala Gly Ala Phe Ala
 100 105 110
 Arg Gln Pro Pro Leu Ala Asp Leu Glu Ala Leu Asn Leu Ser Gly Asn
 115 120 125
 His Leu Lys Glu Val Cys Ala Gly Ala Phe Glu His Leu Pro Gly Leu
 130 135 140

395/617

Arg Arg Leu Asp Leu Ser His Asn Pro Leu Thr Asn Leu Ser Ala Phe
145 150 155 160
Val Phe Ala Gly Ser Asn Ala Ser Val Ser Ala Pro Ser Pro Leu Glu
165 170 175
Glu Leu Ile Leu Asn His Ile Val Pro Pro Glu Asp Gln Arg Gln Asn
180 185 190
Gly Ser Phe Glu Gly Met Val Ala Phe Glu Gly Met Val Ala Ala Ala
195 200 205
Leu Arg Ser Gly Leu Ala Leu Arg Gly Leu Thr Arg Leu Glu Leu Ala
210 215 220
Ser Asn His Phe Leu Phe Leu Pro Arg Asp Leu Leu Ala Gln Leu Pro
225 230 235 240
Ser Leu Arg Tyr Leu Asp Leu Arg Asn Asn Ser Leu Val Ser Leu Thr
245 250 255
Tyr Ala Ser Phe Arg Asn Leu Thr His Leu Glu Ser Leu His Leu Glu
260 265 270
Asp Asn Ala Leu Lys Val Leu His Asn Ser Thr Leu Ala Glu Trp Gln
275 280 285
Gly Leu Ala His Val Lys Val Phe Leu Asp Asn Asn Pro Trp Val Cys
290 295 300
Asp Cys Tyr Met Ala Asp Met Val Ala Trp Leu Lys Glu Thr Glu Val
305 310 315 320
Val Pro Asp Lys Ala Arg Leu Thr Cys Ala Phe Pro Glu Lys Met Arg
325 330 335
Asn Arg Gly Leu Leu Asp Leu Asn Ser Ser Asp Leu Asp Cys Asp Ala
340 345 350
Val Leu Pro Gln Ser Leu Gln Thr Ser Tyr Val Phe Leu Gly Ile Val

355 360 365
 Leu Ala Leu Ile Gly Ala Ile Phe Leu Leu Val Leu Tyr Leu Asn Arg
 370 375 380
 Lys Gly Ile Lys Lys Trp Met His Asn Ile Arg Asp Ala Cys Arg Asp
 385 390 395 400
 His Met Glu Gly Tyr His Tyr Arg Tyr Glu Ile Asn Ala Asp Pro Arg
 405 410 415
 Leu Thr Asn Leu Ser Ser Asn Ser Asp Val
 420 425

<210> 125

<211> 2557

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (556)..(1833)

<400> 125

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 gccaggggct ggggtgagag gagagtgcgc gcccgagca ggagctggga aggcgcgtgg 180
 actcgggtgg ccctcggagt tggctttgca ggcgcggggt gcggaggtcg ctcatccgat 240
 cctgccctga gagaggcgcc aacaaaggag ttgaggaggt gccaccacc ccagctgcgg 300
 cgggaggagg agcgccaagg cccgtgtccc gaccgcgct gcgtactcac tggagggaag 360
 ggcggggtgc cgctccggga gggggacgcc cgggtggctcg gggttagcca agttccagct 420
 tttggcgtcc cctcctctgc tcccacgcga ggaaagtttg ccgtcgacgc ttgcggccgg 480
 ctgcgccccg ccggggcccag gcggtcgagt cttcggagcg ggcgctgtcc cagctccggg 540

gaaccgag cgcg atg cct ggg gcg ggc tcc cgg ggc ccc tcc gcc ggg 591
 Met Pro Gly Ala Gly Ser Arg Gly Pro Ser Ala Gly
 1 5 10
 gac gga cgg ctg agg ttg gca agg ctg gcg cta gtg ctg ctg ggt tgg 639
 Asp Gly Arg Leu Arg Leu Ala Arg Leu Ala Leu Val Leu Leu Gly Trp
 15 20 25
 gtc tcc gcg tcg gcc ccc agc tct tcg gta ccc tcg tct tcc acc tcc 687
 Val Ser Ala Ser Ala Pro Ser Ser Ser Val Pro Ser Ser Ser Thr Ser
 30 35 40
 ccg gca gac ttc ctg gcc tcg ggg tct gcg cag cct ccg cca gcc gag 735
 Pro Ala Asp Phe Leu Ala Ser Gly Ser Ala Gln Pro Pro Pro Ala Glu
 45 50 55 60
 aga tgc ccc gcg gcg tgc gag tgc tcc gag gcg gcg cgc acg gtt aag 783
 Arg Cys Pro Ala Ala Cys Glu Cys Ser Glu Ala Ala Arg Thr Val Lys
 65 70 75
 tgc gtg aac cgc aac ctg ctg gag gtg ccg gcg gat cta ccg cct tac 831
 Cys Val Asn Arg Asn Leu Leu Glu Val Pro Ala Asp Leu Pro Pro Tyr
 80 85 90
 gtg cgc aac ctt ttc ctt acc ggc aac cag atg acc gtg ctc ccc gcg 879
 Val Arg Asn Leu Phe Leu Thr Gly Asn Gln Met Thr Val Leu Pro Ala
 95 100 105
 ggc gcc ttc gcc cgc cag ccg ccg ctc gcc gac ctg gag gcg ctc aac 927
 Gly Ala Phe Ala Arg Gln Pro Pro Leu Ala Asp Leu Glu Ala Leu Asn
 110 115 120
 ctc agc ggc aac cac ctg aag gag gtg tgt gca ggt gcc ttc gag cat 975
 Leu Ser Gly Asn His Leu Lys Glu Val Cys Ala Gly Ala Phe Glu His
 125 130 135 140

ctg ccg ggt ctg cgc cgg ctt gac ctc agc cac aac cct ctc acc aac	1023
Leu Pro Gly Leu Arg Arg Leu Asp Leu Ser His Asn Pro Leu Thr Asn	
145 150 155	
ctc agc gcc ttc gtc ttt gcg ggc agc aac gcc agc gtc tcg gcc ccc	1071
Leu Ser Ala Phe Val Phe Ala Gly Ser Asn Ala Ser Val Ser Ala Pro	
160 165 170	
agc ccc ctg gag gag ctg atc ctg aat cac atc gtg ccc cct gag gat	1119
Ser Pro Leu Glu Glu Leu Ile Leu Asn His Ile Val Pro Pro Glu Asp	
175 180 185	
cag agg cag aac ggg agc ttc gag ggt atg gtg gcc ttc gaa ggc atg	1167
Gln Arg Gln Asn Gly Ser Phe Glu Gly Met Val Ala Phe Glu Gly Met	
190 195 200	
gtg gca gca gct ctg cgc tca ggc ctt gca ctc cga ggt ctt aca cgc	1215
Val Ala Ala Ala Leu Arg Ser Gly Leu Ala Leu Arg Gly Leu Thr Arg	
205 210 215 220	
ctg gag cta gcc agc aat cac ttt ctt ttc ctg cct cgg gac tta cta	1263
Leu Glu Leu Ala Ser Asn His Phe Leu Phe Leu Pro Arg Asp Leu Leu	
225 230 235	
gcc caa ctg ccg agt ctc aga tac ctg gac ctc agg aac aat tcc ctg	1311
Ala Gln Leu Pro Ser Leu Arg Tyr Leu Asp Leu Arg Asn Asn Ser Leu	
240 245 250	
gtg agc ctg acc tac gca tcc ttc cgc aac ctg aca cac ctc gaa agc	1359
Val Ser Leu Thr Tyr Ala Ser Phe Arg Asn Leu Thr His Leu Glu Ser	
255 260 265	
ctc cac ttg gag gac aat gcc ctc aag gtc ctt cac aac tcc acc ttg	1407
Leu His Leu Glu Asp Asn Ala Leu Lys Val Leu His Asn Ser Thr Leu	
270 275 280	

gct gag tgg caa ggc ctg gct cat gtc aag gtg ttc ctg gac aac aat 1455
 Ala Glu Trp Gln Gly Leu Ala His Val Lys Val Phe Leu Asp Asn Asn
 285 290 295 300
 ccc tgg gtt tgc gac tgc tac atg gct gac atg gtg gct tgg ctt aaa 1503
 Pro Trp Val Cys Asp Cys Tyr Met Ala Asp Met Val Ala Trp Leu Lys
 305 310 315
 gag aca gag gtg gtg cca gat aaa gcc agg ctt acc tgc gca ttc ccg 1551
 Glu Thr Glu Val Val Pro Asp Lys Ala Arg Leu Thr Cys Ala Phe Pro
 320 325 330
 gag aag atg agg aat cgt ggc ctc tta gac ctc aac agc tct gac ctg 1599
 Glu Lys Met Arg Asn Arg Gly Leu Leu Asp Leu Asn Ser Ser Asp Leu
 335 340 345
 gac tgt gac gct gtc ctt ccc caa tcc ctg cag act tcc tat gtc ttc 1647
 Asp Cys Asp Ala Val Leu Pro Gln Ser Leu Gln Thr Ser Tyr Val Phe
 350 355 360
 cta ggt att gtt tta gct ctg ata ggc gct att ttc ctc ctc gtt ttg 1695
 Leu Gly Ile Val Leu Ala Leu Ile Gly Ala Ile Phe Leu Leu Val Leu
 365 370 375 380
 tat ttg aac cgt aaa ggc ata aaa aag tgg atg cat aac atc aga gat 1743
 Tyr Leu Asn Arg Lys Gly Ile Lys Lys Trp Met His Asn Ile Arg Asp
 385 390 395
 gcc tgc agg gat cac atg gaa ggg tat cat tac aga tac gaa atc aat 1791
 Ala Cys Arg Asp His Met Glu Gly Tyr His Tyr Arg Tyr Glu Ile Asn
 400 405 410
 gcg gac ccc aga tta aca aat ctt agt tcc aac tcg gat gtc 1833
 Ala Asp Pro Arg Leu Thr Asn Leu Ser Ser Asn Ser Asp Val
 415 420 425

tgagaaacag gacccatcaa ggaggactct gcatgaggtg tagacttaag ggtttttttt 1893
 ttccccitta ctaggcttgc tccacttcca cacttcaccg tagacactat tgactttgat 1953
 ccttgttatg taaaatcccg gtgtgttctg ttaatgtaag gacatgaaca actgcacatg 2013
 tttatitttc ctattccttt cggctactcct cgatgcctgc ggagggattg tttttttttt 2073
 tctctctctc tcaagtcgca gcatggactt ggattagttc agticaaggt gtagcacaga 2133
 taacattcaa cggaagctgc ctcagttttt tttttttttt ttttgagaaa agtactttat 2193
 tcataaatat gagtttcata ctcacctacc taaatgatgg aggaaatatt gcatccccaa 2253
 actgcctgca gaccgtagca agctcttaca tagaactttg tagtgcatag gagcacctgc 2313
 atccaagagc atgcgtacat tttactgttc tgcataataa aaagaaaaag ttgcaacttc 2373
 agataacttc ttgacaaac taaattactt ttgattgca gtttatagga aactgacctg 2433
 agatittttcg gtgttttttt tttttgttt gttttggttt tgttttgttt tgttttttaa 2493
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 aaag 2557

<210> 126

<211> 426

<212> PRT

<213> Mus musculus

<400> 126

Met Pro Gly Ala Gly Ser Arg Gly Pro Ser Ala Gly Asp Gly Arg Leu

1 5 10 15

Arg Leu Ala Arg Leu Ala Leu Val Leu Leu Gly Trp Val Ser Ala Ser

20 25 30

Ala Pro Ser Ser Ser Val Pro Ser Ser Ser Thr Ser Pro Ala Asp Phe

35 40 45

Leu Ala Ser Gly Ser Ala Gln Pro Pro Pro Ala Glu Arg Cys Pro Ala

50 55 60

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275 280 285
 Gly Leu Ala His Val Lys Val Phe Leu Asp Asn Asn Pro Trp Val Cys
 290 295 300
 Asp Cys Tyr Met Ala Asp Met Val Ala Trp Leu Lys Glu Thr Glu Val
 305 310 315 320
 Val Pro Asp Lys Ala Arg Leu Thr Cys Ala Phe Pro Glu Lys Met Arg
 325 330 335
 Asn Arg Gly Leu Leu Asp Leu Asn Ser Ser Asp Leu Asp Cys Asp Ala
 340 345 350
 Val Leu Pro Gln Ser Leu Gln Thr Ser Tyr Val Phe Leu Gly Ile Val
 355 360 365
 Leu Ala Leu Ile Gly Ala Ile Phe Leu Leu Val Leu Tyr Leu Asn Arg
 370 375 380
 Lys Gly Ile Lys Lys Trp Met His Asn Ile Arg Asp Ala Cys Arg Asp
 385 390 395 400
 His Met Glu Gly Tyr His Tyr Arg Tyr Glu Ile Asn Ala Asp Pro Arg
 405 410 415
 Leu Thr Asn Leu Ser Ser Asn Ser Asp Val
 420 425

<210> 127
 <211> 2361
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (426)..(1685)

<400> 127

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 gtagggaagg aattgggat taagcggtcc ctgagaggat ccagcgagggt gtgccaacaa 120
 gaggcgaaga ggtggcacca gggcggcggc aggaagagga gcgggagcag gagcgcgagg 180
 cggagcggtcc cgacccgccg tgcgtacttt ctggagggaa gggcggggg aatcggtccc 240
 tgagggaagc gcccgtggc gaggggggta gccaggttcc ggctgcggcg ccaactccctc 300
 ggttccacga gaggaagtt ttttttttcc agacgcttcc gccggctcgc gccctccggg 360
 cccagcctcc cgagccttcg gagcgggcgc cgtcccagcc cagctccggg gaaacgcgag 420
 ccgcg atg cct ggg ggg tgc tcc cgg ggc ccc gcc gcc ggg gac ggg cgt 470
 Met Pro Gly Gly Cys Ser Arg Gly Pro Ala Ala Gly Asp Gly Arg
 1 5 10 15
 ctg cgg ctg gcg cga cta gcg ctg gta ctc ctg ggc tgg gtc tcc tcg 518
 Leu Arg Leu Ala Arg Leu Ala Leu Val Leu Leu Gly Trp Val Ser Ser
 20 25 30
 tct tct ccc acc tcc tcg gca tcc tcc ttc tcc tcc tcg gcg ccg ttc 566
 Ser Ser Pro Thr Ser Ser Ala Ser Ser Phe Ser Ser Ser Ala Pro Phe
 35 40 45
 ctg gct tcc gcc gtg tcc gcc cag ccc ccg ctg ccg gac cag tgc ccc 614
 Leu Ala Ser Ala Val Ser Ala Gln Pro Pro Leu Pro Asp Gln Cys Pro
 50 55 60
 gcg ctg tgc gag tgc tcc gag gca gcg cgc aca gtc aag tgc gtt aac 662
 Ala Leu Cys Glu Cys Ser Glu Ala Ala Arg Thr Val Lys Cys Val Asn
 65 70 75
 cgc aat ctg acc gag gtg ccc acg gac ctg ccc gcc tac gtg cgc aac 710
 Arg Asn Leu Thr Glu Val Pro Thr Asp Leu Pro Ala Tyr Val Arg Asn
 80 85 90 95
 etc ttc ctt acc ggc aac cag ctg gcc gtg ctc cct gcc ggc gcc ttc 758

404/617

Leu Phe Leu Thr Gly Asn Gln Leu Ala Val Leu Pro Ala Gly Ala Phe
 100 105 110
 gcc cgc cgg ccg ccg ctg gcg gag ctg gcc gcg ctc aac ctc agc ggc 806
 Ala Arg Arg Pro Pro Leu Ala Glu Leu Ala Ala Leu Asn Leu Ser Gly
 115 120 125
 agc cgc ctg gac gag gtg cgc gcg ggc gcc ttc gag cat ctg ccc agc 854
 Ser Arg Leu Asp Glu Val Arg Ala Gly Ala Phe Glu His Leu Pro Ser
 130 135 140
 ctg cgc cag ctc gac ctc agc cac aac cca ctg gcc gac ctc agt ccc 902
 Leu Arg Gln Leu Asp Leu Ser His Asn Pro Leu Ala Asp Leu Ser Pro
 145 150 155
 ttc gct ttc tcg ggc agc aat gcc agc gtc tcg gcc ccc agt ccc ctt 950
 Phe Ala Phe Ser Gly Ser Asn Ala Ser Val Ser Ala Pro Ser Pro Leu
 160 165 170 175
 gtg gaa ctg atc ctg aac cac atc gtg ccc cct gaa gat gag cgg cag 998
 Val Glu Leu Ile Leu Asn His Ile Val Pro Pro Glu Asp Glu Arg Gln
 180 185 190
 aac cgg agc ttc gag ggc atg gtg gtg gcg gcc ctg ctg gcg ggc cgt 1046
 Asn Arg Ser Phe Glu Gly Met Val Val Ala Ala Leu Leu Ala Gly Arg
 195 200 205
 gca ctg cag ggg ctc cgc cgc ttg gag ctg gcc agc aac cac ttc ctt 1094
 Ala Leu Gln Gly Leu Arg Arg Leu Glu Leu Ala Ser Asn His Phe Leu
 210 215 220
 tac ctg ccg cgg gat gtg ctg gcc caa ctg ccc agc ctc agg cac ctg 1142
 Tyr Leu Pro Arg Asp Val Leu Ala Gln Leu Pro Ser Leu Arg His Leu
 225 230 235
 gac tta agt aat aat tcg ctg gtg agc ctg acc tac gtg tcc ttc cgc 1190

Asp Leu Ser Asn Asn Ser Leu Val Ser Leu Thr Tyr Val Ser Phe Arg
 240 245 250 255
 aac ctg aca cat cta gaa agc ctc cac ctg gag gac aat gcc ctc aag 1238
 Asn Leu Thr His Leu Glu Ser Leu His Leu Glu Asp Asn Ala Leu Lys
 260 265 270
 gtc ctt cac aat ggc acc ctg gct gag ttg caa ggt cta ccc cac att 1286
 Val Leu His Asn Gly Thr Leu Ala Glu Leu Gln Gly Leu Pro His Ile
 275 280 285
 agg gtt ttc ctg gac aac aat ccc tgg gtc tgc gac tgc cac atg gca 1334
 Arg Val Phe Leu Asp Asn Asn Pro Trp Val Cys Asp Cys His Met Ala
 290 295 300
 gac atg gtg acc tgg ctc aag gaa aca gag gta gtg cag ggc aaa gac 1382
 Asp Met Val Thr Trp Leu Lys Glu Thr Glu Val Val Gln Gly Lys Asp
 305 310 315
 cgg ctc acc tgt gca tat ccg gaa aaa atg agg aat cgg gtc ctc ttg 1430
 Arg Leu Thr Cys Ala Tyr Pro Glu Lys Met Arg Asn Arg Val Leu Leu
 320 325 330 335
 gaa ctc aac agt gct gac ctg gac tgt gac ccg att ctt ccc cca tcc 1478
 Glu Leu Asn Ser Ala Asp Leu Asp Cys Asp Pro Ile Leu Pro Pro Ser
 340 345 350
 ctg caa acc tct tat gtc ttc ctg ggt att gtt tta gcc ctg ata ggc 1526
 Leu Gln Thr Ser Tyr Val Phe Leu Gly Ile Val Leu Ala Leu Ile Gly
 355 360 365
 gct att ttc ctc ctg gtt ttg tat ttg aac cgc aag ggg ata aaa aag 1574
 Ala Ile Phe Leu Leu Val Leu Tyr Leu Asn Arg Lys Gly Ile Lys Lys
 370 375 380
 tgg atg cat aac atc aga gat gcc tgc agg gat cac atg gaa ggg tat 1622

Trp Met His Asn Ile Arg Asp Ala Cys Arg Asp His Met Glu Gly Tyr
 385 390 395
 cat tac aga tat gaa atc aat gcg gac ccc aga tta aca aac ctc agt 1670
 His Tyr Arg Tyr Glu Ile Asn Ala Asp Pro Arg Leu Thr Asn Leu Ser
 400 405 410 415
 tct aac tcg gat gtc tgagaaatat tagaggacag accaaggaca actctgcatg 1725
 Ser Asn Ser Asp Val
 420
 agatgtagac ttaagcttta tccctactag gcttgctcca ctttcatcct ccactataga 1785
 tacaacggac tttgactaaa agcagtgaag gggatttgct tccttggtat gtaaagtttc 1845
 tcggtgtgtt ctgttaatgt aagacgatga acagttgtgt atagtgtttt accctcttct 1905
 ttttcttgga actcctcaac acgtatggag ggatttttca ggtttcagca tgaacatggg 1965
 cttcttgctg tctgtctctc tctcagtaca gttcaagggtg tagcaagtgt acccacacag 2025
 atagcattca acaaaagctg cctcaacttt ttcgagaaaa atactttatt cataaatatc 2085
 agttttattc tcatgtacct aagttgtgga gaaaataatt gcacccataa aactgcctgc 2145
 agacgttagc aggctcttca aaataactcc atgggtgcaca ggagcacctg catccaagag 2205
 catgcttaca ttttactgtt ctgcatatta caaaaaataa cttgcaactt cataacttct 2265
 ttgacaaagt aaattacttt tttgattgca gtttatatga aaatgtactg attttttttt 2325
 aataaactgc atcgagatcc aaccgactga attggt 2361

<210> 128

<211> 420

<212> PRT

<213> Homo sapiens

<400> 128

Met Pro Gly Gly Cys Ser Arg Gly Pro Ala Ala Gly Asp Gly Arg Leu

1

5

10

15

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Arg Leu Ala Arg Leu Ala Leu Val Leu Leu Gly Trp Val Ser Ser Ser
20 25 30
Ser Pro Thr Ser Ser Ala Ser Ser Phe Ser Ser Ser Ala Pro Phe Leu
35 40 45
Ala Ser Ala Val Ser Ala Gln Pro Pro Leu Pro Asp Gln Cys Pro Ala
50 55 60
Leu Cys Glu Cys Ser Glu Ala Ala Arg Thr Val Lys Cys Val Asn Arg
65 70 75 80
Asn Leu Thr Glu Val Pro Thr Asp Leu Pro Ala Tyr Val Arg Asn Leu
85 90 95
Phe Leu Thr Gly Asn Gln Leu Ala Val Leu Pro Ala Gly Ala Phe Ala
100 105 110
Arg Arg Pro Pro Leu Ala Glu Leu Ala Ala Leu Asn Leu Ser Gly Ser
115 120 125
Arg Leu Asp Glu Val Arg Ala Gly Ala Phe Glu His Leu Pro Ser Leu
130 135 140
Arg Gln Leu Asp Leu Ser His Asn Pro Leu Ala Asp Leu Ser Pro Phe
145 150 155 160
Ala Phe Ser Gly Ser Asn Ala Ser Val Ser Ala Pro Ser Pro Leu Val
165 170 175
Glu Leu Ile Leu Asn His Ile Val Pro Pro Glu Asp Glu Arg Gln Asn
180 185 190
Arg Ser Phe Glu Gly Met Val Val Ala Ala Leu Leu Ala Gly Arg Ala
195 200 205
Leu Gln Gly Leu Arg Arg Leu Glu Leu Ala Ser Asn His Phe Leu Tyr
210 215 220
Leu Pro Arg Asp Val Leu Ala Gln Leu Pro Ser Leu Arg His Leu Asp

225 230 235 240
Leu Ser Asn Asn Ser Leu Val Ser Leu Thr Tyr Val Ser Phe Arg Asn
245 250 255
Leu Thr His Leu Glu Ser Leu His Leu Glu Asp Asn Ala Leu Lys Val
260 265 270
Leu His Asn Gly Thr Leu Ala Glu Leu Gln Gly Leu Pro His Ile Arg
275 280 285
Val Phe Leu Asp Asn Asn Pro Trp Val Cys Asp Cys His Met Ala Asp
290 295 300
Met Val Thr Trp Leu Lys Glu Thr Glu Val Val Gln Gly Lys Asp Arg
305 310 315 320
Leu Thr Cys Ala Tyr Pro Glu Lys Met Arg Asn Arg Val Leu Leu Glu
325 330 335
Leu Asn Ser Ala Asp Leu Asp Cys Asp Pro Ile Leu Pro Pro Ser Leu
340 345 350
Gln Thr Ser Tyr Val Phe Leu Gly Ile Val Leu Ala Leu Ile Gly Ala
355 360 365
Ile Phe Leu Leu Val Leu Tyr Leu Asn Arg Lys Gly Ile Lys Lys Trp
370 375 380
Met His Asn Ile Arg Asp Ala Cys Arg Asp His Met Glu Gly Tyr His
385 390 395 400
Tyr Arg Tyr Glu Ile Asn Ala Asp Pro Arg Leu Thr Asn Leu Ser Ser
405 410 415
Asn Ser Asp Val
420

<210> 129

409/617

<211> 1617

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (144).. (1160)

<223>

<400> 129

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gtccccgcac ccgcaccgca gccctgcccc gcggccccgcc gcccttcgc cagcctcccg 120

gaggacaccc gtgggtcacg gcc atg ccg cgc gtc tac ata gga cgc ctg agc 173

Met Pro Arg Val Tyr Ile Gly Arg Leu Ser

1

5

10

tac aac gtc ggc gag aag gac atc cag cgc ttt ttc agc ggc tac ggc 221

Tyr Asn Val Gly Glu Lys Asp Ile Gln Arg Phe Phe Ser Gly Tyr Gly

15

20

25

cgc ctc ctc gag atc gac ctc aaa aat ggg tac ggt ttc gtg gag ttc 269

Arg Leu Leu Glu Ile Asp Leu Lys Asn Gly Tyr Gly Phe Val Glu Phe

30

35

40

gag gac tcc cgg gat gcc gac gat gcc gtg tac gag ctc aac agc aag 317

Glu Asp Ser Arg Asp Ala Asp Asp Ala Val Tyr Glu Leu Asn Ser Lys

45

50

55

gag ctg tgc ggc gag cgc gtg atc gta gag cac gcc cgg ggc ccg cgc 365

Glu Leu Cys Gly Glu Arg Val Ile Val Glu His Ala Arg Gly Pro Arg

60

65

70

cgc gac cgc gat ggc tac agc tac gga agc cgc agt ggt gga ggt gga 413

Arg Asp Arg Asp Gly Tyr Ser Tyr Gly Ser Arg Ser Gly Gly Gly Gly

410/617

75	80	85	90	
tac agc agt cgg aga act tct ggc aga gac aaa tat gga cca cct gtt				461
Tyr Ser Ser Arg Arg Thr Ser Gly Arg Asp Lys Tyr Gly Pro Pro Val				
	95	100	105	
cgt aca gag tac agg ctt att gta gaa aat ctg tct agt cgt tgc agt				509
Arg Thr Glu Tyr Arg Leu Ile Val Glu Asn Leu Ser Ser Arg Cys Ser				
	110	115	120	
tgg caa gac tta aag gat ttc atg cgg caa gca gga gaa gtg act tat				557
Trp Gln Asp Leu Lys Asp Phe Met Arg Gln Ala Gly Glu Val Thr Tyr				
	125	130	135	
gca gat gct cac aaa gaa cga aca aat gag ggt gtg att gaa ttt aga				605
Ala Asp Ala His Lys Glu Arg Thr Asn Glu Gly Val Ile Glu Phe Arg				
	140	145	150	
tcc tac tcc gac atg aag cgt gct ttg gat aaa ctg gat ggt aca gaa				653
Ser Tyr Ser Asp Met Lys Arg Ala Leu Asp Lys Leu Asp Gly Thr Glu				
	155	160	165	170
ata aat ggc aga aat att agg ctt att gaa gat aag cca aga aca agc				701
Ile Asn Gly Arg Asn Ile Arg Leu Ile Glu Asp Lys Pro Arg Thr Ser				
	175	180	185	
cat agg cgc tcc tac tct ggc agt aga tcc aga tca cgg tct aga aga				749
His Arg Arg Ser Tyr Ser Gly Ser Arg Ser Arg Ser Arg Ser Arg Arg				
	190	195	200	
agg tct cgg agt agg agt cgc aga agc agc cgc agt aga tct cga agt				797
Arg Ser Arg Ser Arg Ser Arg Arg Ser Ser Arg Ser Arg Ser Arg Ser				
	205	210	215	
atc tca aaa agt cgc tcc cga tct agg tct cgg agc aaa ggt cga tcc				845
Ile Ser Lys Ser Arg Ser Arg Ser Arg Ser Arg Ser Lys Gly Arg Ser				

220	225	230	
cga tcc cgc tca aaa ggc agg aaa tcc aga tca aag agc aaa tcg aag			893
Arg Ser Arg Ser Lys Gly Arg Lys Ser Arg Ser Lys Ser Lys Ser Lys			
235	240	245	250
ccc aag tct gac cgg ggc tcc cat tcc cac tca aga agc agg tct aag			941
Pro Lys Ser Asp Arg Gly Ser His Ser His Ser Arg Ser Arg Ser Lys			
255	260	265	
gat aag tat ggg aag tca cgt agt agg tca cgg tct cgg tcc ccc aaa			989
Asp Lys Tyr Gly Lys Ser Arg Ser Arg Ser Arg Ser Arg Ser Pro Lys			
270	275	280	
gag aac ggc aaa gga gac ata aag tca aag tcc aga tcc cgg agc cag			1037
Glu Asn Gly Lys Gly Asp Ile Lys Ser Lys Ser Arg Ser Arg Ser Gln			
285	290	295	
tct cgg tcc cac tcg cct cta cct gct cca ccc tca aag gct cgg tcc			1085
Ser Arg Ser His Ser Pro Leu Pro Ala Pro Pro Ser Lys Ala Arg Ser			
300	305	310	
atg tcc cct ccg cca aaa aga gct tca agg tcc cgt tct aga tct cgt			1133
Met Ser Pro Pro Pro Lys Arg Ala Ser Arg Ser Arg Ser Arg Ser Arg			
315	320	325	330
tca agg tcc aga tca agt tcc aga gat taaccctgac ctgcagcttc			1180
Ser Arg Ser Arg Ser Ser Ser Arg Asp			
335			
tttgcacact ataacagaac actttcctac ttgcttaggc agttactctt ccgagtttat			1240
actgcctct tctttaagag gatttcctga aaaggaaca ccggaatttg atttgtggcc			1300
aaatttactg agaaaaagat gaggttctaa aatggtggta tgaagccctc tcccttcttt			1360
gtagaattaa gataattttg attttgtagc ctttgagcta aaataacttt tgtaaagatt			1420
aagctcattt agattttttt taaagtattg cagcaggatc tgctgcaggg ttctgttggtt			1480

ttgttttgct tatttttaaa ttaactgttc aggctttgga tactgcaggc tttagaggga 1540
 gaacccaaat tttcaattat gttggctttt tataaagctt gagttatgta agatttaa 1600
 aaaagtttgc taccaag 1617

<210> 130

<211> 339

<212> PRT

<213> Mus musculus

<400> 130

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 Asp Ile Gln Arg Phe Phe Ser Gly Tyr Gly Arg Leu Leu Glu Ile Asp
 20 25 30
 Leu Lys Asn Gly Tyr Gly Phe Val Glu Phe Glu Asp Ser Arg Asp Ala
 35 40 45
 Asp Asp Ala Val Tyr Glu Leu Asn Ser Lys Glu Leu Cys Gly Glu Arg
 50 55 60
 Val Ile Val Glu His Ala Arg Gly Pro Arg Arg Asp Arg Asp Gly Tyr
 65 70 75 80
 Ser Tyr Gly Ser Arg Ser Gly Gly Gly Tyr Ser Ser Arg Arg Thr
 85 90 95
 Ser Gly Arg Asp Lys Tyr Gly Pro Pro Val Arg Thr Glu Tyr Arg Leu
 100 105 110
 Ile Val Glu Asn Leu Ser Ser Arg Cys Ser Trp Gln Asp Leu Lys Asp
 115 120 125
 Phe Met Arg Gln Ala Gly Glu Val Thr Tyr Ala Asp Ala His Lys Glu
 130 135 140

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Arg Thr Asn Glu Gly Val Ile Glu Phe Arg Ser Tyr Ser Asp Met Lys
145 150 155 160
Arg Ala Leu Asp Lys Leu Asp Gly Thr Glu Ile Asn Gly Arg Asn Ile
165 170 175
Arg Leu Ile Glu Asp Lys Pro Arg Thr Ser His Arg Arg Ser Tyr Ser
180 185 190
Gly Ser Arg Ser Arg Ser Arg Ser Arg Arg Arg Ser Arg Ser Arg Ser
195 200 205
Arg Arg Ser Ser Arg Ser Arg Ser Arg Ser Ile Ser Lys Ser Arg Ser
210 215 220
Arg Ser Arg Ser Arg Ser Lys Gly Arg Ser Arg Ser Arg Ser Lys Gly
225 230 235 240
Arg Lys Ser Arg Ser Lys Ser Lys Ser Lys Pro Lys Ser Asp Arg Gly
245 250 255
Ser His Ser His Ser Arg Ser Arg Ser Lys Asp Lys Tyr Gly Lys Ser
260 265 270
Arg Ser Arg Ser Arg Ser Arg Ser Pro Lys Glu Asn Gly Lys Gly Asp
275 280 285
Ile Lys Ser Lys Ser Arg Ser Arg Ser Gln Ser Arg Ser His Ser Pro
290 295 300
Leu Pro Ala Pro Pro Ser Lys Ala Arg Ser Met Ser Pro Pro Pro Lys
305 310 315 320
Arg Ala Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Ser
325 330 335
Ser Arg Asp

<210> 131

<211> 1617

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (144).. (1160)

<223>

<400> 131

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gaggacaccc gtgggtcagc gcc atg ccg cgc gtc tac ata gga cgc ctg agc      173
      Met Pro Arg Val Tyr Ile Gly Arg Leu Ser
              1              5              10
tac aac gtc cgc gag aag gac atc cag cgc ttt ttc agc ggc tac ggc      221
Tyr Asn Val Arg Glu Lys Asp Ile Gln Arg Phe Phe Ser Gly Tyr Gly
              15              20              25
cgc ctc ctc gag atc gac ctc aaa aat ggg tac ggt ttc gtg gag ttc      269
Arg Leu Leu Glu Ile Asp Leu Lys Asn Gly Tyr Gly Phe Val Glu Phe
              30              35              40
gag gac tcc cgg gat gcc gac gat gcc gtg tac gag ctc aac agc aag      317
Glu Asp Ser Arg Asp Ala Asp Asp Ala Val Tyr Glu Leu Asn Ser Lys
              45              50              55
gag ctg tgc ggc gag cgc gtg atc gta gag cac gcc cgg ggc ccg cgc      365
Glu Leu Cys Gly Glu Arg Val Ile Val Glu His Ala Arg Gly Pro Arg
              60              65              70
cgc gac cgc gat ggc tac agc tac gga agc cgc agt ggt gga ggt gga      413
Arg Asp Arg Asp Gly Tyr Ser Tyr Gly Ser Arg Ser Gly Gly Gly Gly

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415/617

75	80	85	90	
tac agc agt cgg aga act tct ggc aga gac aaa tat gga cca cct gtt				461
Tyr Ser Ser Arg Arg Thr Ser Gly Arg Asp Lys Tyr Gly Pro Pro Val				
	95	100	105	
cgt aca gag tac agg ctt att gta gaa aat ctg tct agt cgt tgc agt				509
Arg Thr Glu Tyr Arg Leu Ile Val Glu Asn Leu Ser Ser Arg Cys Ser				
	110	115	120	
tgg caa gac tta aag gat ttc atg cgg caa gca gga gaa gtg act tat				557
Trp Gln Asp Leu Lys Asp Phe Met Arg Gln Ala Gly Glu Val Thr Tyr				
	125	130	135	
gca gat gct cac aaa gaa cga aca aat gag ggt gtg att gaa ttt aga				605
Ala Asp Ala His Lys Glu Arg Thr Asn Glu Gly Val Ile Glu Phe Arg				
	140	145	150	
tcc tac tcc gac atg aag cgt gct ttg gat aaa ctg gat ggt aca gaa				653
Ser Tyr Ser Asp Met Lys Arg Ala Leu Asp Lys Leu Asp Gly Thr Glu				
	155	160	165	170
ata aat ggc aga aat att agg ctt att gaa gat aag cca aga aca agc				701
Ile Asn Gly Arg Asn Ile Arg Leu Ile Glu Asp Lys Pro Arg Thr Ser				
	175	180	185	
cat agg cgc tcc tac tct ggc agt aga tcc aga tca cgg tct aga aga				749
His Arg Arg Ser Tyr Ser Gly Ser Arg Ser Arg Ser Arg Ser Arg Arg				
	190	195	200	
agg tct cgg agt agg agt cgc aga agc agc cgc agt aga tct cga agt				797
Arg Ser Arg Ser Arg Ser Arg Arg Ser Ser Arg Ser Arg Ser Arg Ser				
	205	210	215	
atc tca aaa agt cgc tcc cga tct agg tct cgg agc aaa ggt cga tcc				845
Ile Ser Lys Ser Arg Ser Arg Ser Arg Ser Arg Ser Lys Gly Arg Ser				

220 225 230
 cga tcc cgc tca aaa ggc agg aaa tcc aga tca aag agc aaa tcg aag 893
 Arg Ser Arg Ser Lys Gly Arg Lys Ser Arg Ser Lys Ser Lys Ser Lys
 235 240 245 250
 ccc aag tct gac cgg ggc tcc cat tcc cac tca aga agc agg tct aag 941
 Pro Lys Ser Asp Arg Gly Ser His Ser His Ser Arg Ser Arg Ser Lys
 255 260 265
 gat aag tat ggg aag tca cgt agt agg tca cgg tct cgg tcc ccc aaa 989
 Asp Lys Tyr Gly Lys Ser Arg Ser Arg Ser Arg Ser Arg Ser Pro Lys
 270 275 280
 gag aac ggc aaa gga gac ata aag tca aag tcc aga tcc cgg agc cag 1037
 Glu Asn Gly Lys Gly Asp Ile Lys Ser Lys Ser Arg Ser Arg Ser Gln
 285 290 295
 tct cgg tcc cac tcg cct cta cct gct cca ccc tca aag gct cgg tcc 1085
 Ser Arg Ser His Ser Pro Leu Pro Ala Pro Pro Ser Lys Ala Arg Ser
 300 305 310
 atg tcc cct ccg cca aaa aga gct tca agg tcc cgt tct aga tct cgt 1133
 Met Ser Pro Pro Pro Lys Arg Ala Ser Arg Ser Arg Ser Arg Ser Arg
 315 320 325 330
 tca agg tcc aga tca agt tcc aga gat taaccctgac ctgcagcttc 1180
 Ser Arg Ser Arg Ser Ser Ser Arg Asp
 335
 ttgcacact ataacagaac actttcctac ttgcttaggc agttactctt ccgagtttat 1240
 actcgctct tctttaagag gatttcctga aaagggaaca ccggaatttg atttgtggcc 1300
 aaatttactg agaaaaagat gaggttctaa aatggtggta tgaagccctc tcccttcttt 1360
 gtagaattaa gataattttg attttgtagc ctttgagcta aaataacttt tgtaaagatt 1420
 aagctcattt agattttttt taaagtattg cagcaggatc tgctgcaggg ttctgttggt 1480

ttgttttgc ttttttaaa ttaactgttc aggctttgga tactgcaggc tttagaggga 1540
 gaacccaaat tttcaattat gttggctttt tataaagctt gagttatgta agatttaa at 1600
 aaaagtttgc taccaag 1617

<210> 132

<211> 339

<212> PRT

<213> Mus musculus

<400> 132

Met Pro Arg Val Tyr Ile Gly Arg Leu Ser Tyr Asn Val Arg Glu Lys
 1 5 10 15
 Asp Ile Gln Arg Phe Phe Ser Gly Tyr Gly Arg Leu Leu Glu Ile Asp
 20 25 30
 Leu Lys Asn Gly Tyr Gly Phe Val Glu Phe Glu Asp Ser Arg Asp Ala
 35 40 45
 Asp Asp Ala Val Tyr Glu Leu Asn Ser Lys Glu Leu Cys Gly Glu Arg
 50 55 60
 Val Ile Val Glu His Ala Arg Gly Pro Arg Arg Asp Arg Asp Gly Tyr
 65 70 75 80
 Ser Tyr Gly Ser Arg Ser Gly Gly Gly Gly Tyr Ser Ser Arg Arg Thr
 85 90 95
 Ser Gly Arg Asp Lys Tyr Gly Pro Pro Val Arg Thr Glu Tyr Arg Leu
 100 105 110
 Ile Val Glu Asn Leu Ser Ser Arg Cys Ser Trp Gln Asp Leu Lys Asp
 115 120 125
 Phe Met Arg Gln Ala Gly Glu Val Thr Tyr Ala Asp Ala His Lys Glu
 130 135 140

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Arg Thr Asn Glu Gly Val Ile Glu Phe Arg Ser Tyr Ser Asp Met Lys
145 150 155 160
Arg Ala Leu Asp Lys Leu Asp Gly Thr Glu Ile Asn Gly Arg Asn Ile
165 170 175
Arg Leu Ile Glu Asp Lys Pro Arg Thr Ser His Arg Arg Ser Tyr Ser
180 185 190
Gly Ser Arg Ser Arg Ser Arg Ser Arg Arg Ser Arg Ser Arg Ser
195 200 205
Arg Arg Ser Ser Arg Ser Arg Ser Arg Ser Ile Ser Lys Ser Arg Ser
210 215 220
Arg Ser Arg Ser Arg Ser Lys Gly Arg Ser Arg Ser Arg Ser Lys Gly
225 230 235 240
Arg Lys Ser Arg Ser Lys Ser Lys Ser Lys Pro Lys Ser Asp Arg Gly
245 250 255
Ser His Ser His Ser Arg Ser Arg Ser Lys Asp Lys Tyr Gly Lys Ser
260 265 270
Arg Ser Arg Ser Arg Ser Arg Ser Pro Lys Glu Asn Gly Lys Gly Asp
275 280 285
Ile Lys Ser Lys Ser Arg Ser Arg Ser Gln Ser Arg Ser His Ser Pro
290 295 300
Leu Pro Ala Pro Pro Ser Lys Ala Arg Ser Met Ser Pro Pro Pro Lys
305 310 315 320
Arg Ala Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Arg Ser Ser
325 330 335
Ser Arg Asp

<210> 133

<211> 1650

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (137)..(1168)

<223>

<400> 133

cggacgcgtg ggctcggccg cccctgtggt gtgaggcgcg tgttcgggct cttgccgtcc 60

cgcacccgc accgcggtta ctggcttgcg gtccgccgtt cgacaaccag ccttgggtc 120

cccgccgcc acggac atg ccg cgc gtc tac ata gga cgc ctg agc tac aac 172

Met Pro Arg Val Tyr Ile Gly Arg Leu Ser Tyr Asn

1

5

10

gtc cgg gag aag gac atc cag cgc ttt ttc agt ggc tat ggc cgc ctc 220

Val Arg Glu Lys Asp Ile Gln Arg Phe Phe Ser Gly Tyr Gly Arg Leu

15

20

25

ctc gaa gta gac ctc aaa aat ggg tac ggc ttc gtg gag ttc gag gac 268

Leu Glu Val Asp Leu Lys Asn Gly Tyr Gly Phe Val Glu Phe Glu Asp

30

35

40

tcc cgc gac gcc gac gac gcc gtt tac gag ctg aac ggc aag gag ctc 316

Ser Arg Asp Ala Asp Asp Ala Val Tyr Glu Leu Asn Gly Lys Glu Leu

45

50

55

60

tgc ggc gag cgc gtg atc gta gag cac gcc cgg ggc ccg cgt cgc gat 364

Cys Gly Glu Arg Val Ile Val Glu His Ala Arg Gly Pro Arg Arg Asp

65

70

75

cgc gac ggc tac agc tac gga agc cgc agt ggt gga ggt gga tac agc 412

Arg Asp Gly Tyr Ser Tyr Gly Ser Arg Ser Gly Gly Gly Gly Tyr Ser

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80	85	90	
agt cgg aga aca tct ggc aga gac aaa tac gga cca cct gtt cgt aca			460
Ser Arg Arg Thr Ser Gly Arg Asp Lys Tyr Gly Pro Pro Val Arg Thr			
95	100	105	
gaa tac agg ctt att gta gaa aat ctt tct agt cgg tgc agt tgg caa			508
Glu Tyr Arg Leu Ile Val Glu Asn Leu Ser Ser Arg Cys Ser Trp Gln			
110	115	120	
gat tta aag gat ttt atg cga caa gca ggt gaa gta acc tat gcg gat			556
Asp Leu Lys Asp Phe Met Arg Gln Ala Gly Glu Val Thr Tyr Ala Asp			
125	130	135	140
gcc cac aag gaa cga aca aat gag ggt gta att gag ttt cgc tcc tac			604
Ala His Lys Glu Arg Thr Asn Glu Gly Val Ile Glu Phe Arg Ser Tyr			
145	150	155	
tct gac atg aag cgt gct ttg gac aaa ctg gat ggc aca gaa ata aat			652
Ser Asp Met Lys Arg Ala Leu Asp Lys Leu Asp Gly Thr Glu Ile Asn			
160	165	170	
ggc aga aat att agg ctt att gaa gat aag cca cgc aca agc cat agg			700
Gly Arg Asn Ile Arg Leu Ile Glu Asp Lys Pro Arg Thr Ser His Arg			
175	180	185	
cga tct tac tct gga agc aga tcc agg tct cga tct aga aga cgg tca			748
Arg Ser Tyr Ser Gly Ser Arg Ser Arg Ser Arg Ser Arg Arg Ser			
190	195	200	
cga agt agg agt cgc agg agc agc cgc agt aga tct cga agt atc tca			796
Arg Ser Arg Ser Arg Arg Ser Ser Arg Ser Arg Ser Arg Ser Ile Ser			
205	210	215	220
aaa agt cgc tcc cgt tcc agg tcg cgg agc aaa ggt cga tca cgt tct			844
Lys Ser Arg Ser Arg Ser Arg Ser Arg Ser Lys Gly Arg Ser Arg Ser			

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225	230	235	
cga tca aaa ggc agg aaa tct aga tca aag agc aaa tct aag ccc aag			892
Arg Ser Lys Gly Arg Lys Ser Arg Ser Lys Ser Lys Ser Lys Pro Lys			
240	245	250	
tct gat cgg ggc tcc cat tca cat tct cga agc aga tct aag gat gag			940
Ser Asp Arg Gly Ser His Ser His Ser Arg Ser Arg Ser Lys Asp Glu			
255	260	265	
tat gag aaa tct cga agc agg tct cgg tcc cga tcc ccc aaa gaa aat			988
Tyr Glu Lys Ser Arg Ser Arg Ser Arg Ser Arg Ser Pro Lys Glu Asn			
270	275	280	
gga aag ggt gat ata aag tca aaa tcc aga tca agg agc cag tcc cgt			1036
Gly Lys Gly Asp Ile Lys Ser Lys Ser Arg Ser Arg Ser Gln Ser Arg			
285	290	295	300
tcc aat tcg ccg cta cct gtt cca ccc tca aag gcc cgt tct gtg tcc			1084
Ser Asn Ser Pro Leu Pro Val Pro Pro Ser Lys Ala Arg Ser Val Ser			
305	310	315	
cct cca cca aaa aga gct act tca aga tcc cgt tct aga tct cgc tca			1132
Pro Pro Pro Lys Arg Ala Thr Ser Arg Ser Arg Ser Arg Ser Arg Ser			
320	325	330	
aag tca aga tca agg tcc agg tcg agt tcc aga gat taactcagaa			1178
Lys Ser Arg Ser Arg Ser Arg Ser Ser Ser Arg Asp			
335	340		
ctccttgttt gcacattatt atggaacact ttctactta ggcagttact cttccatgtt			1238
tatacttggc ctcttctgca agaggaatct cttgaaaaca ggggcacaca gaaatttgat			1298
ttgtggccaa attggatgaa aaagatgagg ctctaaggaa atggtggcat gaagaccctc			1358
tcccttcttt gtagaattaa gataactttg attttatage ttttgagcta acgtaacttt			1418
tgtaaagatt aagctcattt agtgttgttt tttttttttt tttttttttt ttttttagt			1478

atttcagcag gatctgctgg cagggttttt ttgttttatt tgtttgctta tttttaaat 1538
 aactgttttg agctttgaat acttaaggct ttagaggag aaccaattt tcaattatgt 1598
 tggcttttta taaagcttga gttatgtaag atttaaataa aagtttgcta cc 1650

<210> 134

<211> 344

<212> PRT

<213> Homo sapiens

<400> 134

Met Pro Arg Val Tyr Ile Gly Arg Leu Ser Tyr Asn Val Arg Glu Lys
 1 5 10 15
 Asp Ile Gln Arg Phe Phe Ser Gly Tyr Gly Arg Leu Leu Glu Val Asp
 20 25 30
 Leu Lys Asn Gly Tyr Gly Phe Val Glu Phe Glu Asp Ser Arg Asp Ala
 35 40 45
 Asp Asp Ala Val Tyr Glu Leu Asn Gly Lys Glu Leu Cys Gly Glu Arg
 50 55 60
 Val Ile Val Glu His Ala Arg Gly Pro Arg Arg Asp Arg Asp Gly Tyr
 65 70 75 80
 Ser Tyr Gly Ser Arg Ser Gly Gly Gly Gly Tyr Ser Ser Arg Arg Thr
 85 90 95
 Ser Gly Arg Asp Lys Tyr Gly Pro Pro Val Arg Thr Glu Tyr Arg Leu
 100 105 110
 Ile Val Glu Asn Leu Ser Ser Arg Cys Ser Trp Gln Asp Leu Lys Asp
 115 120 125
 Phe Met Arg Gln Ala Gly Glu Val Thr Tyr Ala Asp Ala His Lys Glu
 130 135 140

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Arg Thr Asn Glu Gly Val Ile Glu Phe Arg Ser Tyr Ser Asp Met Lys
145 150 155 160
Arg Ala Leu Asp Lys Leu Asp Gly Thr Glu Ile Asn Gly Arg Asn Ile
165 170 175
Arg Leu Ile Glu Asp Lys Pro Arg Thr Ser His Arg Arg Ser Tyr Ser
180 185 190
Gly Ser Arg Ser Arg Ser Arg Ser Arg Arg Ser Arg Ser Arg Ser
195 200 205
Arg Arg Ser Ser Arg Ser Arg Ser Arg Ser Ile Ser Lys Ser Arg Ser
210 215 220
Arg Ser Arg Ser Arg Ser Lys Gly Arg Ser Arg Ser Arg Ser Lys Gly
225 230 235 240
Arg Lys Ser Arg Ser Lys Ser Lys Ser Lys Pro Lys Ser Asp Arg Gly
245 250 255
Ser His Ser His Ser Arg Ser Arg Ser Lys Asp Glu Tyr Glu Lys Ser
260 265 270
Arg Ser Arg Ser Arg Ser Arg Ser Pro Lys Glu Asn Gly Lys Gly Asp
275 280 285
Ile Lys Ser Lys Ser Arg Ser Arg Ser Gln Ser Arg Ser Asn Ser Pro
290 295 300
Leu Pro Val Pro Pro Ser Lys Ala Arg Ser Val Ser Pro Pro Pro Lys
305 310 315 320
Arg Ala Thr Ser Arg Ser Arg Ser Arg Ser Arg Ser Lys Ser Arg Ser
325 330 335
Arg Ser Arg Ser Ser Ser Arg Asp
340

<210> 135

<211> 1231

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (79).. (957)

<223>

<400> 135

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agcttccacg ttaagacc atg gct gag ccc agt gac aac tct ctg agg att      111
      Met Ala Glu Pro Ser Asp Asn Ser Leu Arg Ile
              1              5              10
gtt ctg gta ggg aaa aca gga agt gga aag agc gcc aca gca aac acc      159
Val Leu Val Gly Lys Thr Gly Ser Gly Lys Ser Ala Thr Ala Asn Thr
              15              20              25
atc ctg ggg caa aag aga ttt gtt tct aga atc gca ccc cat gct gtc      207
Ile Leu Gly Gln Lys Arg Phe Val Ser Arg Ile Ala Pro His Ala Val
              30              35              40
acc cag aac tgt cag agt gac tcc cgc agg tgg aag gaa aga gac ctc      255
Thr Gln Asn Cys Gln Ser Asp Ser Arg Arg Trp Lys Glu Arg Asp Leu
              45              50              55
ctg gtt gtt gat acc cca ggg ctc ttc gac acc aag gta aaa ctg gaa      303
Leu Val Val Asp Thr Pro Gly Leu Phe Asp Thr Lys Val Lys Leu Glu
60              65              70              75
acc acc tgc ctt gaa atc agc cgg tgt gtc ctc cag tcc tgc cct ggg      351
Thr Thr Cys Leu Glu Ile Ser Arg Cys Val Leu Gln Ser Cys Pro Gly

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80	85	90	
cct cat gcc atc att ctg gtt ctg caa ctg aac cgc ttc acg gtg gaa			399
Pro His Ala Ile Ile Leu Val Leu Gln Leu Asn Arg Phe Thr Val Glu			
95	100	105	
gag caa gaa act gtt atc agg atc aag gct atc ttt ggg gag gaa gtc			447
Glu Gln Glu Thr Val Ile Arg Ile Lys Ala Ile Phe Gly Glu Glu Val			
110	115	120	
atg aag tac atg att gtc ttg ttc acc cgc aaa gat gat ctg gag gac			495
Met Lys Tyr Met Ile Val Leu Phe Thr Arg Lys Asp Asp Leu Glu Asp			
125	130	135	
cag agc tta agc gac ttc att gct gac tca gat aca aac ctg aaa agc			543
Gln Ser Leu Ser Asp Phe Ile Ala Asp Ser Asp Thr Asn Leu Lys Ser			
140	145	150	155
atc atc aag gag tgt ggc aat cgt tgc ctg gcc atc aat aac aaa gca			591
Ile Ile Lys Glu Cys Gly Asn Arg Cys Leu Ala Ile Asn Asn Lys Ala			
160	165	170	
gag agg gct gag agg gaa acg cag gtg cag gag ctg atg ggg ctt gta			639
Glu Arg Ala Glu Arg Glu Thr Gln Val Gln Glu Leu Met Gly Leu Val			
175	180	185	
gaa acc ctg gtg cag aac aat ggt ggt ctc tac ttc tcc cat ccc gta			687
Glu Thr Leu Val Gln Asn Asn Gly Gly Leu Tyr Phe Ser His Pro Val			
190	195	200	
tac aag gac gcg gag cga agg ctg aag aag caa gtg gag atc ttg agg			735
Tyr Lys Asp Ala Glu Arg Arg Leu Lys Lys Gln Val Glu Ile Leu Arg			
205	210	215	
aaa att tac act gac cta cca gag aag gag att aga ata gtg gag gag			783
Lys Ile Tyr Thr Asp Leu Pro Glu Lys Glu Ile Arg Ile Val Glu Glu			

3NSDOCID: <WO_____03104277A2_I_>

20 25 30
 Arg Phe Val Ser Arg Ile Ala Pro His Ala Val Thr Gln Asn Cys Gln
 35 40 45
 Ser Asp Ser Arg Arg Trp Lys Glu Arg Asp Leu Leu Val Val Asp Thr
 50 55 60
 Pro Gly Leu Phe Asp Thr Lys Val Lys Leu Glu Thr Thr Cys Leu Glu
 65 70 75 80
 Ile Ser Arg Cys Val Leu Gln Ser Cys Pro Gly Pro His Ala Ile Ile
 85 90 95
 Leu Val Leu Gln Leu Asn Arg Phe Thr Val Glu Glu Gln Glu Thr Val
 100 105 110
 Ile Arg Ile Lys Ala Ile Phe Gly Glu Glu Val Met Lys Tyr Met Ile
 115 120 125
 Val Leu Phe Thr Arg Lys Asp Asp Leu Glu Asp Gln Ser Leu Ser Asp
 130 135 140
 Phe Ile Ala Asp Ser Asp Thr Asn Leu Lys Ser Ile Ile Lys Glu Cys
 145 150 155 160
 Gly Asn Arg Cys Leu Ala Ile Asn Asn Lys Ala Glu Arg Ala Glu Arg
 165 170 175
 Glu Thr Gln Val Gln Glu Leu Met Gly Leu Val Glu Thr Leu Val Gln
 180 185 190
 Asn Asn Gly Gly Leu Tyr Phe Ser His Pro Val Tyr Lys Asp Ala Glu
 195 200 205
 Arg Arg Leu Lys Lys Gln Val Glu Ile Leu Arg Lys Ile Tyr Thr Asp
 210 215 220
 Leu Pro Glu Lys Glu Ile Arg Ile Val Glu Glu Glu Tyr Ala Leu Arg
 225 230 235 240

Lys Phe Ser Ala Gln Glu Arg Glu Lys Lys Ile Gln Ala Ile Arg Glu
 245 250 255
 Asn Tyr Asn Leu Lys Ile Arg Asn Leu Arg Glu Glu Ala Glu Lys Asn
 260 265 270
 Ile Phe Asn Gln Ile Ile Glu Glu Val Lys Lys Val Leu Leu Lys Ile
 275 280 285
 Trp His Leu Phe Ser
 290

<210> 137

<211> 1222

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (120).. (1019)

<223>

<400> 137

agcgtgggta aaagcaaaag caacagctca agcagcctcc ttggagaaaa cctgaaaatt 60
 caacttggtc aagagaaggt cttgtacgtg cctaagttct agagcctcct gacgtgagc 119
 atg gct gag agt gag gac cgc tcc ctg agg atc gtt ctg gta ggg aaa 167
 Met Ala Glu Ser Glu Asp Arg Ser Leu Arg Ile Val Leu Val Gly Lys
 1 5 10 15
 act gga agt ggg aaa agt gca aca gcg aac acc atc ctt gga gag gaa 215
 Thr Gly Ser Gly Lys Ser Ala Thr Ala Asn Thr Ile Leu Gly Glu Glu
 20 25 30
 atc ttt gat tct aga att gct gcc caa gct gtt acc aag aac tgt caa 263

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Ile Phe Asp Ser Arg Ile Ala Ala Gln Ala Val Thr Lys Asn Cys Gln
 35 40 45
 aaa gca tcc cgg gaa tgg cag ggg aga gac ctt ctt gtt gta gac act 311
 Lys Ala Ser Arg Glu Trp Gln Gly Arg Asp Leu Leu Val Val Asp Thr
 50 55 60
 cca ggg ctc ttt gac acc aag gag agc ctg gac acc acc tgc aag gaa 359
 Pro Gly Leu Phe Asp Thr Lys Glu Ser Leu Asp Thr Thr Cys Lys Glu
 65 70 75 80
 atc agc cgc tgc atc atc tcc tcc tgc cca ggg ccc cat gct att gtc 407
 Ile Ser Arg Cys Ile Ile Ser Ser Cys Pro Gly Pro His Ala Ile Val
 85 90 95
 cta gtt ctg ctg ctg ggc cgc tac aca gag gag gag cag aaa acc gtt 455
 Leu Val Leu Leu Leu Gly Arg Tyr Thr Glu Glu Glu Gln Lys Thr Val
 100 105 110
 gca ttg atc aag gct gtc ttt ggg aag tca gcc atg aag cac atg gtc 503
 Ala Leu Ile Lys Ala Val Phe Gly Lys Ser Ala Met Lys His Met Val
 115 120 125
 atc ttg ttc act cgc aaa gaa gag ttg gag ggc cag agc ttc cat gac 551
 Ile Leu Phe Thr Arg Lys Glu Glu Leu Glu Gly Gln Ser Phe His Asp
 130 135 140
 ttc ata gca gat gcg gat gtg ggc cta aaa agc atc gtc aag gag tgc 599
 Phe Ile Ala Asp Ala Asp Val Gly Leu Lys Ser Ile Val Lys Glu Cys
 145 150 155 160
 ggg aac cgc tgc tgt gcc ttt agc aac agc aag aaa acc agt aag gca 647
 Gly Asn Arg Cys Cys Ala Phe Ser Asn Ser Lys Lys Thr Ser Lys Ala
 165 170 175
 gag aag gaa agt caa gtg cag gag ttg gtg gag ctg ata gag aaa atg 695

Glu Lys Glu Ser Gln Val Gln Glu Leu Val Glu Leu Ile Glu Lys Met
 180 185 190
 gtg cag tgc aac gaa ggg gct tac ttt tct gat gac ata tac aag gac 743
 Val Gln Cys Asn Glu Gly Ala Tyr Phe Ser Asp Asp Ile Tyr Lys Asp
 195 200 205
 aca gag gaa agg ctg aaa caa cgg gaa gag gtt ttg agg aaa atc tac 791
 Thr Glu Glu Arg Leu Lys Gln Arg Glu Glu Val Leu Arg Lys Ile Tyr
 210 215 220
 act gac caa tta aat gaa gaa att aaa cta gta gaa gag gat aag cat 839
 Thr Asp Gln Leu Asn Glu Glu Ile Lys Leu Val Glu Glu Asp Lys His
 225 230 235 240
 aaa tca gag gaa gaa aag gag aaa gaa att aaa tta cta aaa tta aaa 887
 Lys Ser Glu Glu Glu Lys Glu Lys Glu Ile Lys Leu Leu Lys Leu Lys
 245 250 255
 tat gat gaa aaa ata aaa aat ata agg gaa gaa gct gag aga aat ata 935
 Tyr Asp Glu Lys Ile Lys Asn Ile Arg Glu Glu Ala Glu Arg Asn Ile
 260 265 270
 ttt aaa gat gtt ttt aat agg att tgg aag atg ctt tca gaa ata tgg 983
 Phe Lys Asp Val Phe Asn Arg Ile Trp Lys Met Leu Ser Glu Ile Trp
 275 280 285
 cat agg ttt ttg tgc aaa tgt aag ttt tat tct tcc taatttactg 1029
 His Arg Phe Leu Ser Lys Cys Lys Phe Tyr Ser Ser
 290 295 300
 tgatttgta atggatgaat tgtattttgc aaagatagtt agagaaatac ctccttcccc 1089
 ttagctttat taaggatatca ttgataaata aaaataaaat atgtttaatg tatataatgt 1149
 gatttttaaa tatatatata tatatacaca cattgtgaaa taatgaaata aaggtaatta 1209
 acacatctaa aac 1222

<210> 138

<211> 300

<212> PRT

<213> Homo sapiens

<400> 138

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 20 25 30
 Ile Phe Asp Ser Arg Ile Ala Ala Gln Ala Val Thr Lys Asn Cys Gln
 35 40 45
 Lys Ala Ser Arg Glu Trp Gln Gly Arg Asp Leu Leu Val Val Asp Thr
 50 55 60
 Pro Gly Leu Phe Asp Thr Lys Glu Ser Leu Asp Thr Thr Cys Lys Glu
 65 70 75 80
 Ile Ser Arg Cys Ile Ile Ser Ser Cys Pro Gly Pro His Ala Ile Val
 85 90 95
 Leu Val Leu Leu Leu Gly Arg Tyr Thr Glu Glu Glu Gln Lys Thr Val
 100 105 110
 Ala Leu Ile Lys Ala Val Phe Gly Lys Ser Ala Met Lys His Met Val
 115 120 125
 Ile Leu Phe Thr Arg Lys Glu Glu Leu Glu Gly Gln Ser Phe His Asp
 130 135 140
 Phe Ile Ala Asp Ala Asp Val Gly Leu Lys Ser Ile Val Lys Glu Cys
 145 150 155 160
 Gly Asn Arg Cys Cys Ala Phe Ser Asn Ser Lys Lys Thr Ser Lys Ala

165 170 175
 Glu Lys Glu Ser Gln Val Gln Glu Leu Val Glu Leu Ile Glu Lys Met
 180 185 190
 Val Gln Cys Asn Glu Gly Ala Tyr Phe Ser Asp Asp Ile Tyr Lys Asp
 195 200 205
 Thr Glu Glu Arg Leu Lys Gln Arg Glu Glu Val Leu Arg Lys Ile Tyr
 210 215 220
 Thr Asp Gln Leu Asn Glu Glu Ile Lys Leu Val Glu Glu Asp Lys His
 225 230 235 240
 Lys Ser Glu Glu Glu Lys Glu Lys Glu Ile Lys Leu Leu Lys Leu Lys
 245 250 255
 Tyr Asp Glu Lys Ile Lys Asn Ile Arg Glu Glu Ala Glu Arg Asn Ile
 260 265 270
 Phe Lys Asp Val Phe Asn Arg Ile Trp Lys Met Leu Ser Glu Ile Trp
 275 280 285
 His Arg Phe Leu Ser Lys Cys Lys Phe Tyr Ser Ser
 290 295 300

<210> 139
 <211> 1850
 <212> DNA
 <213> Mus musculus
 <220>
 <221> CDS
 <222> (58).. (1284)
 <223>
 <400> 139

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atg ttt atc tgg cgt tcc tta cta cag ctg ccg gaa aat cat act gca	105
Met Phe Ile Trp Arg Ser Leu Leu Gln Leu Pro Glu Asn His Thr Ala	
1 5 10 15	
ttt agt agc ttg gtg gac aaa ggg act cat gcg gct tat ctc agc ctt	153
Phe Ser Ser Leu Val Asp Lys Gly Thr His Ala Ala Tyr Leu Ser Leu	
20 25 30	
cag aag aaa tac ccc atc aaa agc agg aaa cta ctg aga gta ttg cag	201
Gln Lys Lys Tyr Pro Ile Lys Ser Arg Lys Leu Leu Arg Val Leu Gln	
35 40 45	
aga acc ctc tct gca tta gct cac tgg tct gca atc ttc agt gac aca	249
Arg Thr Leu Ser Ala Leu Ala His Trp Ser Ala Ile Phe Ser Asp Thr	
50 55 60	
cca tac ctt cca ctc ttg gca ttt cca ttt gta aaa tta ttc cag aac	297
Pro Tyr Leu Pro Leu Leu Ala Phe Pro Phe Val Lys Leu Phe Gln Asn	
65 70 75 80	
aat cag ctc atc tgt ttt gaa gtt gtg gct act ctc ata atc aat tgg	345
Asn Gln Leu Ile Cys Phe Glu Val Val Ala Thr Leu Ile Ile Asn Trp	
85 90 95	
tgt caa cat tgg ttt gag tac ttt cct aat cct cct atc aac att ctt	393
Cys Gln His Trp Phe Glu Tyr Phe Pro Asn Pro Pro Ile Asn Ile Leu	
100 105 110	
agc atg ata gaa aat gtt ttg gca ttt cat gac aag gag ctg ctg cag	441
Ser Met Ile Glu Asn Val Leu Ala Phe His Asp Lys Glu Leu Leu Gln	
115 120 125	
cac ttc ata gat cgt gat ata act tcc cag gtg tat gcc tgg cct ctc	489
His Phe Ile Asp Arg Asp Ile Thr Ser Gln Val Tyr Ala Trp Pro Leu	

130	135	140	
ctg gaa aca ctg ttc tca gaa gtg ctg acg aga gag gag tgg ctc cgc			537
Leu Glu Thr Leu Phe Ser Glu Val Leu Thr Arg Glu Glu Trp Leu Arg			
145	150	155	160
ctc ttc gat aac atc ttc tcc aat cac cct tcc ttc ctc ctg atg act			585
Leu Phe Asp Asn Ile Phe Ser Asn His Pro Ser Phe Leu Leu Met Thr			
165	170	175	
gtg gtg gcc tac agt acc tgc tcc aga gcg cct ttg ctc aac tgt act			633
Val Val Ala Tyr Ser Thr Cys Ser Arg Ala Pro Leu Leu Asn Cys Thr			
180	185	190	
ctt aag aat gac ttt gag tat ttt ttt cac cat cgg aat aac ctg gac			681
Leu Lys Asn Asp Phe Glu Tyr Phe Phe His His Arg Asn Asn Leu Asp			
195	200	205	
ata aat gtt gta att aga gaa gtt tat cat ctc atg gag aca acg cct			729
Ile Asn Val Val Ile Arg Glu Val Tyr His Leu Met Glu Thr Thr Pro			
210	215	220	
gct gat atc cac cca aat agc atg ctg gat gct ttc gtt gca ctg acg			777
Ala Asp Ile His Pro Asn Ser Met Leu Asp Ala Phe Val Ala Leu Thr			
225	230	235	240
aaa ggg cag tac cct ata ttt aat caa tat cca aag ttc att gtg gac			825
Lys Gly Gln Tyr Pro Ile Phe Asn Gln Tyr Pro Lys Phe Ile Val Asp			
245	250	255	
tac cag aca cgg gaa tgg gaa agg ata agg aac gat gaa ctg gac ttc			873
Tyr Gln Thr Arg Glu Trp Glu Arg Ile Arg Asn Asp Glu Leu Asp Phe			
260	265	270	
ttg aga gag agg cag aca gtt gaa aat atg caa gct gaa gtg gat gag			921
Leu Arg Glu Arg Gln Thr Val Glu Asn Met Gln Ala Glu Val Asp Glu			

435/617

275	280	285	
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Gln Arg Ala Lys Asp Glu Ala Trp Tyr Gln Lys Gln Glu Leu Leu Arg			
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aga gct gag gag aca aga aga gag ata ctt ctt caa gaa gag gag aag			1017
Arg Ala Glu Glu Thr Arg Arg Glu Ile Leu Leu Gln Glu Glu Lys			
305	310	315	320
atg gcc cag cag aga caa agg cta gct gcc gtg aaa agg gaa ctg gag			1065
Met Ala Gln Gln Arg Gln Arg Leu Ala Ala Val Lys Arg Glu Leu Glu			
325	330	335	
ata aag gaa ata cac tta cag ggt gct gcg agg aga cgc ttg ctg aag			1113
Ile Lys Glu Ile His Leu Gln Gly Ala Ala Arg Arg Arg Leu Leu Lys			
340	345	350	
ctt cag caa gat caa cgg gaa atg gag ctg cgc agg ctg gag gat gaa			1161
Leu Gln Gln Asp Gln Arg Glu Met Glu Leu Arg Arg Leu Glu Asp Glu			
355	360	365	
att gag aga aag gta caa atg aga gat caa gaa atc gct gcc aca gcc			1209
Ile Glu Arg Lys Val Gln Met Arg Asp Gln Glu Ile Ala Ala Thr Ala			
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aag gac ctg gaa ata agg cag ctg gaa ctc gaa gca caa aag cga ctt			1257
Lys Asp Leu Glu Ile Arg Gln Leu Glu Leu Glu Ala Gln Lys Arg Leu			
385	390	395	400
tat gag aag gta gaa agc agc tct ctc tgaaggagg aaagcgtgc			1304
Tyr Glu Lys Val Glu Ser Ser Ser Leu			
405			
ccttcagctg acctgtggac aaggctggac ccccttgtgg tttctagtat tcattctctt			1364
tatcctttat gcagaatata gtgtaactta gcaaatggca gaatgcatat gtgtaatgct			1424

tcgactcctg gttccccaac agtgtggcca catttccacg gtaccagatt gagcccaagt 1484
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<212> PRT

<213> Mus musculus

<400> 140

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 35 40 45
 Arg Thr Leu Ser Ala Leu Ala His Trp Ser Ala Ile Phe Ser Asp Thr
 50 55 60
 Pro Tyr Leu Pro Leu Leu Ala Phe Pro Phe Val Lys Leu Phe Gln Asn
 65 70 75 80
 Asn Gln Leu Ile Cys Phe Glu Val Val Ala Thr Leu Ile Ile Asn Trp
 85 90 95
 Cys Gln His Trp Phe Glu Tyr Phe Pro Asn Pro Pro Ile Asn Ile Leu

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100 105 110
Ser Met Ile Glu Asn Val Leu Ala Phe His Asp Lys Glu Leu Leu Gln
115 120 125
His Phe Ile Asp Arg Asp Ile Thr Ser Gln Val Tyr Ala Trp Pro Leu
130 135 140
Leu Glu Thr Leu Phe Ser Glu Val Leu Thr Arg Glu Glu Trp Leu Arg
145 150 155 160
Leu Phe Asp Asn Ile Phe Ser Asn His Pro Ser Phe Leu Leu Met Thr
165 170 175
Val Val Ala Tyr Ser Thr Cys Ser Arg Ala Pro Leu Leu Asn Cys Thr
180 185 190
Leu Lys Asn Asp Phe Glu Tyr Phe Phe His His Arg Asn Asn Leu Asp
195 200 205
Ile Asn Val Val Ile Arg Glu Val Tyr His Leu Met Glu Thr Thr Pro
210 215 220
Ala Asp Ile His Pro Asn Ser Met Leu Asp Ala Phe Val Ala Leu Thr
225 230 235 240
Lys Gly Gln Tyr Pro Ile Phe Asn Gln Tyr Pro Lys Phe Ile Val Asp
245 250 255
Tyr Gln Thr Arg Glu Trp Glu Arg Ile Arg Asn Asp Glu Leu Asp Phe
260 265 270
Leu Arg Glu Arg Gln Thr Val Glu Asn Met Gln Ala Glu Val Asp Glu
275 280 285
Gln Arg Ala Lys Asp Glu Ala Trp Tyr Gln Lys Gln Glu Leu Leu Arg
290 295 300
Arg Ala Glu Glu Thr Arg Arg Glu Ile Leu Leu Gln Glu Glu Lys
305 310 315 320

Met Ala Gln Gln Arg Gln Arg Leu Ala Ala Val Lys Arg Glu Leu Glu
 325 330 335
 Ile Lys Glu Ile His Leu Gln Gly Ala Ala Arg Arg Arg Leu Leu Lys
 340 345 350
 Leu Gln Gln Asp Gln Arg Glu Met Glu Leu Arg Arg Leu Glu Asp Glu
 355 360 365
 Ile Glu Arg Lys Val Gln Met Arg Asp Gln Glu Ile Ala Ala Thr Ala
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 Tyr Glu Lys Val Glu Ser Ser Ser Leu
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<222> (63).. (3050)

<223>

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 Met Gln Ser Thr Asp Leu Gly Asn Lys Glu Ser Gly Lys Ile Trp
 1 5 10 15
 cac cgc aag cca tcg cca gcc act cac gac gga att ata gtg aac att 155

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His Arg Lys Pro Ser Pro Ala Thr His Asp Gly Ile Ile Val Asn Ile
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 35 40 45
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 Val Ala Phe Asp Gly Ser Gly Asn Ser Phe Ile Ala Gly Asp His Gln
 50 55 60
 gga aac atc tat gtt ttt gac ttg cat gga aac agg ttt aat ctt gtt 299
 Gly Asn Ile Tyr Val Phe Asp Leu His Gly Asn Arg Phe Asn Leu Val
 65 70 75
 cag cga aca gca caa gcg tgc aca gct ctg gcc ttt aat ctt cgt aga 347
 Gln Arg Thr Ala Gln Ala Cys Thr Ala Leu Ala Phe Asn Leu Arg Arg
 80 85 90 95
 aag tct gag ttc ctt gtg gcg tta gct gat tat tct att aaa tgt ttt 395
 Lys Ser Glu Phe Leu Val Ala Leu Ala Asp Tyr Ser Ile Lys Cys Phe
 100 105 110
 gat aca gtc acc aag gag ctg gtt agc tgg atg aga gga cac gag tcg 443
 Asp Thr Val Thr Lys Glu Leu Val Ser Trp Met Arg Gly His Glu Ser
 115 120 125
 tcg gtg tgt tcc att tct gtg cac gca tct ggg aga tac gcc atc acc 491
 Ser Val Cys Ser Ile Ser Val His Ala Ser Gly Arg Tyr Ala Ile Thr
 130 135 140
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 Thr Ser Ser Asp Thr Ala Gln Leu Trp Asp Leu Asp Thr Phe Gln Arg
 145 150 155
 aag aga aag ctg aac atc cgc cag tcg gtg ggc ata cag aag gtt ttc 587

Lys Arg Lys Leu Asn Ile Arg Gln Ser Val Gly Ile Gln Lys Val Phe
 160 165 170 175
 ttt cta cca tta agt aac acc atc ctc agc tgt ttt aaa gac aac tcc 635
 Phe Leu Pro Leu Ser Asn Thr Ile Leu Ser Cys Phe Lys Asp Asn Ser
 180 185 190
 atc ttc gcc tgg gaa cgt gat act ctg ttt tgc aaa tac caa ttg cca 683
 Ile Phe Ala Trp Glu Arg Asp Thr Leu Phe Cys Lys Tyr Gln Leu Pro
 195 200 205
 ggt cca cct gag ggc tct aac atc tta tac aaa gtg ttt gct gtg acc 731
 Gly Pro Pro Glu Gly Ser Asn Ile Leu Tyr Lys Val Phe Ala Val Thr
 210 215 220
 aga gat ggc cga atc ttg gct gct gga ggc aaa tcc aat cac ctg cat 779
 Arg Asp Gly Arg Ile Leu Ala Ala Gly Gly Lys Ser Asn His Leu His
 225 230 235
 ttg tgg tgc ttg gag gcc aca ggg ctc ttc aga atc att cag atg cct 827
 Leu Trp Cys Leu Glu Ala Thr Gly Leu Phe Arg Ile Ile Gln Met Pro
 240 245 250 255
 gcg aag gta cga gct gtt cgc cat ctg gaa ttc ctg cct gat agc ttt 875
 Ala Lys Val Arg Ala Val Arg His Leu Glu Phe Leu Pro Asp Ser Phe
 260 265 270
 gat gcc ggt tcc aat cag gtt ctt ggt gtg cta agt caa gat ggg att 923
 Asp Ala Gly Ser Asn Gln Val Leu Gly Val Leu Ser Gln Asp Gly Ile
 275 280 285
 atg cgg ttt gtc aac ata cag act tgt aaa ctt ctc ttt gaa att ggg 971
 Met Arg Phe Val Asn Ile Gln Thr Cys Lys Leu Leu Phe Glu Ile Gly
 290 295 300
 act gtt gaa gaa gga att agc tcg tca gta att agt cca cac ggt cgg 1019

Thr Val Glu Glu Gly Ile Ser Ser Ser Val Ile Ser Pro His Gly Arg
 305 310 315
 tac ata gca tcc att atg gaa aat gga agt ctg aat gta tat tca gtt 1067
 Tyr Ile Ala Ser Ile Met Glu Asn Gly Ser Leu Asn Val Tyr Ser Val
 320 325 330 335
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 Gln Ala Leu Thr Gln Glu Ile Asn Lys Pro Pro Pro Pro Leu Val Lys
 340 345 350
 gtg att gaa gat ttg ccc agt aac aca gtg agt tcc agc aat ctt aaa 1163
 Val Ile Glu Asp Leu Pro Ser Asn Thr Val Ser Ser Ser Asn Leu Lys
 355 360 365
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 Met Lys Ile Met Pro Gly Arg Val Gln Arg Pro Ala Arg Cys Lys Glu
 370 375 380
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 Ser Lys Ile Pro Thr Arg Val Leu Lys Gln Asp Leu Thr Gly Asp Leu
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 Glu Asn Lys Glu Asn Glu Leu Ser Glu Gly Leu Asn Lys Lys Arg Leu
 400 405 410 415
 caa atc tta tta aaa ggc tat ggg gaa tat cca aca aaa tac aga atg 1355
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Ser Ser Leu Val Asp Lys Gly Thr His Ala Ala Tyr Leu Ser Leu Gln
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 aag aaa tac ccc atc aaa agc agg aaa cta ctg aga gta ttg cag aga 1499
 Lys Lys Tyr Pro Ile Lys Ser Arg Lys Leu Leu Arg Val Leu Gln Arg
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 acc ctc tct gca tta gct cac tgg tct gca atc ttc agt gac aca cca 1547
 Thr Leu Ser Ala Leu Ala His Trp Ser Ala Ile Phe Ser Asp Thr Pro
 480 485 490 495
 tac ctt cca ctc ttg gca ttt cca ttt gta aaa tta ttc cag aac aat 1595
 Tyr Leu Pro Leu Leu Ala Phe Pro Phe Val Lys Leu Phe Gln Asn Asn
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 Gln Leu Ile Cys Phe Glu Val Val Ala Thr Leu Ile Ile Asn Trp Cys
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 caa cat tgg ttt gag tac ttt cct aat cct cct atc aac att ctt agc 1691
 Gln His Trp Phe Glu Tyr Phe Pro Asn Pro Pro Ile Asn Ile Leu Ser
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 atg ata gaa aat gtt ttg gca ttt cat gac aag gag ctg ctg cag cac 1739
 Met Ile Glu Asn Val Leu Ala Phe His Asp Lys Glu Leu Leu Gln His
 545 550 555
 ttc ata gat cgt gat ata act tcc cag gtg tat gcc tgg cct ctc ctg 1787
 Phe Ile Asp Arg Asp Ile Thr Ser Gln Val Tyr Ala Trp Pro Leu Leu
 560 565 570 575
 gaa aca ctg ttc tca gaa gtg ctg acg aga gag gag tgg ctc cgc ctc 1835
 Glu Thr Leu Phe Ser Glu Val Leu Thr Arg Glu Glu Trp Leu Arg Leu
 580 585 590
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Phe Asp Asn Ile Phe Ser Asn His Pro Ser Phe Leu Leu Met Thr Val
 595 600 605
 gtg gcc tac agt acc tgc tcc aga gcg cct ttg ctc aac tgt act ctt 1931
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 aag aat gac ttt gag tat ttt ttt cac cat cgg aat aac ctg gac ata 1979
 Lys Asn Asp Phe Glu Tyr Phe Phe His His Arg Asn Asn Leu Asp Ile
 625 630 635
 aat gtt gta att aga gaa gtt tat cat ctc atg gag aca acg cct gct 2027
 Asn Val Val Ile Arg Glu Val Tyr His Leu Met Glu Thr Thr Pro Ala
 640 645 650 655
 gat atc cac cca aat agc atg ctg gat gct ttc gtt gca ctg acg aaa 2075
 Asp Ile His Pro Asn Ser Met Leu Asp Ala Phe Val Ala Leu Thr Lys
 660 665 670
 ggg cag tac cct ata ttt aat caa tat cca aag ttc att gtg gac tac 2123
 Gly Gln Tyr Pro Ile Phe Asn Gln Tyr Pro Lys Phe Ile Val Asp Tyr
 675 680 685
 cag aca cgg gaa tgg gaa agg ata agg aac gat gaa ctg gac ttc ttg 2171
 Gln Thr Arg Glu Trp Glu Arg Ile Arg Asn Asp Glu Leu Asp Phe Leu
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 Arg Glu Arg Gln Thr Val Glu Asn Met Gln Ala Glu Val Asp Glu Gln
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 aga gct aag gat gag gcg tgg tac cag aag cag gag ctg ctc cgc aga 2267
 Arg Ala Lys Asp Glu Ala Trp Tyr Gln Lys Gln Glu Leu Leu Arg Arg
 720 725 730 735
 gct gag gag aca aga aga gag ata ctt ctt caa gaa gag gag aag atg 2315

Ala Glu Glu Thr Arg Arg Glu Ile Leu Leu Gln Glu Glu Glu Lys Met
740 745 750
gcc cag cag aga caa agg cta gct gcc gtg aaa agg gaa ctg gag ata 2363
Ala Gln Gln Arg Gln Arg Leu Ala Ala Val Lys Arg Glu Leu Glu Ile
755 760 765
aag gaa ata cac tta cag gat gct gcg agg aga cgc ttg ctg aag ctt 2411
Lys Glu Ile His Leu Gln Asp Ala Ala Arg Arg Arg Leu Leu Lys Leu
770 775 780
cag caa gat caa cgg gaa atg gag ctg cgc agg ctg gag gat gaa att 2459
Gln Gln Asp Gln Arg Glu Met Glu Leu Arg Arg Leu Glu Asp Glu Ile
785 790 795
gag aga aag gta caa atg gga gat caa gaa atc gct gcc aca gcc aag 2507
Glu Arg Lys Val Gln Met Gly Asp Gln Glu Ile Ala Ala Thr Ala Lys
800 805 810 815
gac ctg gaa ata agg cag ctg gaa ctc gaa gca caa aag cga ctt tat 2555
Asp Leu Glu Ile Arg Gln Leu Glu Leu Glu Ala Gln Lys Arg Leu Tyr
820 825 830
gag aag gat ctt act aca agt caa gag gct gtt gcc aaa gaa atc cga 2603
Glu Lys Asp Leu Thr Thr Ser Gln Glu Ala Val Ala Lys Glu Ile Arg
835 840 845
gaa gat aca gat gcc cat agg cgg aaa gcg gct ctg gaa gaa cac atg 2651
Glu Asp Thr Asp Ala His Arg Arg Lys Ala Ala Leu Glu Glu His Met
850 855 860
ttc cag aag ctg cta gag aac agc cag atg ggg ggc aga agg gcg cag 2699
Phe Gln Lys Leu Leu Glu Asn Ser Gln Met Gly Gly Arg Arg Ala Gln
865 870 875
agg tgg aag gaa gcc gaa gag aag gaa ttc cat ttg caa tca gca aag 2747

Arg Trp Lys Glu Ala Glu Glu Lys Glu Phe His Leu Gln Ser Ala Lys
 880 885 890 895
 aaa gcc tct gcc ctt tca gat gcc tct cga aag tgg ttt tta agg cag 2795
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 Gln Tyr Met Asp Ser Ala Tyr Leu Pro Gln Thr Ser Arg Leu His Asp
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 Val Ser Asp Met Asp Pro Ser Thr His Ile Phe Ser Arg Asn Tyr Pro
 945 950 955
 aca gaa tgg aac cac atg gaa cac gac ctt ctc aag aac gtg cga gat 2987
 Thr Glu Trp Asn His Met Glu His Asp Leu Leu Lys Asn Val Arg Asp
 960 965 970 975
 ctt cgc agg aga ctc aca gcc cgg gct cgg aac agc tgt cgg cac cct 3035
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 980 985 990
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 995
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 ttttgtatag agaaatatgt ctataaaatt atgttttcta ttgaattata atgctttggc 3210
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<211> 996

<212> PRT

<213> Mus musculus

<400> 142

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 35 40 45
 Ala Phe Asp Gly Ser Gly Asn Ser Phe Ile Ala Gly Asp His Gln Gly
 50 55 60
 Asn Ile Tyr Val Phe Asp Leu His Gly Asn Arg Phe Asn Leu Val Gln
 65 70 75 80
 Arg Thr Ala Gln Ala Cys Thr Ala Leu Ala Phe Asn Leu Arg Arg Lys
 85 90 95
 Ser Glu Phe Leu Val Ala Leu Ala Asp Tyr Ser Ile Lys Cys Phe Asp
 100 105 110
 Thr Val Thr Lys Glu Leu Val Ser Trp Met Arg Gly His Glu Ser Ser
 115 120 125
 Val Cys Ser Ile Ser Val His Ala Ser Gly Arg Tyr Ala Ile Thr Thr
 130 135 140
 Ser Ser Asp Thr Ala Gln Leu Trp Asp Leu Asp Thr Phe Gln Arg Lys
 145 150 155 160
 Arg Lys Leu Asn Ile Arg Gln Ser Val Gly Ile Gln Lys Val Phe Phe
 165 170 175

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Leu Pro Leu Ser Asn Thr Ile Leu Ser Cys Phe Lys Asp Asn Ser Ile
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Phe Ala Trp Glu Arg Asp Thr Leu Phe Cys Lys Tyr Gln Leu Pro Gly
195 200 205
Pro Pro Glu Gly Ser Asn Ile Leu Tyr Lys Val Phe Ala Val Thr Arg
210 215 220
Asp Gly Arg Ile Leu Ala Ala Gly Gly Lys Ser Asn His Leu His Leu
225 230 235 240
Trp Cys Leu Glu Ala Thr Gly Leu Phe Arg Ile Ile Gln Met Pro Ala
245 250 255
Lys Val Arg Ala Val Arg His Leu Glu Phe Leu Pro Asp Ser Phe Asp
260 265 270
Ala Gly Ser Asn Gln Val Leu Gly Val Leu Ser Gln Asp Gly Ile Met
275 280 285
Arg Phe Val Asn Ile Gln Thr Cys Lys Leu Leu Phe Glu Ile Gly Thr
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Val Glu Glu Gly Ile Ser Ser Ser Val Ile Ser Pro His Gly Arg Tyr
305 310 315 320
Ile Ala Ser Ile Met Glu Asn Gly Ser Leu Asn Val Tyr Ser Val Gln
325 330 335
Ala Leu Thr Gln Glu Ile Asn Lys Pro Pro Pro Pro Leu Val Lys Val
340 345 350
Ile Glu Asp Leu Pro Ser Asn Thr Val Ser Ser Ser Asn Leu Lys Met
355 360 365
Lys Ile Met Pro Gly Arg Val Gln Arg Pro Ala Arg Cys Lys Glu Ser
370 375 380
Lys Ile Pro Thr Arg Val Leu Lys Gln Asp Leu Thr Gly Asp Leu Glu

385 390 395 400
Asn Lys Glu Asn Glu Leu Ser Glu Gly Leu Asn Lys Lys Arg Leu Gln
 405 410 415
Ile Leu Leu Lys Gly Tyr Gly Glu Tyr Pro Thr Lys Tyr Arg Met Phe
 420 425 430
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 435 440 445
Ser Leu Val Asp Lys Gly Thr His Ala Ala Tyr Leu Ser Leu Gln Lys
 450 455 460
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465 470 475 480
Leu Ser Ala Leu Ala His Trp Ser Ala Ile Phe Ser Asp Thr Pro Tyr
 485 490 495
Leu Pro Leu Leu Ala Phe Pro Phe Val Lys Leu Phe Gln Asn Asn Gln
 500 505 510
Leu Ile Cys Phe Glu Val Val Ala Thr Leu Ile Ile Asn Trp Cys Gln
 515 520 525
His Trp Phe Glu Tyr Phe Pro Asn Pro Pro Ile Asn Ile Leu Ser Met
 530 535 540
Ile Glu Asn Val Leu Ala Phe His Asp Lys Glu Leu Leu Gln His Phe
545 550 555 560
Ile Asp Arg Asp Ile Thr Ser Gln Val Tyr Ala Trp Pro Leu Leu Glu
 565 570 575
Thr Leu Phe Ser Glu Val Leu Thr Arg Glu Glu Trp Leu Arg Leu Phe
 580 585 590
Asp Asn Ile Phe Ser Asn His Pro Ser Phe Leu Leu Met Thr Val Val
 595 600 605

Ala Tyr Ser Thr Cys Ser Arg Ala Pro Leu Leu Asn Cys Thr Leu Lys
610 615 620
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Ile His Pro Asn Ser Met Leu Asp Ala Phe Val Ala Leu Thr Lys Gly
660 665 670
Gln Tyr Pro Ile Phe Asn Gln Tyr Pro Lys Phe Ile Val Asp Tyr Gln
675 680 685
Thr Arg Glu Trp Glu Arg Ile Arg Asn Asp Glu Leu Asp Phe Leu Arg
690 695 700
Glu Arg Gln Thr Val Glu Asn Met Gln Ala Glu Val Asp Glu Gln Arg
705 710 715 720
Ala Lys Asp Glu Ala Trp Tyr Gln Lys Gln Glu Leu Leu Arg Arg Ala
725 730 735
Glu Glu Thr Arg Arg Glu Ile Leu Leu Gln Glu Glu Glu Lys Met Ala
740 745 750
Gln Gln Arg Gln Arg Leu Ala Ala Val Lys Arg Glu Leu Glu Ile Lys
755 760 765
Glu Ile His Leu Gln Asp Ala Ala Arg Arg Arg Leu Leu Lys Leu Gln
770 775 780
Gln Asp Gln Arg Glu Met Glu Leu Arg Arg Leu Glu Asp Glu Ile Glu
785 790 795 800
Arg Lys Val Gln Met Gly Asp Gln Glu Ile Ala Ala Thr Ala Lys Asp
805 810 815
Leu Glu Ile Arg Gln Leu Glu Leu Glu Ala Gln Lys Arg Leu Tyr Glu

820 825 830
Lys Asp Leu Thr Thr Ser Gln Glu Ala Val Ala Lys Glu Ile Arg Glu
835 840 845
Asp Thr Asp Ala His Arg Arg Lys Ala Ala Leu Glu Glu His Met Phe
850 855 860
Gln Lys Leu Leu Glu Asn Ser Gln Met Gly Gly Arg Arg Ala Gln Arg
865 870 875 880
Trp Lys Glu Ala Glu Glu Lys Glu Phe His Leu Gln Ser Ala Lys Lys
885 890 895
Ala Ser Ala Leu Ser Asp Ala Ser Arg Lys Trp Phe Leu Arg Gln Glu
900 905 910
Thr Ser Ala Ala Leu Glu His Glu Glu Met Pro Trp Leu Gln Arg Gln
915 920 925
Tyr Met Asp Ser Ala Tyr Leu Pro Gln Thr Ser Arg Leu His Asp Val
930 935 940
Ser Asp Met Asp Pro Ser Thr His Ile Phe Ser Arg Asn Tyr Pro Thr
945 950 955 960
Glu Trp Asn His Met Glu His Asp Leu Leu Lys Asn Val Arg Asp Leu
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<211> 3503

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<221> CDS

<222> (92).. (3289)

<223>

<400> 143

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Asn Lys Glu Ser Gly Lys Ile Trp His Arg Lys Pro Ser Pro Ala Thr
      10             15             20

cgg gac gga att ata gtg aac att att cac aac act tcc gat tac cat      208
Arg Asp Gly Ile Ile Val Asn Ile Ile His Asn Thr Ser Asp Tyr His
      25             30             35

cca aaa gtt ttg cga ttt ttg aat gtg gct ttt gac ggc aca ggc gac      256
Pro Lys Val Leu Arg Phe Leu Asn Val Ala Phe Asp Gly Thr Gly Asp
      40             45             50             55

tgc tta att gct ggg gac cac caa gga aat att tat gtt ttt gac tta      304
Cys Leu Ile Ala Gly Asp His Gln Gly Asn Ile Tyr Val Phe Asp Leu
      60             65             70

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His Gly Asn Arg Phe Asn Leu Val Gln Arg Thr Ala Gln Ala Cys Thr
      75             80             85

gct ctg gcc ttt aat ctt cgt agg aaa tct gaa ttc ctt gtg gca tta      400
Ala Leu Ala Phe Asn Leu Arg Arg Lys Ser Glu Phe Leu Val Ala Leu

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90	95	100	
gct gat tat tct att aaa tgt ttt gat aca gtc acc aag gag cta gtt			448
Ala Asp Tyr Ser Ile Lys Cys Phe Asp Thr Val Thr Lys Glu Leu Val			
105	110	115	
agc tgg atg aga gga cat gaa tca tca gta ttt tcg atc tct gtg cat			496
Ser Trp Met Arg Gly His Glu Ser Ser Val Phe Ser Ile Ser Val His			
120	125	130	135
gca tca ggg aaa tat gcc atc aca act tct tct gat aca gca caa tta			544
Ala Ser Gly Lys Tyr Ala Ile Thr Thr Ser Ser Asp Thr Ala Gln Leu			
	140	145	150
tgg gac ttg gat acc ttt cag aga aaa aga aag ctg aat att cgc cag			592
Trp Asp Leu Asp Thr Phe Gln Arg Lys Arg Lys Leu Asn Ile Arg Gln			
	155	160	165
tct gtg ggt ata cag aag gtt ttc ttt cta cca tta agt aat acc atc			640
Ser Val Gly Ile Gln Lys Val Phe Phe Leu Pro Leu Ser Asn Thr Ile			
170	175	180	
ctc agc tgt ttt aaa gat aat tcc att ttt gcc tgg gaa tgt gac aca			688
Leu Ser Cys Phe Lys Asp Asn Ser Ile Phe Ala Trp Glu Cys Asp Thr			
185	190	195	
ctt ttt tgc aaa tat caa ttg cca gct cca cct gaa agc tct agt ata			736
Leu Phe Cys Lys Tyr Gln Leu Pro Ala Pro Pro Glu Ser Ser Ser Ile			
200	205	210	215
tta tac aaa gtg ttt gct gta acc aga gat ggc cga atc ctg gct gct			784
Leu Tyr Lys Val Phe Ala Val Thr Arg Asp Gly Arg Ile Leu Ala Ala			
	220	225	230
gga ggc aag tca aat cat ctt cat ttg tgg tgc ttg gaa gct agg cag			832
Gly Gly Lys Ser Asn His Leu His Leu Trp Cys Leu Glu Ala Arg Gln			

235	240	245	
ctc ttt aga att atc cag atg ccc act aaa gtt cga gcc att cgc cat			880
Leu Phe Arg Ile Ile Gln Met Pro Thr Lys Val Arg Ala Ile Arg His			
250	255	260	
ctg gaa ttt ctt cct gat agt ttt gat gct ggt tct aat cag gtt ctt			928
Leu Glu Phe Leu Pro Asp Ser Phe Asp Ala Gly Ser Asn Gln Val Leu			
265	270	275	
gga gta cta agt caa gat ggt att atg aga ttt atc aat atg cag act			976
Gly Val Leu Ser Gln Asp Gly Ile Met Arg Phe Ile Asn Met Gln Thr			
280	285	290	295
tgt aaa ctt ctc ttt gag att ggg agc ctc gat gaa gga att agc tca			1024
Cys Lys Leu Leu Phe Glu Ile Gly Ser Leu Asp Glu Gly Ile Ser Ser			
300	305	310	
tca gca att agc cca cat gga cgg tac att gca tct att atg gaa aat			1072
Ser Ala Ile Ser Pro His Gly Arg Tyr Ile Ala Ser Ile Met Glu Asn			
315	320	325	
gga agt cta aac ata tat tca gtt cag gct tta aca caa gaa ata aat			1120
Gly Ser Leu Asn Ile Tyr Ser Val Gln Ala Leu Thr Gln Glu Ile Asn			
330	335	340	
aag cca cct ccg cct tta gtg aaa gtt att gaa gat ttg ccc aat aat			1168
Lys Pro Pro Pro Pro Leu Val Lys Val Ile Glu Asp Leu Pro Asn Asn			
345	350	355	
aaa ctg agt tcc agt gat ctt aag atg aaa gta aca tca ggg aga gta			1216
Lys Leu Ser Ser Ser Asp Leu Lys Met Lys Val Thr Ser Gly Arg Val			
360	365	370	375
cag cag cca gca aaa tct agg gaa agc aaa atg caa act aga ata tta			1264
Gln Gln Pro Ala Lys Ser Arg Glu Ser Lys Met Gln Thr Arg Ile Leu			

380	385	390	
aaa caa gac ctg act ggt gat ttt gaa agt aaa aag aat gaa tta cca			1312
Lys Gln Asp Leu Thr Gly Asp Phe Glu Ser Lys Lys Asn Glu Leu Pro			
395	400	405	
gat gga tta aac aaa aag cgt tta caa atc tta tta aaa ggc tat ggt			1360
Asp Gly Leu Asn Lys Lys Arg Leu Gln Ile Leu Leu Lys Gly Tyr Gly			
410	415	420	
gaa tat cca aca aaa tac aga atg ttc att tgg cgc tct ctg cta caa			1408
Glu Tyr Pro Thr Lys Tyr Arg Met Phe Ile Trp Arg Ser Leu Leu Gln			
425	430	435	
ctg cct gaa aat cat act gcg ttt agt acc ctc ata gat aag ggg act			1456
Leu Pro Glu Asn His Thr Ala Phe Ser Thr Leu Ile Asp Lys Gly Thr			
440	445	450	455
cat gtg gcg ttt ctc aac ctt cag aag aaa tac ccc atc aaa agt agg			1504
His Val Ala Phe Leu Asn Leu Gln Lys Lys Tyr Pro Ile Lys Ser Arg			
460	465	470	
aag cta ctc aga gta tta cag aga acc tta tct gca tta gct cac tgg			1552
Lys Leu Leu Arg Val Leu Gln Arg Thr Leu Ser Ala Leu Ala His Trp			
475	480	485	
tct gtc att ttt agt gac aca cca tat ctt cca ctc ttg gca ttt cca			1600
Ser Val Ile Phe Ser Asp Thr Pro Tyr Leu Pro Leu Leu Ala Phe Pro			
490	495	500	
ttt gta aaa tta ttc cag aac aac caa ctc atc tgt ttt gaa gtt att			1648
Phe Val Lys Leu Phe Gln Asn Asn Gln Leu Ile Cys Phe Glu Val Ile			
505	510	515	
gct act ctc ata atc aat tgg tgt caa cac tgg ttt gaa tat ttt cct			1696
Ala Thr Leu Ile Ile Asn Trp Cys Gln His Trp Phe Glu Tyr Phe Pro			

520	525	530	535	
aat cct cct atc aat att ctt agc atg ata gaa aat gtt ttg gca ttt				1744
Asn Pro Pro Ile Asn Ile Leu Ser Met Ile Glu Asn Val Leu Ala Phe				
540	545	550		
cat gac aag gaa ctg ctg caa cac ttc ata gat cat gat ata acc tcc				1792
His Asp Lys Glu Leu Leu Gln His Phe Ile Asp His Asp Ile Thr Ser				
555	560	565		
cag cta tat gca tgg cct ctt ctt gaa act gtg ttc tca gaa gtg ctg				1840
Gln Leu Tyr Ala Trp Pro Leu Leu Glu Thr Val Phe Ser Glu Val Leu				
570	575	580		
aca aga gag gag tgg ctg aaa ttg ttc gat aat atc ttt tcc aac cat				1888
Thr Arg Glu Glu Trp Leu Lys Leu Phe Asp Asn Ile Phe Ser Asn His				
585	590	595		
cct tcc ttc ctt ctg atg act gtt gta gcc tac aac ata tgt tct aga				1936
Pro Ser Phe Leu Leu Met Thr Val Val Ala Tyr Asn Ile Cys Ser Arg				
600	605	610	615	
acg cct ctg ctc agc tgt aat ctt aaa gat gac ttt gag ttt ttt ttt				1984
Thr Pro Leu Leu Ser Cys Asn Leu Lys Asp Asp Phe Glu Phe Phe Phe				
620	625	630		
cac cat cgg aat aac ctg gat ata aat gtt gtg att aga caa gtt tat				2032
His His Arg Asn Asn Leu Asp Ile Asn Val Val Ile Arg Gln Val Tyr				
635	640	645		
cat ctc atg gag acc acg cct act gac att cat cca gac agc atg ctt				2080
His Leu Met Glu Thr Thr Pro Thr Asp Ile His Pro Asp Ser Met Leu				
650	655	660		
aat gtt ttt gtt gca ctg aca aaa ggg cag tat cca gta ttt aat caa				2128
Asn Val Phe Val Ala Leu Thr Lys Gly Gln Tyr Pro Val Phe Asn Gln				

665	670	675	
tat cca aag ttt att gtg gac tat caa aca cag gaa cga gaa aga ata			2176
Tyr Pro Lys Phe Ile Val Asp Tyr Gln Thr Gln Glu Arg Glu Arg Ile			
680	685	690	695
agg aat gat gaa ttg gat tac tta aga gag agg cag aca gtt gaa gat			2224
Arg Asn Asp Glu Leu Asp Tyr Leu Arg Glu Arg Gln Thr Val Glu Asp			
700	705	710	
atg caa gct aaa gtc gac cag caa aga gtt gaa gat gaa gct tgg tac			2272
Met Gln Ala Lys Val Asp Gln Gln Arg Val Glu Asp Glu Ala Trp Tyr			
715	720	725	
cag aaa cag gag ctg ctt cgt aaa gct gaa gaa aca aga aga gaa atg			2320
Gln Lys Gln Glu Leu Leu Arg Lys Ala Glu Glu Thr Arg Arg Glu Met			
730	735	740	
ctc tta caa gag gag gag aaa atg ata caa caa aga cag agg cta gct			2368
Leu Leu Gln Glu Glu Glu Lys Met Ile Gln Gln Arg Gln Arg Leu Ala			
745	750	755	
gct gtg aaa aga gag ctg aaa gta aag gaa atg cac tta caa gat gct			2416
Ala Val Lys Arg Glu Leu Lys Val Lys Glu Met His Leu Gln Asp Ala			
760	765	770	775
gca aga agg cgt ttt ctg aag ctt cag caa gat caa cag gaa atg gag			2464
Ala Arg Arg Arg Phe Leu Lys Leu Gln Gln Asp Gln Gln Glu Met Glu			
780	785	790	
cta aga aga ctg gat gat gaa att ggg aga aag gta tat atg aga gat			2512
Leu Arg Arg Leu Asp Asp Glu Ile Gly Arg Lys Val Tyr Met Arg Asp			
795	800	805	
cga gaa att gct gcc aca gcc aga gac cta gaa atg aga cag ctg gaa			2560
Arg Glu Ile Ala Ala Thr Ala Arg Asp Leu Glu Met Arg Gln Leu Glu			

810	815	820	
ctc gaa tca caa aag aga ctt tat gag aag aat ctt act gaa aat caa			2608
Leu Glu Ser Gln Lys Arg Leu Tyr Glu Lys Asn Leu Thr Glu Asn Gln			
825	830	835	
gaa gct ctt gca aaa gaa atg cga gca gat gca gat gcc tat aga cga			2656
Glu Ala Leu Ala Lys Glu Met Arg Ala Asp Ala Asp Ala Tyr Arg Arg			
840	845	850	855
aaa gtg gat ctt gaa gaa cac atg ttt cat aag ctg ata gaa gca ggt			2704
Lys Val Asp Leu Glu Glu His Met Phe His Lys Leu Ile Glu Ala Gly			
860	865	870	
gaa acc cag agc cag aaa act cag aag gtg att aaa gaa aat ttg gca			2752
Glu Thr Gln Ser Gln Lys Thr Gln Lys Val Ile Lys Glu Asn Leu Ala			
875	880	885	
aag gct gaa caa gca tgc cta aat acc gac tgg cag att cag tct tta			2800
Lys Ala Glu Gln Ala Cys Leu Asn Thr Asp Trp Gln Ile Gln Ser Leu			
890	895	900	
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His Lys Gln Lys Cys Asp Asp Leu Gln Arg Asn Lys Cys Tyr Gln Glu			
905	910	915	
gta gcc aaa ctc ctt agg gaa aac aga agg aaa gaa ata gag ata ata			2896
Val Ala Lys Leu Leu Arg Glu Asn Arg Arg Lys Glu Ile Glu Ile Ile			
920	925	930	935
aat gca atg gtg gag gag gaa gcc aag aag tgg aag gaa gct gaa gga			2944
Asn Ala Met Val Glu Glu Glu Ala Lys Lys Trp Lys Glu Ala Glu Gly			
940	945	950	
aaa gag ttc cgt ttg aga tca gca aag aaa gct tct gct ctt tca gat			2992
Lys Glu Phe Arg Leu Arg Ser Ala Lys Lys Ala Ser Ala Leu Ser Asp			

955	960	965	
gcg tct aga aag tgg ttt tta aag caa gag ata aat gcg gct gta gaa			3040
Ala Ser Arg Lys Trp Phe Leu Lys Gln Glu Ile Asn Ala Ala Val Glu			
970	975	980	
cat gct gaa aat cca tgt cat aaa gaa gaa ccc agg ttc caa aat gaa			3088
His Ala Glu Asn Pro Cys His Lys Glu Glu Pro Arg Phe Gln Asn Glu			
985	990	995	
cag gac tca agc tgt ttg cct aga acc tca caa tta aat gac tct			3133
Gln Asp Ser Ser Cys Leu Pro Arg Thr Ser Gln Leu Asn Asp Ser			
1000	1005	1010	
tct gaa atg gat ccc tca aca cag att tct tta aat aga aga gca			3178
Ser Glu Met Asp Pro Ser Thr Gln Ile Ser Leu Asn Arg Arg Ala			
1015	1020	1025	
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Val Glu Trp Asp Thr Thr Gly Gln Asn Leu Ile Lys Lys Val Arg			
1030	1035	1040	
aat ctt cgc cag aga ctc act gcc egg gct cgt cac aga tgt caa			3268
Asn Leu Arg Gln Arg Leu Thr Ala Arg Ala Arg His Arg Cys Gln			
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Thr Pro His Leu Leu Ala Ala			
1060	1065		
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taaagatcag ccctttgtac agaaaaatgt gtctataaaa attatgtgtt atttaattct			3439
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tggt			3503

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35 40 45

Ala Phe Asp Gly Thr Gly Asp Cys Leu Ile Ala Gly Asp His Gln Gly

50 55 60

Asn Ile Tyr Val Phe Asp Leu His Gly Asn Arg Phe Asn Leu Val Gln

65 70 75 80

Arg Thr Ala Gln Ala Cys Thr Ala Leu Ala Phe Asn Leu Arg Arg Lys

85 90 95

Ser Glu Phe Leu Val Ala Leu Ala Asp Tyr Ser Ile Lys Cys Phe Asp

100 105 110

Thr Val Thr Lys Glu Leu Val Ser Trp Met Arg Gly His Glu Ser Ser

115 120 125

Val Phe Ser Ile Ser Val His Ala Ser Gly Lys Tyr Ala Ile Thr Thr

130 135 140

Ser Ser Asp Thr Ala Gln Leu Trp Asp Leu Asp Thr Phe Gln Arg Lys

145 150 155 160

Arg Lys Leu Asn Ile Arg Gln Ser Val Gly Ile Gln Lys Val Phe Phe

165 170 175

Leu Pro Leu Ser Asn Thr Ile Leu Ser Cys Phe Lys Asp Asn Ser Ile
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Phe Ala Trp Glu Cys Asp Thr Leu Phe Cys Lys Tyr Gln Leu Pro Ala
195 200 205
Pro Pro Glu Ser Ser Ser Ile Leu Tyr Lys Val Phe Ala Val Thr Arg
210 215 220
Asp Gly Arg Ile Leu Ala Ala Gly Gly Lys Ser Asn His Leu His Leu
225 230 235 240
Trp Cys Leu Glu Ala Arg Gln Leu Phe Arg Ile Ile Gln Met Pro Thr
245 250 255
Lys Val Arg Ala Ile Arg His Leu Glu Phe Leu Pro Asp Ser Phe Asp
260 265 270
Ala Gly Ser Asn Gln Val Leu Gly Val Leu Ser Gln Asp Gly Ile Met
275 280 285
Arg Phe Ile Asn Met Gln Thr Cys Lys Leu Leu Phe Glu Ile Gly Ser
290 295 300
Leu Asp Glu Gly Ile Ser Ser Ser Ala Ile Ser Pro His Gly Arg Tyr
305 310 315 320
Ile Ala Ser Ile Met Glu Asn Gly Ser Leu Asn Ile Tyr Ser Val Gln
325 330 335
Ala Leu Thr Gln Glu Ile Asn Lys Pro Pro Pro Pro Leu Val Lys Val
340 345 350
Ile Glu Asp Leu Pro Asn Asn Lys Leu Ser Ser Ser Asp Leu Lys Met
355 360 365
Lys Val Thr Ser Gly Arg Val Gln Gln Pro Ala Lys Ser Arg Glu Ser
370 375 380
Lys Met Gln Thr Arg Ile Leu Lys Gln Asp Leu Thr Gly Asp Phe Glu

385 390 395 400
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 405 410 415
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 530 535 540
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545 550 555 560
Ile Asp His Asp Ile Thr Ser Gln Leu Tyr Ala Trp Pro Leu Leu Glu
 565 570 575
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Asp Asn Ile Phe Ser Asn His Pro Ser Phe Leu Leu Met Thr Val Val
 595 600 605

Ala Tyr Asn Ile Cys Ser Arg Thr Pro Leu Leu Ser Cys Asn Leu Lys
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Asp Asp Phe Glu Phe Phe Phe His His Arg Asn Asn Leu Asp Ile Asn
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Val Val Ile Arg Gln Val Tyr His Leu Met Glu Thr Thr Pro Thr Asp
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Gln Tyr Pro Val Phe Asn Gln Tyr Pro Lys Phe Ile Val Asp Tyr Gln
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690 695 700
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705 710 715 720
Val Glu Asp Glu Ala Trp Tyr Gln Lys Gln Glu Leu Leu Arg Lys Ala
725 730 735
Glu Glu Thr Arg Arg Glu Met Leu Leu Gln Glu Glu Glu Lys Met Ile
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755 760 765
Glu Met His Leu Gln Asp Ala Ala Arg Arg Arg Phe Leu Lys Leu Gln
770 775 780
Gln Asp Gln Gln Glu Met Glu Leu Arg Arg Leu Asp Asp Glu Ile Gly
785 790 795 800
Arg Lys Val Tyr Met Arg Asp Arg Glu Ile Ala Ala Thr Ala Arg Asp
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Leu Glu Met Arg Gln Leu Glu Leu Glu Ser Gln Lys Arg Leu Tyr Glu

820 825 830
Lys Asn Leu Thr Glu Asn Gln Glu Ala Leu Ala Lys Glu Met Arg Ala
835 840 845
Asp Ala Asp Ala Tyr Arg Arg Lys Val Asp Leu Glu Glu His Met Phe
850 855 860
His Lys Leu Ile Glu Ala Gly Glu Thr Gln Ser Gln Lys Thr Gln Lys
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Val Ile Lys Glu Asn Leu Ala Lys Ala Glu Gln Ala Cys Leu Asn Thr
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900 905 910
Arg Asn Lys Cys Tyr Gln Glu Val Ala Lys Leu Leu Arg Glu Asn Arg
915 920 925
Arg Lys Glu Ile Glu Ile Ile Asn Ala Met Val Glu Glu Glu Ala Lys
930 935 940
Lys Trp Lys Glu Ala Glu Gly Lys Glu Phe Arg Leu Arg Ser Ala Lys
945 950 955 960
Lys Ala Ser Ala Leu Ser Asp Ala Ser Arg Lys Trp Phe Leu Lys Gln
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980 985 990
Glu Pro Arg Phe Gln Asn Glu Gln Asp Ser Ser Cys Leu Pro Arg Thr
995 1000 1005
Ser Gln Leu Asn Asp Ser Ser Glu Met Asp Pro Ser Thr Gln Ile
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Ser Leu Asn Arg Arg Ala Val Glu Trp Asp Thr Thr Gly Gln Asn
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Leu Ile Lys Lys Val Arg Asn Leu Arg Gln Arg Leu Thr Ala Arg

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1045

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Ile Trp Arg Pro Lys Arg Phe Thr Arg Leu Val Tyr Cys Asn Leu Cys

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Glu Gln Ser Ile Ser Leu Gly Lys Gln Gly Leu Ser Cys Asn Phe Cys

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Lys Tyr Ile Val His Asp His Cys Ala Met Lys Ala Gln Pro Cys Glu

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465/617

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 Leu Trp Val Arg Gly Gly Cys His Ser Gly Arg Cys Asp Arg Cys Gln
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 aaa aag atc cgg acc tac cac agc cta aca gga ctg cac tgt gtg tgg 341
 Lys Lys Ile Arg Thr Tyr His Ser Leu Thr Gly Leu His Cys Val Trp
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 Cys His Leu Glu Ile His Asp Asp Cys Leu Gln Ala Val Gly Pro Glu
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 Cys Asp Cys Gly Leu Leu Arg Asp His Ile Leu Pro Pro Cys Ser Ile
 125 130 135
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 Tyr Pro Ser Val Leu Val Ser Gly Gln Glu Cys Lys His Lys Thr Thr
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 Ser Asn Thr His Pro Leu Leu Val Phe Ile Asn Leu Lys Ser Gly Gly
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Arg Gln Val Phe Asp Leu Lys Asp Gly Pro Glu Pro Gly Leu Arg Phe
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 Phe Leu Glu Val Ile Pro Gln Gln Asn Gly Glu Lys Ser Asp Pro Val
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 Gly Asp Thr Lys Arg Pro His Gly Asp Thr Cys Glu Ile Asn Gln Ala
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 tgt gtg cca gac atg agt gac aag cgg ctg gaa gtg gta gga ata gag 1397
 Cys Val Pro Asp Met Ser Asp Lys Arg Leu Glu Val Val Gly Ile Glu
 445 450 455
 ggt gca att gag atg ggc cag atc tat acc agg ctc aag agt gct gga 1445
 Gly Ala Ile Glu Met Gly Gln Ile Tyr Thr Arg Leu Lys Ser Ala Gly
 460 465 470 475
 cac cgg ctg gcc aag tgc tcc gag atc aca ttc cag acc aca aaa acc 1493
 His Arg Leu Ala Lys Cys Ser Glu Ile Thr Phe Gln Thr Thr Lys Thr
 480 485 490
 ctc ccc atg caa att gac ggg gag ccc tgg atg cag gca ccc tgt aca 1541

Leu Pro Met Gln Ile Asp Gly Glu Pro Trp Met Gln Ala Pro Cys Thr
 495 500 505
 atc aag atc acc cat aag aac cag atg cct atg ctt atg ggt cca cct 1589
 Ile Lys Ile Thr His Lys Asn Gln Met Pro Met Leu Met Gly Pro Pro
 510 515 520
 tcc aac tcc tac aat ttc ttt ggc ttt tgg agc tgaagaagct ctctgccttg 1642
 Ser Asn Ser Tyr Asn Phe Phe Gly Phe Trp Ser
 525 530
 agcctacctc ccagttcctg aagatttcct actgtctaga tgctgccaca ctttctgcc 1702
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 tgctcccata cagacatcct tacacaacca gcaacgcaac aaggaacact gaaaaaatgc 1822
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<210> 146

<211> 534

<212> PRT

<213> Mus musculus

<400> 146

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 20 25 30
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 35 40 45
 Asp His Cys Ala Met Lys Ala Gln Pro Cys Glu Val Ser Thr Tyr Ala
 50 55 60

Lys Ser Arg Lys Asp Ile Gly Val Gln Ser His Leu Trp Val Arg Gly
 65 70 75 80
 Gly Cys His Ser Gly Arg Cys Asp Arg Cys Gln Lys Lys Ile Arg Thr
 85 90 95
 Tyr His Ser Leu Thr Gly Leu His Cys Val Trp Cys His Leu Glu Ile
 100 105 110
 His Asp Asp Cys Leu Gln Ala Val Gly Pro Glu Cys Asp Cys Gly Leu
 115 120 125
 Leu Arg Asp His Ile Leu Pro Pro Cys Ser Ile Tyr Pro Ser Val Leu
 130 135 140
 Val Ser Gly Gln Glu Cys Lys His Lys Thr Thr Asp Asp Thr Ser Leu
 145 150 155 160
 Cys Thr Pro Glu Ala Phe Arg Ile Glu Pro Val Ser Asn Thr His Pro
 165 170 175
 Leu Leu Val Phe Ile Asn Leu Lys Ser Gly Gly Lys Gln Gly Gln Ser
 180 185 190
 Val Leu Trp Lys Phe Gln Tyr Ile Leu Asn Pro Arg Gln Val Phe Asp
 195 200 205
 Leu Lys Asp Gly Pro Glu Pro Gly Leu Arg Phe Phe Lys Asp Val Pro
 210 215 220
 Gln Phe Arg Ile Leu Val Cys Gly Gly Asp Gly Thr Val Gly Trp Val
 225 230 235 240
 Leu Glu Thr Ile Asp Lys Ala Asn Phe Ala Thr Val Pro Pro Val Ala
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 Val Leu Pro Leu Gly Thr Gly Asn Asp Leu Ala Arg Cys Leu Arg Trp
 260 265 270
 Gly Arg Gly Tyr Glu Gly Glu Asn Leu Arg Lys Ile Leu Lys Asp Ile

275	280	285
Glu Leu Ser Lys Val Val Tyr Leu Asp Arg Trp Phe Leu Glu Val Ile		
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Pro Gln Gln Asn Gly Glu Lys Ser Asp Pro Val Pro Ser Gln Ile Ile		
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Asn Asn Tyr Phe Ser Ile Gly Val Asp Ala Ser Ile Ala His Arg Phe		
325	330	335
His Leu Met Arg Glu Lys Tyr Pro Glu Lys Phe Asn Ser Arg Met Lys		
340	345	350
Asn Lys Leu Trp Tyr Phe Glu Phe Ala Thr Ser Glu Ser Ile Phe Ser		
355	360	365
Thr Cys Lys Lys Leu Glu Glu Ser Val Thr Val Glu Ile Cys Gly Lys		
370	375	380
Leu Leu Asp Leu Ser Asp Leu Ser Leu Glu Gly Ile Ala Val Leu Asn		
385	390	395
Ile Pro Ser Thr His Gly Gly Ser Asn Leu Trp Gly Asp Thr Lys Arg		
405	410	415
Pro His Gly Asp Thr Cys Glu Ile Asn Gln Ala Leu Gly Ser Ala Ala		
420	425	430
Lys Ile Ile Thr Asp Pro Asp Ile Leu Lys Thr Cys Val Pro Asp Met		
435	440	445
Ser Asp Lys Arg Leu Glu Val Val Gly Ile Glu Gly Ala Ile Glu Met		
450	455	460
Gly Gln Ile Tyr Thr Arg Leu Lys Ser Ala Gly His Arg Leu Ala Lys		
465	470	475
Cys Ser Glu Ile Thr Phe Gln Thr Thr Lys Thr Leu Pro Met Gln Ile		
485	490	495

471/617

Asp Gly Glu Pro Trp Met Gln Ala Pro Cys Thr Ile Lys Ile Thr His

500

505

510

Lys Asn Gln Met Pro Met Leu Met Gly Pro Pro Ser Asn Ser Tyr Asn

515

520

525

Phe Phe Gly Phe Trp Ser

530

<210> 147

<211> 2811

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (334).. (2523)

<223>

<400> 147

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 tgcgcaagac gcaagaccgg ggctaaccct ctgaaaaaca agaagctgta ctaccaggct 300
 gtctctgtga tcaacttcag gaagagaaga agg atg gcc aaa gag aag ggc ctc 354

Met Ala Lys Glu Lys Gly Leu

1

5

atc agc cca gaa gac ttc gct cag ctg caa aag tac ata gaa tac tcc 402

Ile Ser Pro Glu Asp Phe Ala Gln Leu Gln Lys Tyr Ile Glu Tyr Ser

10

15

20

acc aaa agg gtc agc gat gta ctg aag gtc ttt gac gat ggt gag atg 450
 Thr Lys Arg Val Ser Asp Val Leu Lys Val Phe Asp Asp Gly Glu Met
 25 30 35
 aac aga ttt tgc cag gga gat gcc att ggg tac cta gga ttt gaa caa 498
 Asn Arg Phe Cys Gln Gly Asp Ala Ile Gly Tyr Leu Gly Phe Glu Gln
 40 45 50 55
 ttc atg aaa atg tat ctg gaa atg gag gag gtt ccc cat cac cta tgc 546
 Phe Met Lys Met Tyr Leu Glu Met Glu Glu Val Pro His His Leu Cys
 60 65 70
 tgg gct ctg ttt tgg tcc ttc cat act agt caa gtt gcg gct gag aag 594
 Trp Ala Leu Phe Trp Ser Phe His Thr Ser Gln Val Ala Ala Glu Lys
 75 80 85
 acc aag tca aaa gcc aat gtg atc tgt ctc agt gat gtg tac tgc tac 642
 Thr Lys Ser Lys Ala Asn Val Ile Cys Leu Ser Asp Val Tyr Cys Tyr
 90 95 100
 ttc acc ctc cta gaa ggt ggc cgg cca gaa gac aag cta gag ttc acc 690
 Phe Thr Leu Leu Glu Gly Gly Arg Pro Glu Asp Lys Leu Glu Phe Thr
 105 110 115
 ttc aag cta tat gac atg gac aga aat ggg atc ctg gat agc acg gaa 738
 Phe Lys Leu Tyr Asp Met Asp Arg Asn Gly Ile Leu Asp Ser Thr Glu
 120 125 130 135
 gtg gaa aaa atc atc ctt cag atg atg cga gtg gcc gaa tat cta gac 786
 Val Glu Lys Ile Ile Leu Gln Met Met Arg Val Ala Glu Tyr Leu Asp
 140 145 150
 tgg gat gtg tct gag ctg aga ccg atc ctt cag gag atg atg aga gag 834
 Trp Asp Val Ser Glu Leu Arg Pro Ile Leu Gln Glu Met Met Arg Glu
 155 160 165

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 Met Asp Gln Asp Gly Ser Gly Ser Val Ser Leu Asp Glu Trp Val Arg
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 Ala Gly Ala Thr Thr Val Pro Leu Leu Val Leu Leu Gly Met Asp Val
 185 190 195
 act atg aaa gat gat ggc aac cat ata tgg aga ccc aag aga ttc acc 978
 Thr Met Lys Asp Asp Gly Asn His Ile Trp Arg Pro Lys Arg Phe Thr
 200 205 210 215
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 Arg Leu Val Tyr Cys Asn Leu Cys Glu Gln Ser Ile Ser Leu Gly Lys
 220 225 230
 cag ggc ctg agc tgt aac ttc tgt aag tac att gtt cat gac cac tgt 1074
 Gln Gly Leu Ser Cys Asn Phe Cys Lys Tyr Ile Val His Asp His Cys
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 gcc atg aag gcc cag cct tgt gaa gtc agc acc tat gcc aag tct cgg 1122
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 aaa gac att ggt gtc cag tca cac tta tgg gtt cga gga ggc tgt cat 1170
 Lys Asp Ile Gly Val Gln Ser His Leu Trp Val Arg Gly Gly Cys His
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 tcc ggg cgt tgt gac cgc tgc cag aaa aag atc cgg acc tac cac agc 1218
 Ser Gly Arg Cys Asp Arg Cys Gln Lys Lys Ile Arg Thr Tyr His Ser
 280 285 290 295
 cta aca gga ctg cac tgt gtg tgg tgc cac ctg gag atc cat gat gac 1266
 Leu Thr Gly Leu His Cys Val Trp Cys His Leu Glu Ile His Asp Asp
 300 305 310

tgt ctg cag gct gta ggt cct gag tgt gac tgt ggg ttg ctc cgt gat	1314
Cys Leu Gln Ala Val Gly Pro Glu Cys Asp Cys Gly Leu Leu Arg Asp	
315 320 325	
cat atc ctg cct ccg tgt tcc atc tac ccc agc gtc ctg gta tct gga	1362
His Ile Leu Pro Pro Cys Ser Ile Tyr Pro Ser Val Leu Val Ser Gly	
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Gln Glu Cys Lys His Lys Thr Thr Asp Asp Thr Ser Leu Cys Thr Pro	
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gag gct ttt cgg att gaa ccc gtt tct aac acc cac ccc ctt cta gtc	1458
Glu Ala Phe Arg Ile Glu Pro Val Ser Asn Thr His Pro Leu Leu Val	
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Phe Ile Asn Leu Lys Ser Gly Gly Lys Gln Gly Gln Ser Val Leu Trp	
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Lys Phe Gln Tyr Ile Leu Asn Pro Arg Gln Val Phe Asp Leu Lys Asp	
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Gly Pro Glu Pro Gly Leu Arg Phe Phe Lys Asp Val Pro Gln Phe Arg	
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Ile Leu Val Cys Gly Gly Asp Gly Thr Val Gly Trp Val Leu Glu Thr	
425 430 435	
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Ile Asp Lys Ala Asn Phe Ala Thr Val Pro Pro Val Ala Val Leu Pro	
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ctg ggc act gga aat gat ctg gct cgg tgc cta aga tgg gga aga ggt	1746
Leu Gly Thr Gly Asn Asp Leu Ala Arg Cys Leu Arg Trp Gly Arg Gly	
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tat gaa ggt gag aat ttg aga aag att ctc aag gat ata gag cta agt	1794
Tyr Glu Gly Glu Asn Leu Arg Lys Ile Leu Lys Asp Ile Glu Leu Ser	
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Lys Val Val Tyr Leu Asp Arg Trp Phe Leu Glu Val Ile Pro Gln Gln	
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Asn Gly Glu Lys Ser Asp Pro Val Pro Ser Gln Ile Ile Asn Asn Tyr	
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Phe Ser Ile Gly Val Asp Ala Ser Ile Ala His Arg Phe His Leu Met	
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540 545 550	
tgg tac ttt gag ttt gcc aca tct gag tcc atc ttc tca aca tgc aaa	2034
Trp Tyr Phe Glu Phe Ala Thr Ser Glu Ser Ile Phe Ser Thr Cys Lys	
555 560 565	
aag ctg gaa gag tct gta acc gtt gag ata tgc ggg aag ctg ctg gat	2082
Lys Leu Glu Glu Ser Val Thr Val Glu Ile Cys Gly Lys Leu Leu Asp	
570 575 580	
ctg agc gac cta tcc cta gaa ggc att gcg gta ttg aac atc ccg agc	2130
Leu Ser Asp Leu Ser Leu Glu Gly Ile Ala Val Leu Asn Ile Pro Ser	
585 590 595	

acg cac ggt ggc tcc aac ctc tgg ggt gac acc aag aga cct cat ggg 2178
 Thr His Gly Gly Ser Asn Leu Trp Gly Asp Thr Lys Arg Pro His Gly
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 Asp Thr Cys Glu Ile Asn Gln Ala Leu Gly Ser Ala Ala Lys Ile Ile
 620 625 630
 aca gac ccc gat atc ctg aag acc tgt gtg cca gac atg agt gac aag 2274
 Thr Asp Pro Asp Ile Leu Lys Thr Cys Val Pro Asp Met Ser Asp Lys
 635 640 645
 cgg ctg gaa gtg gta gga ata gag ggt gca att gag atg ggc cag atc 2322
 Arg Leu Glu Val Val Gly Ile Glu Gly Ala Ile Glu Met Gly Gln Ile
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 tat acc agg ctc aag agt gct gga cac cgg ctg gcc aag tgc tcc gag 2370
 Tyr Thr Arg Leu Lys Ser Ala Gly His Arg Leu Ala Lys Cys Ser Glu
 665 670 675
 atc aca ttc cag acc aca aaa acc ctc ccc atg caa att gac ggg gag 2418
 Ile Thr Phe Gln Thr Thr Lys Thr Leu Pro Met Gln Ile Asp Gly Glu
 680 685 690 695
 ccc tgg atg cag gca ccc tgt aca atc aag atc acc cat aag aac cag 2466
 Pro Trp Met Gln Ala Pro Cys Thr Ile Lys Ile Thr His Lys Asn Gln
 700 705 710
 atg cct atg ctt atg ggt cca cct tcc aac tcc tac aat ttc ttt ggc 2514
 Met Pro Met Leu Met Gly Pro Pro Ser Asn Ser Tyr Asn Phe Phe Gly
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 Phe Trp Ser
 730

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 tacacaacca gcaacgcaac aaggaacact gaaaaaatgc ctcatcttaa taaagtgact 2743
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<210> 148

<211> 730

<212> PRT

<213> Mus musculus

<400> 148

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 Gly Tyr Leu Gly Phe Glu Gln Phe Met Lys Met Tyr Leu Glu Met Glu
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 Ser Gln Val Ala Ala Glu Lys Thr Lys Ser Lys Ala Asn Val Ile Cys
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 Leu Ser Asp Val Tyr Cys Tyr Phe Thr Leu Leu Glu Gly Gly Arg Pro
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 Glu Asp Lys Leu Glu Phe Thr Phe Lys Leu Tyr Asp Met Asp Arg Asn
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Gly Ile Leu Asp Ser Thr Glu Val Glu Lys Ile Ile Leu Gln Met Met
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Arg Val Ala Glu Tyr Leu Asp Trp Asp Val Ser Glu Leu Arg Pro Ile
145 150 155 160
Leu Gln Glu Met Met Arg Glu Met Asp Gln Asp Gly Ser Gly Ser Val
165 170 175
Ser Leu Asp Glu Trp Val Arg Ala Gly Ala Thr Thr Val Pro Leu Leu
180 185 190
Val Leu Leu Gly Met Asp Val Thr Met Lys Asp Asp Gly Asn His Ile
195 200 205
Trp Arg Pro Lys Arg Phe Thr Arg Leu Val Tyr Cys Asn Leu Cys Glu
210 215 220
Gln Ser Ile Ser Leu Gly Lys Gln Gly Leu Ser Cys Asn Phe Cys Lys
225 230 235 240
Tyr Ile Val His Asp His Cys Ala Met Lys Ala Gln Pro Cys Glu Val
245 250 255
Ser Thr Tyr Ala Lys Ser Arg Lys Asp Ile Gly Val Gln Ser His Leu
260 265 270
Trp Val Arg Gly Gly Cys His Ser Gly Arg Cys Asp Arg Cys Gln Lys
275 280 285
Lys Ile Arg Thr Tyr His Ser Leu Thr Gly Leu His Cys Val Trp Cys
290 295 300
His Leu Glu Ile His Asp Asp Cys Leu Gln Ala Val Gly Pro Glu Cys
305 310 315 320
Asp Cys Gly Leu Leu Arg Asp His Ile Leu Pro Pro Cys Ser Ile Tyr
325 330 335
Pro Ser Val Leu Val Ser Gly Gln Glu Cys Lys His Lys Thr Thr Asp

340 345 350
Asp Thr Ser Leu Cys Thr Pro Glu Ala Phe Arg Ile Glu Pro Val Ser
355 360 365
Asn Thr His Pro Leu Leu Val Phe Ile Asn Leu Lys Ser Gly Gly Lys
370 375 380
Gln Gly Gln Ser Val Leu Trp Lys Phe Gln Tyr Ile Leu Asn Pro Arg
385 390 395 400
Gln Val Phe Asp Leu Lys Asp Gly Pro Glu Pro Gly Leu Arg Phe Phe
405 410 415
Lys Asp Val Pro Gln Phe Arg Ile Leu Val Cys Gly Gly Asp Gly Thr
420 425 430
Val Gly Trp Val Leu Glu Thr Ile Asp Lys Ala Asn Phe Ala Thr Val
435 440 445
Pro Pro Val Ala Val Leu Pro Leu Gly Thr Gly Asn Asp Leu Ala Arg
450 455 460
Cys Leu Arg Trp Gly Arg Gly Tyr Glu Gly Glu Asn Leu Arg Lys Ile
465 470 475 480
Leu Lys Asp Ile Glu Leu Ser Lys Val Val Tyr Leu Asp Arg Trp Phe
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Ser Gln Ile Ile Asn Asn Tyr Phe Ser Ile Gly Val Asp Ala Ser Ile
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Ala His Arg Phe His Leu Met Arg Glu Lys Tyr Pro Glu Lys Phe Asn
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Ser Arg Met Lys Asn Lys Leu Trp Tyr Phe Glu Phe Ala Thr Ser Glu
545 550 555 560

Ser Ile Phe Ser Thr Cys Lys Lys Leu Glu Glu Ser Val Thr Val Glu
 565 570 575
 Ile Cys Gly Lys Leu Leu Asp Leu Ser Asp Leu Ser Leu Glu Gly Ile
 580 585 590
 Ala Val Leu Asn Ile Pro Ser Thr His Gly Gly Ser Asn Leu Trp Gly
 595 600 605
 Asp Thr Lys Arg Pro His Gly Asp Thr Cys Glu Ile Asn Gln Ala Leu
 610 615 620
 Gly Ser Ala Ala Lys Ile Ile Thr Asp Pro Asp Ile Leu Lys Thr Cys
 625 630 635 640
 Val Pro Asp Met Ser Asp Lys Arg Leu Glu Val Val Gly Ile Glu Gly
 645 650 655
 Ala Ile Glu Met Gly Gln Ile Tyr Thr Arg Leu Lys Ser Ala Gly His
 660 665 670
 Arg Leu Ala Lys Cys Ser Glu Ile Thr Phe Gln Thr Thr Lys Thr Leu
 675 680 685
 Pro Met Gln Ile Asp Gly Glu Pro Trp Met Gln Ala Pro Cys Thr Ile
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<210> 149

<211> 2690

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (210).. (2414)

<223>

<400> 149

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atattaacgc ctaccctctg aagaggtcca agcaacggaa gtactactac gaagctgcct    180
ttctggccat ccttgagaaa aatagacag atg gcc aag gag agg ggc cta ata    233
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agc ccc agt gat ttt gcc cag ctg caa aaa tac atg gaa tac tcc acc    281
Ser Pro Ser Asp Phe Ala Gln Leu Gln Lys Tyr Met Glu Tyr Ser Thr
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aaa aag gtc agt gat gtc cta aag ctc ttc gag gat ggc gag atg gct    329
Lys Lys Val Ser Asp Val Leu Lys Leu Phe Glu Asp Gly Glu Met Ala
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Lys Tyr Val Gln Gly Asp Ala Ile Gly Tyr Glu Gly Phe Gln Gln Phe
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ctg aaa atc tat ctc gaa gtg gat aat gtt ccc aga cac cta agc ctg    425
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gca ctg ttt caa tcc ttt gag act ggt cac tgc tta aat gag aca aat    473
Ala Leu Phe Gln Ser Phe Glu Thr Gly His Cys Leu Asn Glu Thr Asn
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Val Thr Lys Asp Val Val Cys Leu Asn Asp Val Ser Cys Tyr Phe Ser
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 105 110 115 120
 ctg tac gac acg gac aga aat ggg atc ctg gac agc tca gaa gtg gac 617
 Leu Tyr Asp Thr Asp Arg Asn Gly Ile Leu Asp Ser Ser Glu Val Asp
 125 130 135
 aaa att atc cta cag atg atg cga gtg gct gaa tac ctg gat tgg gat 665
 Lys Ile Ile Leu Gln Met Met Arg Val Ala Glu Tyr Leu Asp Trp Asp
 140 145 150
 gtg tct gag ctg agg ccg att ctt cag gag atg atg aaa gag att gac 713
 Val Ser Glu Leu Arg Pro Ile Leu Gln Glu Met Met Lys Glu Ile Asp
 155 160 165
 tat gat ggc agt ggc tct gtc tct caa gct gag tgg gtc cgg gct ggg 761
 Tyr Asp Gly Ser Gly Ser Val Ser Gln Ala Glu Trp Val Arg Ala Gly
 170 175 180
 gcc acc acc gtg cca ctg cta gtg ctg ctg ggt ctg gag atg act ctg 809
 Ala Thr Thr Val Pro Leu Leu Val Leu Leu Gly Leu Glu Met Thr Leu
 185 190 195 200
 aag gac gac gga cag cac atg tgg agg ccc aag agg ttc ccc aga cca 857
 Lys Asp Asp Gly Gln His Met Trp Arg Pro Lys Arg Phe Pro Arg Pro
 205 210 215
 gtc tac tgc aat ctg tgc gag tca agc att ggt ctt ggc aaa cag gga 905
 Val Tyr Cys Asn Leu Cys Glu Ser Ser Ile Gly Leu Gly Lys Gln Gly
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 ctg agc tgt aac ctc tgt aag tac act gtt cac gac cag tgt gcc atg 953

483/617

Leu Ser Cys Asn Leu Cys Lys Tyr Thr Val His Asp Gln Cys Ala Met
 235 240 245
 aaa gcc ctg cct tgt gaa gtc agc acc tat gcc aag tct cgg aag gac 1001
 Lys Ala Leu Pro Cys Glu Val Ser Thr Tyr Ala Lys Ser Arg Lys Asp
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 Ile Gly Val Gln Ser His Val Trp Val Arg Gly Gly Cys Glu Ser Gly
 265 270 275 280
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 Arg Cys Asp Arg Cys Gln Lys Lys Ile Arg Ile Tyr His Ser Leu Thr
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 Gly Leu His Cys Val Trp Cys His Leu Glu Ile His Asp Asp Cys Leu
 300 305 310
 caa gcg gtg ggc cat gag tgt gac tgt ggg ctg ctc cgg gat cac atc 1193
 Gln Ala Val Gly His Glu Cys Asp Cys Gly Leu Leu Arg Asp His Ile
 315 320 325
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 330 335 340
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 Arg Lys Asn Ser Lys Thr Ser Gln Lys Thr Met Asp Asp Leu Asn Leu
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 Ser Thr Ser Glu Ala Leu Arg Ile Asp Pro Val Pro Asn Thr His Pro
 365 370 375
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 gtg ctc tgg aag ttc cag tat ata tta aac cct cga cag gtg ttc aac 1433
 Val Leu Trp Lys Phe Gln Tyr Ile Leu Asn Pro Arg Gln Val Phe Asn
 395 400 405
 ctc cta aag gat ggt cct gag ata ggg ctc cga tta ttc aag gat gtt 1481
 Leu Leu Lys Asp Gly Pro Glu Ile Gly Leu Arg Leu Phe Lys Asp Val
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 Pro Asp Ser Arg Ile Leu Val Cys Gly Gly Asp Gly Thr Val Gly Trp
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 445 450 455
 gct gtg ttg ccc ctg ggt act gga aat gat ctg gct cga tgc cta aga 1625
 Ala Val Leu Pro Leu Gly Thr Gly Asn Asp Leu Ala Arg Cys Leu Arg
 460 465 470
 tgg gga gga ggt tat gaa gga cag aat ctg gca aag atc ctc aag gat 1673
 Trp Gly Gly Gly Tyr Glu Gly Gln Asn Leu Ala Lys Ile Leu Lys Asp
 475 480 485
 tta gag atg agt aaa gtg gta cat atg gat cga tgg tct gtg gag gtg 1721
 Leu Glu Met Ser Lys Val Val His Met Asp Arg Trp Ser Val Glu Val
 490 495 500
 ata cct caa caa act gaa gaa aaa agt gac cca gtc ccc ttt caa atc 1769
 Ile Pro Gln Gln Thr Glu Glu Lys Ser Asp Pro Val Pro Phe Gln Ile
 505 510 515 520
 atc aat aac tac ttc tct att ggc gtg gat gcc tct att gct cat cga 1817

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Ile Asn Asn Tyr Phe Ser Ile Gly Val Asp Ala Ser Ile Ala His Arg
 525 530 535
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 Phe His Ile Met Arg Glu Lys Tyr Pro Glu Lys Phe Asn Ser Arg Met
 540 545 550
 aag aac aag cta tgg tac ttc gaa ttt gcc aca tct gaa tcc atc ttc 1913
 Lys Asn Lys Leu Trp Tyr Phe Glu Phe Ala Thr Ser Glu Ser Ile Phe
 555 560 565
 tca aca tgc aaa aag ctg gag gag tct ttg aca gtt gag atc tgt ggg 1961
 Ser Thr Cys Lys Lys Leu Glu Glu Ser Leu Thr Val Glu Ile Cys Gly
 570 575 580
 aaa ccg ctg gat ctg agc aac ctg tcc cta gaa ggc atc gca gtg cta 2009
 Lys Pro Leu Asp Leu Ser Asn Leu Ser Leu Glu Gly Ile Ala Val Leu
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 aac atc cct agc atg cat ggt ggc tcc aac ctc tgg ggt gat acc agg 2057
 Asn Ile Pro Ser Met His Gly Gly Ser Asn Leu Trp Gly Asp Thr Arg
 605 610 615
 aga ccc cat ggg gat atc tat ggg atc aac cag gcc tta ggt gct aca 2105
 Arg Pro His Gly Asp Ile Tyr Gly Ile Asn Gln Ala Leu Gly Ala Thr
 620 625 630
 gct aaa gtc atc acc gac cct gat atc ctg aaa acc tgt gta cca gac 2153
 Ala Lys Val Ile Thr Asp Pro Asp Ile Leu Lys Thr Cys Val Pro Asp
 635 640 645
 cta agt gac aag aga ctg gaa gtg gtt ggg ctg gag ggt gca att gag 2201
 Leu Ser Asp Lys Arg Leu Glu Val Val Gly Leu Glu Gly Ala Ile Glu
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$\langle 400 \rangle$	150

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Gln Lys Tyr Met Glu Tyr Ser Thr Lys Lys Val Ser Asp Val Leu Lys
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 Asn Val Pro Arg His Leu Ser Leu Ala Leu Phe Gln Ser Phe Glu Thr
 65 70 75 80
 Gly His Cys Leu Asn Glu Thr Asn Val Thr Lys Asp Val Val Cys Leu
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 Asn Asp Val Ser Cys Tyr Phe Ser Leu Leu Glu Gly Gly Arg Pro Glu
 100 105 110
 Asp Lys Leu Glu Phe Thr Phe Lys Leu Tyr Asp Thr Asp Arg Asn Gly
 115 120 125
 Ile Leu Asp Ser Ser Glu Val Asp Lys Ile Ile Leu Gln Met Met Arg
 130 135 140
 Val Ala Glu Tyr Leu Asp Trp Asp Val Ser Glu Leu Arg Pro Ile Leu
 145 150 155 160
 Gln Glu Met Met Lys Glu Ile Asp Tyr Asp Gly Ser Gly Ser Val Ser
 165 170 175
 Gln Ala Glu Trp Val Arg Ala Gly Ala Thr Thr Val Pro Leu Leu Val
 180 185 190
 Leu Leu Gly Leu Glu Met Thr Leu Lys Asp Asp Gly Gln His Met Trp
 195 200 205
 Arg Pro Lys Arg Phe Pro Arg Pro Val Tyr Cys Asn Leu Cys Glu Ser
 210 215 220
 Ser Ile Gly Leu Gly Lys Gln Gly Leu Ser Cys Asn Leu Cys Lys Tyr

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Asn Leu Pro Val Leu Pro Pro Val Ala Val Leu Pro Leu Gly Thr Gly
 450 455 460
 Asn Asp Leu Ala Arg Cys Leu Arg Trp Gly Gly Gly Tyr Glu Gly Gln
 465 470 475 480
 Asn Leu Ala Lys Ile Leu Lys Asp Leu Glu Met Ser Lys Val Val His
 485 490 495
 Met Asp Arg Trp Ser Val Glu Val Ile Pro Gln Gln Thr Glu Glu Lys
 500 505 510
 Ser Asp Pro Val Pro Phe Gln Ile Ile Asn Asn Tyr Phe Ser Ile Gly
 515 520 525
 Val Asp Ala Ser Ile Ala His Arg Phe His Ile Met Arg Glu Lys Tyr
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 Pro Glu Lys Phe Asn Ser Arg Met Lys Asn Lys Leu Trp Tyr Phe Glu
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 565 570 575
 Ser Leu Thr Val Glu Ile Cys Gly Lys Pro Leu Asp Leu Ser Asn Leu
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 Ser Leu Glu Gly Ile Ala Val Leu Asn Ile Pro Ser Met His Gly Gly
 595 600 605
 Ser Asn Leu Trp Gly Asp Thr Arg Arg Pro His Gly Asp Ile Tyr Gly
 610 615 620
 Ile Asn Gln Ala Leu Gly Ala Thr Ala Lys Val Ile Thr Asp Pro Asp
 625 630 635 640
 Ile Leu Lys Thr Cys Val Pro Asp Leu Ser Asp Lys Arg Leu Glu Val
 645 650 655
 Val Gly Leu Glu Gly Ala Ile Glu Met Gly Gln Ile Tyr Thr Lys Leu

660 665 670
 Lys Asn Ala Gly Arg Arg Leu Ala Lys Cys Ser Glu Ile Thr Phe His
 675 680 685
 Thr Thr Lys Thr Leu Pro Met Gln Ile Asp Gly Glu Pro Trp Met Gln
 690 695 700
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 Arg Ser Ala Gly Asp Lys Lys Asn Ala Ser Asp Arg Ser Ala Lys Thr
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 caa gca tct att aaa aaa gaa gag aaa agg tca tct gag aaa tca gaa 207

Gln Ala Ser Ile Lys Lys Glu Glu Lys Arg Ser Ser Glu Lys Ser Glu
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 aaa aaa gaa agc aaa gat act aag aaa ata gag aaa gat gag aag aac 255
 Lys Lys Glu Ser Lys Asp Thr Lys Lys Ile Glu Lys Asp Glu Lys Asn
 45 50 55
 gag gat ggt cca agt ggg cag act tca gag tcc ctg aaa aag agt gaa 303
 Asp Asp Gly Pro Ser Gly Gln Thr Ser Glu Ser Leu Lys Lys Ser Glu
 60 65 70 75
 gag aag aag cgg ata agt tca aag agt cca gga cat atg gtg ata cta 351
 Glu Lys Lys Arg Ile Ser Ser Lys Ser Pro Gly His Met Val Ile Leu
 80 85 90
 aac caa acc aag gga gat cat tgt agg ccg tca aga agg ggc aga tat 399
 Asn Gln Thr Lys Gly Asp His Cys Arg Pro Ser Arg Arg Gly Arg Tyr
 95 100 105
 gag aaa ggt cat gga aga agc aaa gaa aag gag agg gct agc cta gat 447
 Glu Lys Gly His Gly Arg Ser Lys Glu Lys Glu Arg Ala Ser Leu Asp
 110 115 120
 aaa aaa aga gac aaa gac tac aga agg aaa gag atc ttg cct ttt gaa 495
 Lys Lys Arg Asp Lys Asp Tyr Arg Arg Lys Glu Ile Leu Pro Phe Glu
 125 130 135
 aag atg aag gaa caa aga ttg aga gaa cat tta gtt cgt ttt gaa aga 543
 Lys Met Lys Glu Gln Arg Leu Arg Glu His Leu Val Arg Phe Glu Arg
 140 145 150 155
 ctg aaa caa gca gtg gaa ttc aga aga cga aaa gag att gca gaa aga 591
 Leu Lys Gln Ala Val Glu Phe Arg Arg Arg Lys Glu Ile Ala Glu Arg
 160 165 170
 gag cgt cga gag cgt gaa cgc att aga ata att cgt gaa cgg gaa gaa 639

Glu Arg Arg Glu Arg Glu Arg Ile Arg Ile Ile Arg Glu Arg Glu Glu
 175 180 185
 cgg gaa cgc tta cag aga gag aga gag cgc cta gaa att gaa agg caa 687
 Arg Glu Arg Leu Gln Arg Glu Arg Glu Arg Leu Glu Ile Glu Arg Gln
 190 195 200
 aaa cta gag aga gag aga atg gaa cgc gaa cgc ttg gaa agg gaa cgc 735
 Lys Leu Glu Arg Glu Arg Met Glu Arg Glu Arg Leu Glu Arg Glu Arg
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 att cgt att gaa cag gag cgg cgc agg gaa gct gaa agg att gct cgg 783
 Ile Arg Ile Glu Gln Glu Arg Arg Arg Glu Ala Glu Arg Ile Ala Arg
 220 225 230 235
 gag aga gag gag ctc aga agg cag cag cag cag ctt cgc tat gaa caa 831
 Glu Arg Glu Glu Leu Arg Arg Gln Gln Gln Gln Leu Arg Tyr Glu Gln
 240 245 250
 gaa aaa agg aat tct ttg aaa cgc cca cgt gac gta gac cat agg cga 879
 Glu Lys Arg Asn Ser Leu Lys Arg Pro Arg Asp Val Asp His Arg Arg
 255 260 265
 gat gac cct tac tgg agc gag aat aaa aag tta tct cta gat aca gag 927
 Asp Asp Pro Tyr Trp Ser Glu Asn Lys Lys Leu Ser Leu Asp Thr Glu
 270 275 280
 gca cga ttc ggc cat ggg tct gac tat cgt caa cag agc agg ttc ctt 975
 Ala Arg Phe Gly His Gly Ser Asp Tyr Arg Gln Gln Ser Arg Phe Leu
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 gac ttc agt cac cga gaa cgg gcc agg ttt cct gac act gca tct gtg 1023
 Asp Phe Ser His Arg Glu Arg Ala Arg Phe Pro Asp Thr Ala Ser Val
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 cag tca tcc ttt gaa aga cgg gaa cgg ttt gtt ggt caa agt gaa gga 1071

Gln Ser Ser Phe Glu Arg Arg Glu Arg Phe Val Gly Gln Ser Glu Gly
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 Tyr Pro Lys Asn Phe Ser Asp Ser Arg Arg Asn Glu Pro Pro Pro Pro
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 Arg Asn Glu Leu Arg Glu Thr Asp Arg Arg Glu Val Arg Gly Glu Arg
 365 370 375
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 Asp Glu Arg Arg Thr Val Ile Leu His Asp Arg Pro Glu Val Ala His
 380 385 390 395
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 Pro Arg His Pro Arg Glu Thr Val Pro Asn Pro Ser Arg Pro Thr Ser
 400 405 410
 tgg aaa agc gaa gcg aat atg tcc aca gag aaa cgg gag tca cga gtt 1359
 Trp Lys Ser Glu Ala Asn Met Ser Thr Glu Lys Arg Glu Ser Arg Val
 415 420 425
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 Glu Arg Pro Glu Arg Ser Gly Arg Glu Val Ser Gly His Thr Val Arg
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 Gly Val Pro Pro Gly Asn Arg Ser Ser Ala Ser Gly Tyr Gly Thr Arg
 445 450 455
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 Tyr Pro Glu Glu Arg His Val Val Glu Arg His Gly Arg Asp Thr Ser
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 Gly Pro Arg Lys Glu Trp His Gly Pro Pro Ser Gln Gly Pro Ser Tyr
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 cat gac aca aga cga atg ggt gat ggc cga gca gga gca ggc atg ata 1647
 His Asp Thr Arg Arg Met Gly Asp Gly Arg Ala Gly Ala Gly Met Ile
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 Thr Gln His Ser Ser Thr Ala Ser Pro Val Asn Arg Ile Val Gln Met
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 Ser Gly Asn Ser Leu Pro Arg Gly Ser Ser Ser Gly Phe Lys Pro Phe
 540 545 550 555
 aag agt gga cct cca cgg cga ttt taacgcaagc ttctgtctgt ggcttcaaga 1797
 Lys Ser Gly Pro Pro Arg Arg Phe
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Lys Glu Glu Lys Arg Ser Ser Glu Lys Ser Glu Lys Lys Glu Ser Lys

35 40 45

Asp Thr Lys Lys Ile Glu Lys Asp Glu Lys Asn Asp Asp Gly Pro Ser

50 55 60

Gly Gln Thr Ser Glu Ser Leu Lys Lys Ser Glu Glu Lys Lys Arg Ile

65 70 75 80

Ser Ser Lys Ser Pro Gly His Met Val Ile Leu Asn Gln Thr Lys Gly

85 90 95

Asp His Cys Arg Pro Ser Arg Arg Gly Arg Tyr Glu Lys Gly His Gly

100 105 110

Arg Ser Lys Glu Lys Glu Arg Ala Ser Leu Asp Lys Lys Arg Asp Lys

115 120 125

Asp Tyr Arg Arg Lys Glu Ile Leu Pro Phe Glu Lys Met Lys Glu Gln

130 135 140

Arg Leu Arg Glu His Leu Val Arg Phe Glu Arg Leu Lys Gln Ala Val

145 150 155 160
 Glu Phe Arg Arg Arg Lys Glu Ile Ala Glu Arg Glu Arg Arg Glu Arg
 165 170 175
 Glu Arg Ile Arg Ile Ile Arg Glu Arg Glu Glu Arg Glu Arg Leu Gln
 180 185 190
 Arg Glu Arg Glu Arg Leu Glu Ile Glu Arg Gln Lys Leu Glu Arg Glu
 195 200 205
 Arg Met Glu Arg Glu Arg Leu Glu Arg Glu Arg Ile Arg Ile Glu Gln
 210 215 220
 Glu Arg Arg Arg Glu Ala Glu Arg Ile Ala Arg Glu Arg Glu Glu Leu
 225 230 235 240
 Arg Arg Gln Gln Gln Gln Leu Arg Tyr Glu Gln Glu Lys Arg Asn Ser
 245 250 255
 Leu Lys Arg Pro Arg Asp Val Asp His Arg Arg Asp Asp Pro Tyr Trp
 260 265 270
 Ser Glu Asn Lys Lys Leu Ser Leu Asp Thr Glu Ala Arg Phe Gly His
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 Gly Ser Asp Tyr Arg Gln Gln Ser Arg Phe Leu Asp Phe Ser His Arg
 290 295 300
 Glu Arg Ala Arg Phe Pro Asp Thr Ala Ser Val Gln Ser Ser Phe Glu
 305 310 315 320
 Arg Arg Glu Arg Phe Val Gly Gln Ser Glu Gly Lys Lys Pro Arg Pro
 325 330 335
 Ala Ala Arg Arg Glu Glu Pro Ser Phe Glu Arg Tyr Pro Lys Asn Phe
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 Ser Asp Ser Arg Arg Asn Glu Pro Pro Pro Arg Asn Glu Leu Arg
 355 360 365

Glu Thr Asp Arg Arg Glu Val Arg Gly Glu Arg Asp Glu Arg Arg Thr
370 375 380

Val Ile Leu His Asp Arg Pro Glu Val Ala His Pro Arg His Pro Arg
385 390 395 400

Glu Thr Val Pro Asn Pro Ser Arg Pro Thr Ser Trp Lys Ser Glu Ala
405 410 415

Asn Met Ser Thr Glu Lys Arg Glu Ser Arg Val Glu Arg Pro Glu Arg
420 425 430

Ser Gly Arg Glu Val Ser Gly His Thr Val Arg Gly Val Pro Pro Gly
435 440 445

Asn Arg Ser Ser Ala Ser Gly Tyr Gly Thr Arg Glu Gly Glu Arg Gly
450 455 460

Val Ile Ala Asp Arg Gly Ser Gly Thr Gln His Tyr Pro Glu Glu Arg
465 470 475 480

His Val Val Glu Arg His Gly Arg Asp Thr Ser Gly Pro Arg Lys Glu
485 490 495

Trp His Gly Pro Pro Ser Gln Gly Pro Ser Tyr His Asp Thr Arg Arg
500 505 510

Met Gly Asp Gly Arg Ala Gly Ala Gly Met Ile Thr Gln His Ser Ser
515 520 525

Thr Ala Ser Pro Val Asn Arg Ile Val Gln Met Ser Gly Asn Ser Leu
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Arg Arg Phe

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498/617

<211> 2316

<212> DNA

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           1             5             10
cgg agc gct ggt gat aaa aag aac gcg agt gat cgg agt gcc aag aca    159
Arg Ser Ala Gly Asp Lys Lys Asn Ala Ser Asp Arg Ser Ala Lys Thr
           15             20             25
caa gca tct att aaa aaa gaa gag aaa agg tca tct gag aaa tca gaa    207
Gln Ala Ser Ile Lys Lys Glu Glu Lys Arg Ser Ser Glu Lys Ser Glu
           30             35             40
aaa aaa gaa agc aaa gat act aag aaa ata gag aaa gat gag aag aac    255
Lys Lys Glu Ser Lys Asp Thr Lys Lys Ile Glu Lys Asp Glu Lys Asn
           45             50             55
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Asp Asp Gly Pro Ser Gly Gln Thr Ser Glu Ser Leu Lys Lys Ser Glu
           60             65             70             75
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Glu Lys Lys Arg Ile Ser Ser Lys Ser Pro Gly His Met Val Ile Leu
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499/617

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gag aaa ggt cat gga aga agc aaa gaa aag gag agg gct agc cta gat	447
Glu Lys Gly His Gly Arg Ser Lys Glu Lys Glu Arg Ala Ser Leu Asp	
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Lys Lys Arg Asp Lys Asp Tyr Arg Arg Lys Glu Ile Leu Pro Phe Glu	
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Lys Met Lys Glu Gln Arg Leu Arg Glu His Leu Val Arg Phe Glu Arg	
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Arg Glu Arg Leu Gln Arg Glu Arg Glu Arg Leu Glu Ile Glu Arg Gln	
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aaa cta gag aga gag aga atg gaa cgc gaa cgc ttg gaa agg gaa cgc	735
Lys Leu Glu Arg Glu Arg Met Glu Arg Glu Arg Leu Glu Arg Glu Arg	
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Glu Lys Arg Asn Ser Leu Lys Arg Pro Arg Asp Val Asp His Arg Arg	
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gat gac cct tac tgg agc gag aat aaa aag tta tct cta gat aca gag	927
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Lys Lys Pro Arg Pro Ala Ala Arg Arg Glu Glu Pro Ser Phe Glu Arg	
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Tyr Pro Lys Asn Phe Ser Asp Ser Arg Arg Asn Glu Pro Pro Pro Pro	
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Arg Asn Glu Leu Arg Glu Thr Asp Arg Arg Glu Val Arg Gly Glu Arg	
365 370 375	

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 Glu Gly Glu Arg Gly Val Ile Ala Asp Arg Gly Ser Gly Thr Gln His
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 Tyr Pro Glu Glu Arg His Val Val Glu Arg His Gly Arg Asp Thr Ser
 480 485 490
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 Gly Pro Arg Lys Glu Trp His Gly Pro Pro Ser Gln Gly Pro Ser Tyr
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 His Asp Thr Arg Arg Met Gly Asp Gly Arg Ala Gly Ala Gly Met Ile
 510 515 520

acc caa cac tca agc act gcg tcc cca gtg aac agg att gta cag atg 1695
 Thr Gln His Ser Ser Thr Ala Ser Pro Val Asn Arg Ile Val Gln Met
 525 530 535

agt ggt aac tcc ttg cca aga gga agc agc tcg ggg ttt aag ccg ttt 1743
 Ser Gly Asn Ser Leu Pro Arg Gly Ser Ser Ser Gly Phe Lys Pro Phe
 540 545 550 555

aag agt gga cct cca cgg cga ttt taacgcaagc ttcctgctgt ggcttcaaga 1797
 Lys Ser Gly Pro Pro Arg Arg Phe
 560

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<213> Mus musculus

<400> 154

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15

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503/617

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Asp His Cys Arg Pro Ser Arg Arg Gly Arg Tyr Glu Lys Gly His Gly		
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Asp Tyr Arg Arg Lys Glu Ile Leu Pro Phe Glu Lys Met Lys Glu Gln		
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Arg Leu Arg Glu His Leu Val Arg Phe Glu Arg Leu Lys Gln Ala Val		
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Glu Phe Arg Arg Arg Lys Glu Ile Ala Glu Arg Glu Arg Arg Glu Arg		
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Glu Arg Ile Arg Ile Ile Arg Glu Arg Glu Glu Arg Glu Arg Leu Gln		
180	185	190
Arg Glu Arg Glu Arg Leu Glu Ile Glu Arg Gln Lys Leu Glu Arg Glu		
195	200	205
Arg Met Glu Arg Glu Arg Leu Glu Arg Glu Arg Ile Arg Ile Glu Gln		
210	215	220
Glu Arg Arg Arg Glu Ala Glu Arg Ile Ala Arg Glu Arg Glu Glu Leu		
225	230	235
		240

Arg Arg Gln Gln Gln Gln Leu Arg Tyr Glu Gln Glu Lys Arg Asn Ser
245 250 255
Leu Lys Arg Pro Arg Asp Val Asp His Arg Arg Asp Asp Pro Tyr Trp
260 265 270
Ser Glu Asn Lys Lys Leu Ser Leu Asp Thr Glu Ala Arg Phe Gly His
275 280 285
Gly Ser Asp Tyr Arg Gln Gln Ser Arg Phe Leu Asp Phe Ser His Arg
290 295 300
Glu Arg Ala Arg Phe Pro Asp Thr Ala Ser Val Gln Ser Ser Phe Glu
305 310 315 320
Arg Arg Glu Arg Phe Val Gly Gln Ser Glu Gly Lys Lys Pro Arg Pro
325 330 335
Ala Ala Arg Arg Glu Glu Pro Ser Phe Glu Arg Tyr Pro Lys Asn Phe
340 345 350
Ser Asp Ser Arg Arg Asn Glu Pro Pro Pro Arg Asn Glu Leu Arg
355 360 365
Glu Thr Asp Arg Arg Glu Val Arg Gly Glu Arg Asp Glu Arg Arg Thr
370 375 380
Val Ile Leu His Asp Arg Pro Glu Val Ala His Pro Arg His Pro Arg
385 390 395 400
Glu Thr Val Pro Asn Pro Ser Arg Pro Thr Ser Trp Lys Ser Glu Ala
405 410 415
Asn Met Ser Thr Glu Lys Arg Glu Ser Arg Val Glu Arg Pro Glu Arg
420 425 430
Ser Gly Arg Glu Val Ser Gly His Thr Val Arg Gly Ala Pro Pro Gly
435 440 445
Asn Arg Ser Ser Ala Ser Gly Tyr Gly Thr Arg Glu Gly Glu Arg Gly

450 455 460
 Val Ile Ala Asp Arg Gly Ser Gly Thr Gln His Tyr Pro Glu Glu Arg
 465 470 475 480
 His Val Val Glu Arg His Gly Arg Asp Thr Ser Gly Pro Arg Lys Glu
 485 490 495
 Trp His Gly Pro Pro Ser Gln Gly Pro Ser Tyr His Asp Thr Arg Arg
 500 505 510
 Met Gly Asp Gly Arg Ala Gly Ala Gly Met Ile Thr Gln His Ser Ser
 515 520 525
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 Arg Arg Phe

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<211> 3694

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<213> Mus musculus

<220>

<221> CDS

<222> (51).. (3143)

<223>

<400> 155

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Met Ala

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 5 10 15
 ggg aag aag atc acg gag ctg cgg gtt atc gac ctc agg tcc gag ctg 152
 Gly Lys Lys Ile Thr Glu Leu Arg Val Ile Asp Leu Arg Ser Glu Leu
 20 25 30
 aag cgc cgc aac ttg gac atc aac ggg gtc aag acg gta ctg gtc tcc 200
 Lys Arg Arg Asn Leu Asp Ile Asn Gly Val Lys Thr Val Leu Val Ser
 35 40 45 50
 cgg ctg aag cag gct att gaa gag gaa gga ggc gat cca gat aat att 248
 Arg Leu Lys Gln Ala Ile Glu Glu Glu Gly Gly Asp Pro Asp Asn Ile
 55 60 65
 gaa tta act gtt tca act gat act cca aac aag aaa cca acc aaa ggc 296
 Glu Leu Thr Val Ser Thr Asp Thr Pro Asn Lys Lys Pro Thr Lys Gly
 70 75 80
 aaa ggt aaa aaa caa gaa gca gat gag ttg agt gga gat gct tct gtg 344
 Lys Gly Lys Lys Gln Glu Ala Asp Glu Leu Ser Gly Asp Ala Ser Val
 85 90 95
 gaa gat gat tct ttt gtc aag gac tgt gaa ttg gag aat caa gag aca 392
 Glu Asp Asp Ser Phe Val Lys Asp Cys Glu Leu Glu Asn Gln Glu Thr
 100 105 110
 cat gac caa gat gga aat gaa gag cta aag gac ttg gaa gaa ttt ggt 440
 His Asp Gln Asp Gly Asn Glu Glu Leu Lys Asp Leu Glu Glu Phe Gly
 115 120 125 130
 gaa aat gaa gag gaa att gtg cat tcc cag gag ttg ctt tct aca gaa 488
 Glu Asn Glu Glu Glu Ile Val His Ser Gln Glu Leu Leu Ser Thr Glu
 135 140 145

gag aac aag aca act cag gaa ttt gta gag gca gaa gca ata gaa gat 536
 Glu Asn Lys Thr Thr Gln Glu Phe Val Glu Ala Glu Ala Ile Glu Asp
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 Arg Glu Lys Glu Asp Ile Glu Ser Gln Glu Thr Glu Ala Gln Glu Gly
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 gaa gat gac acc ttt cta aca gcc caa gat ggt gag gaa gaa gaa aat 632
 Glu Asp Asp Thr Phe Leu Thr Ala Gln Asp Gly Glu Glu Glu Glu Asn
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 gag aaa gat ata gca ggt tct ggt gat ggc aca caa gaa gta tct aaa 680
 Glu Lys Asp Ile Ala Gly Ser Gly Asp Gly Thr Gln Glu Val Ser Lys
 195 200 205 210
 cct ctt cct tca gaa ggg agc cta gct gag gct gat cac aca gct cat 728
 Pro Leu Pro Ser Glu Gly Ser Leu Ala Glu Ala Asp His Thr Ala His
 215 220 225
 gaa gag atg gaa gct aat gcg act ggg aaa gaa gct gag gat gac aac 776
 Glu Glu Met Glu Ala Asn Ala Thr Gly Lys Glu Ala Glu Asp Asp Asn
 230 235 240
 atc tcg gtc aca atc cag gct gaa gat gcc atc act ctg gat ttt gat 824
 Ile Ser Val Thr Ile Gln Ala Glu Asp Ala Ile Thr Leu Asp Phe Asp
 245 250 255
 ggt gat gac ctc cta gaa aca ggt aaa aat gtg aaa att aca gat tct 872
 Gly Asp Asp Leu Leu Glu Thr Gly Lys Asn Val Lys Ile Thr Asp Ser
 260 265 270
 gaa gca agt aag cca aaa gat gtg cag gac gcc att gca cag agc ccg 920
 Glu Ala Ser Lys Pro Lys Asp Val Gln Asp Ala Ile Ala Gln Ser Pro
 275 280 285 290

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Glu Lys Glu Ala Lys Asp Tyr Glu Met Asn Pro Asn His Lys Asp Gly	
295 300 305	
aag aag gaa gac tcc gtg aag ggt gag cct gtc gag aag gaa gcc aga	1016
Lys Lys Glu Asp Ser Val Lys Gly Glu Pro Val Glu Lys Glu Ala Arg	
310 315 320	
gaa agt gct aag aaa gca gaa tct gga gac aaa gaa aag gat act ttg	1064
Glu Ser Ala Lys Lys Ala Glu Ser Gly Asp Lys Glu Lys Asp Thr Leu	
325 330 335	
aag aaa ggg ccc tcg tct aca ggg gcc tct ggt caa gca aag agc tct	1112
Lys Lys Gly Pro Ser Ser Thr Gly Ala Ser Gly Gln Ala Lys Ser Ser	
340 345 350	
tca aag gaa tct aaa gac agc aag aca tca tct aaa gat gac aaa ggg	1160
Ser Lys Glu Ser Lys Asp Ser Lys Thr Ser Ser Lys Asp Asp Lys Gly	
355 360 365 370	
agc aca ggc agt gct ggt ggg agc agt gga agc tca acc aag aac atc	1208
Ser Thr Gly Ser Ala Gly Gly Ser Ser Gly Ser Ser Thr Lys Asn Ile	
375 380 385	
tgg gtc agt gga ctg tct tct aat acc aaa gct gct gat ttg aag aac	1256
Trp Val Ser Gly Leu Ser Ser Asn Thr Lys Ala Ala Asp Leu Lys Asn	
390 395 400	
ctc ttt ggc aaa tat gga aag gtt cta agt gca aag gta gtt aca aat	1304
Leu Phe Gly Lys Tyr Gly Lys Val Leu Ser Ala Lys Val Val Thr Asn	
405 410 415	
gct cga agt cct ggg gca aaa tgc tat ggc atc gta acc atg tct tca	1352
Ala Arg Ser Pro Gly Ala Lys Cys Tyr Gly Ile Val Thr Met Ser Ser	
420 425 430	

agc aca gaa gtg tcc aga tgt gtt gca cat ctc cat cgc aca gag ctg 1400
 Ser Thr Glu Val Ser Arg Cys Val Ala His Leu His Arg Thr Glu Leu
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 His Gly Gln Leu Ile Ser Val Glu Lys Val Lys Gly Asp Pro Ser Lys
 455 460 465
 aaa gaa atg aag aaa gaa aat gat gag aag agt agc tca cgg agc gct 1496
 Lys Glu Met Lys Lys Glu Asn Asp Glu Lys Ser Ser Ser Arg Ser Ala
 470 475 480
 ggt gat aaa aag aac gcg agt gat cgg agt gcc aag aca caa gca tct 1544
 Gly Asp Lys Lys Asn Ala Ser Asp Arg Ser Ala Lys Thr Gln Ala Ser
 485 490 495
 att aaa aaa gaa gag aaa agg tca tct gag aaa tca gaa aaa aaa gaa 1592
 Ile Lys Lys Glu Glu Lys Arg Ser Ser Glu Lys Ser Glu Lys Lys Glu
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 agc aaa gat act aag aaa ata gag aaa gat gag aag aac gac gat ggt 1640
 Ser Lys Asp Thr Lys Lys Ile Glu Lys Asp Glu Lys Asn Asp Asp Gly
 515 520 525 530
 cca agt ggg cag act tca gag tcc ctg aaa aag agt gaa gag aag aag 1688
 Pro Ser Gly Gln Thr Ser Glu Ser Leu Lys Lys Ser Glu Glu Lys Lys
 535 540 545
 cgg ata agt tca aag agt cca gga cat atg gtg ata cta aac caa acc 1736
 Arg Ile Ser Ser Lys Ser Pro Gly His Met Val Ile Leu Asn Gln Thr
 550 555 560
 aag gga gat cat tgt agg ccg tca aga agg ggc aga tat gag aaa ggt 1784
 Lys Gly Asp His Cys Arg Pro Ser Arg Arg Gly Arg Tyr Glu Lys Gly
 565 570 575

cat gga aga agc aaa gaa aag gag agg gct agc cta gat aaa aaa aga	1832
His Gly Arg Ser Lys Glu Lys Glu Arg Ala Ser Leu Asp Lys Lys Arg	
580 585 590	
gac aaa gac tac aga agg aaa gag atc ttg cct ttt gaa aag atg aag	1880
Asp Lys Asp Tyr Arg Arg Lys Glu Ile Leu Pro Phe Glu Lys Met Lys	
595 600 605 610	
gaa caa aga ttg aga gaa cat tta gtt cgt ttt gaa aga ctg aaa caa	1928
Glu Gln Arg Leu Arg Glu His Leu Val Arg Phe Glu Arg Leu Lys Gln	
615 620 625	
gca gtg gaa ttc aga aga cga aaa gag att gca gaa aga gag cgt cga	1976
Ala Val Glu Phe Arg Arg Arg Lys Glu Ile Ala Glu Arg Glu Arg Arg	
630 635 640	
gag cgt gaa cgc att aga ata att cgt gaa cgg gaa gaa cgg gaa cgc	2024
Glu Arg Glu Arg Ile Arg Ile Ile Arg Glu Arg Glu Glu Arg Glu Arg	
645 650 655	
tta cag aga gag aga gag cgc cta gaa att gaa agg caa aaa cta gag	2072
Leu Gln Arg Glu Arg Glu Arg Leu Glu Ile Glu Arg Gln Lys Leu Glu	
660 665 670	
aga gag aga atg gaa cgc gaa cgc ttg gaa agg gaa cgc att cgt att	2120
Arg Glu Arg Met Glu Arg Glu Arg Leu Glu Arg Glu Arg Ile Arg Ile	
675 680 685 690	
gaa cag gag cgg cgc agg gaa gct gaa agg att gct cgg gag aga gag	2168
Glu Gln Glu Arg Arg Arg Glu Ala Glu Arg Ile Ala Arg Glu Arg Glu	
695 700 705	
gag ctc aga agg cag cag cag cag ctt cgc tat gaa caa gaa aaa agg	2216
Glu Leu Arg Arg Gln Gln Gln Gln Leu Arg Tyr Glu Gln Glu Lys Arg	
710 715 720	

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 Asn Ser Leu Lys Arg Pro Arg Asp Val Asp His Arg Arg Asp Asp Pro
 725 730 735
 tac tgg agc gag aat aaa aag tta tct cta gat aca gag gca cga ttc 2312
 Tyr Trp Ser Glu Asn Lys Lys Leu Ser Leu Asp Thr Glu Ala Arg Phe
 740 745 750
 ggc cat ggg tct gac tat cgt caa cag agc agg ttc ctt gac ttc agt 2360
 Gly His Gly Ser Asp Tyr Arg Gln Gln Ser Arg Phe Leu Asp Phe Ser
 755 760 765 770
 cac cga gaa cgg gcc agg ttt cct gac act gca tct gtg cag tca tcc 2408
 His Arg Glu Arg Ala Arg Phe Pro Asp Thr Ala Ser Val Gln Ser Ser
 775 780 785
 ttt gaa aga cgg gaa cgg ttt gtt ggt caa agt gaa gga aag aaa ccg 2456
 Phe Glu Arg Arg Glu Arg Phe Val Gly Gln Ser Glu Gly Lys Lys Pro
 790 795 800
 aga cca gca gcc cga aga gaa gag cca agt ttt gaa agg tac cct aaa 2504
 Arg Pro Ala Ala Arg Arg Glu Glu Pro Ser Phe Glu Arg Tyr Pro Lys
 805 810 815
 aac ttc agt gat tcc aga aga aat gag cct cca cca cca aga aat gaa 2552
 Asn Phe Ser Asp Ser Arg Arg Asn Glu Pro Pro Pro Pro Arg Asn Glu
 820 825 830
 ctt aga gaa aca gac aga cga gag gtc cga ggg gag aga gac gag aga 2600
 Leu Arg Glu Thr Asp Arg Arg Glu Val Arg Gly Glu Arg Asp Glu Arg
 835 840 845 850
 aga aca gta atc ctt cat gac cga cct gag gtc gct cac ccc aga cac 2648
 Arg Thr Val Ile Leu His Asp Arg Pro Glu Val Ala His Pro Arg His
 855 860 865

cct cga gag act gtg ccc aat cct tct aga cca act tcc tgg aaa agc 2696
 Pro Arg Glu Thr Val Pro Asn Pro Ser Arg Pro Thr Ser Trp Lys Ser
 870 875 880
 gaa gcg aat atg tcc aca gag aaa cgg gag tca cga gtt gaa agg cca 2744
 Glu Ala Asn Met Ser Thr Glu Lys Arg Glu Ser Arg Val Glu Arg Pro
 885 890 895
 gaa aga tct ggg aga gaa gtc tct gga cac act gtg agg gga gcg ccc 2792
 Glu Arg Ser Gly Arg Glu Val Ser Gly His Thr Val Arg Gly Ala Pro
 900 905 910
 ccc ggg aat cgg agt agt gcc tca ggc tat gga acc cga gag gga gag 2840
 Pro Gly Asn Arg Ser Ser Ala Ser Gly Tyr Gly Thr Arg Glu Gly Glu
 915 920 925 930
 cga gga gtc att gct gac aga gga agc gga aca cag cac tac cct gaa 2888
 Arg Gly Val Ile Ala Asp Arg Gly Ser Gly Thr Gln His Tyr Pro Glu
 935 940 945
 gaa cga cat gtc gtg gaa cgt cat gga cgg gac aca agt gga cca agg 2936
 Glu Arg His Val Val Glu Arg His Gly Arg Asp Thr Ser Gly Pro Arg
 950 955 960
 aaa gag tgg cat ggc cca ccc tct cag ggg cct agc tac cat gac aca 2984
 Lys Glu Trp His Gly Pro Pro Ser Gln Gly Pro Ser Tyr His Asp Thr
 965 970 975
 aga cga atg ggt gat ggc cga gca gga gca ggc atg ata acc caa cac 3032
 Arg Arg Met Gly Asp Gly Arg Ala Gly Ala Gly Met Ile Thr Gln His
 980 985 990
 tca agc act gcg tcc cca gtg aac agg att gta cag atg agt ggt 3077
 Ser Ser Thr Ala Ser Pro Val Asn Arg Ile Val Gln Met Ser Gly
 995 1000 1005

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 Asn Ser Leu Pro Arg Gly Ser Ser Ser Gly Phe Lys Pro Phe Lys
 1010 1015 1020
 agt gga cct cca cgg cga ttt taacgcaagc ttcctgctgt ggcttcaaga 3173
 Ser Gly Pro Pro Arg Arg Phe
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<213> Mus musculus

<400> 156

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 35 40 45

Val Ser Arg Leu Lys Gln Ala Ile Glu Glu Glu Gly Gly Asp Pro Asp
 50 55 60
 Asn Ile Glu Leu Thr Val Ser Thr Asp Thr Pro Asn Lys Lys Pro Thr
 65 70 75 80
 Lys Gly Lys Gly Lys Lys Gln Glu Ala Asp Glu Leu Ser Gly Asp Ala
 85 90 95
 Ser Val Glu Asp Asp Ser Phe Val Lys Asp Cys Glu Leu Glu Asn Gln
 100 105 110
 Glu Thr His Asp Gln Asp Gly Asn Glu Glu Leu Lys Asp Leu Glu Glu
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 Phe Gly Glu Asn Glu Glu Glu Ile Val His Ser Gln Glu Leu Leu Ser
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 Thr Glu Glu Asn Lys Thr Thr Gln Glu Phe Val Glu Ala Glu Ala Ile
 145 150 155 160
 Glu Asp Arg Glu Lys Glu Asp Ile Glu Ser Gln Glu Thr Glu Ala Gln
 165 170 175
 Glu Gly Glu Asp Asp Thr Phe Leu Thr Ala Gln Asp Gly Glu Glu Glu
 180 185 190
 Glu Asn Glu Lys Asp Ile Ala Gly Ser Gly Asp Gly Thr Gln Glu Val
 195 200 205
 Ser Lys Pro Leu Pro Ser Glu Gly Ser Leu Ala Glu Ala Asp His Thr
 210 215 220
 Ala His Glu Glu Met Glu Ala Asn Ala Thr Gly Lys Glu Ala Glu Asp
 225 230 235 240
 Asp Asn Ile Ser Val Thr Ile Gln Ala Glu Asp Ala Ile Thr Leu Asp
 245 250 255
 Phe Asp Gly Asp Asp Leu Leu Glu Thr Gly Lys Asn Val Lys Ile Thr

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260 265 270
Asp Ser Glu Ala Ser Lys Pro Lys Asp Val Gln Asp Ala Ile Ala Gln
275 280 285
Ser Pro Glu Lys Glu Ala Lys Asp Tyr Glu Met Asn Pro Asn His Lys
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Asp Gly Lys Lys Glu Asp Ser Val Lys Gly Glu Pro Val Glu Lys Glu
305 310 315 320
Ala Arg Glu Ser Ala Lys Lys Ala Glu Ser Gly Asp Lys Glu Lys Asp
325 330 335
Thr Leu Lys Lys Gly Pro Ser Ser Thr Gly Ala Ser Gly Gln Ala Lys
340 345 350
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355 360 365
Lys Gly Ser Thr Gly Ser Ala Gly Gly Ser Ser Gly Ser Ser Thr Lys
370 375 380
Asn Ile Trp Val Ser Gly Leu Ser Ser Asn Thr Lys Ala Ala Asp Leu
385 390 395 400
Lys Asn Leu Phe Gly Lys Tyr Gly Lys Val Leu Ser Ala Lys Val Val
405 410 415
Thr Asn Ala Arg Ser Pro Gly Ala Lys Cys Tyr Gly Ile Val Thr Met
420 425 430
Ser Ser Ser Thr Glu Val Ser Arg Cys Val Ala His Leu His Arg Thr
435 440 445
Glu Leu His Gly Gln Leu Ile Ser Val Glu Lys Val Lys Gly Asp Pro
450 455 460
Ser Lys Lys Glu Met Lys Lys Glu Asn Asp Glu Lys Ser Ser Ser Arg
465 470 475 480

Ser Ala Gly Asp Lys Lys Asn Ala Ser Asp Arg Ser Ala Lys Thr Gln
 485 490 495
 Ala Ser Ile Lys Lys Glu Glu Lys Arg Ser Ser Glu Lys Ser Glu Lys
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 Lys Glu Ser Lys Asp Thr Lys Lys Ile Glu Lys Asp Glu Lys Asn Asp
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 Asp Gly Pro Ser Gly Gln Thr Ser Glu Ser Leu Lys Lys Ser Glu Glu
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 545 550 555 560
 Gln Thr Lys Gly Asp His Cys Arg Pro Ser Arg Arg Gly Arg Tyr Glu
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 Lys Gly His Gly Arg Ser Lys Glu Lys Glu Arg Ala Ser Leu Asp Lys
 580 585 590
 Lys Arg Asp Lys Asp Tyr Arg Arg Lys Glu Ile Leu Pro Phe Glu Lys
 595 600 605
 Met Lys Glu Gln Arg Leu Arg Glu His Leu Val Arg Phe Glu Arg Leu
 610 615 620
 Lys Gln Ala Val Glu Phe Arg Arg Arg Lys Glu Ile Ala Glu Arg Glu
 625 630 635 640
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 645 650 655
 Glu Arg Leu Gln Arg Glu Arg Glu Arg Leu Glu Ile Glu Arg Gln Lys
 660 665 670
 Leu Glu Arg Glu Arg Met Glu Arg Glu Arg Leu Glu Arg Glu Arg Ile
 675 680 685
 Arg Ile Glu Gln Glu Arg Arg Arg Glu Ala Glu Arg Ile Ala Arg Glu

517/617

690	695	700	
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Lys Arg Asn Ser Leu Lys Arg Pro Arg Asp Val Asp His Arg Arg Asp			
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Asp Pro Tyr Trp Ser Glu Asn Lys Lys Leu Ser Leu Asp Thr Glu Ala			
	740	745	750
Arg Phe Gly His Gly Ser Asp Tyr Arg Gln Gln Ser Arg Phe Leu Asp			
	755	760	765
Phe Ser His Arg Glu Arg Ala Arg Phe Pro Asp Thr Ala Ser Val Gln			
	770	775	780
Ser Ser Phe Glu Arg Arg Glu Arg Phe Val Gly Gln Ser Glu Gly Lys			
785	790	795	800
Lys Pro Arg Pro Ala Ala Arg Arg Glu Glu Pro Ser Phe Glu Arg Tyr			
	805	810	815
Pro Lys Asn Phe Ser Asp Ser Arg Arg Asn Glu Pro Pro Pro Pro Arg			
	820	825	830
Asn Glu Leu Arg Glu Thr Asp Arg Arg Glu Val Arg Gly Glu Arg Asp			
	835	840	845
Glu Arg Arg Thr Val Ile Leu His Asp Arg Pro Glu Val Ala His Pro			
	850	855	860
Arg His Pro Arg Glu Thr Val Pro Asn Pro Ser Arg Pro Thr Ser Trp			
865	870	875	880
Lys Ser Glu Ala Asn Met Ser Thr Glu Lys Arg Glu Ser Arg Val Glu			
	885	890	895
Arg Pro Glu Arg Ser Gly Arg Glu Val Ser Gly His Thr Val Arg Gly			
	900	905	910

Ala Pro Pro Gly Asn Arg Ser Ser Ala Ser Gly Tyr Gly Thr Arg Glu
 915 920 925
 Gly Glu Arg Gly Val Ile Ala Asp Arg Gly Ser Gly Thr Gln His Tyr
 930 935 940
 Pro Glu Glu Arg His Val Val Glu Arg His Gly Arg Asp Thr Ser Gly
 945 950 955 960
 Pro Arg Lys Glu Trp His Gly Pro Pro Ser Gln Gly Pro Ser Tyr His
 965 970 975
 Asp Thr Arg Arg Met Gly Asp Gly Arg Ala Gly Ala Gly Met Ile Thr
 980 985 990
 Gln His Ser Ser Thr Ala Ser Pro Val Asn Arg Ile Val Gln Met Ser
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<212> DNA

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<221> CDS

<222> (641).. (2449)

<223>

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ggcggaactt agacatcacc ggagtcaaga ccgtgctcat ctcccgaactc aagcaggcta	180
ttgaagagga aggaggcgat ccagataata ttgaattaac tgtttcaact gatactccaa	240
acaagaaacc aactaaaggc aaaggtaaaa aacatgaagc agatgagttg agtggagatg	300
cttctgtgga agatgatgct tttatcaagg aaattgaagc tcaagaaggt gaagatgata	360
cctttctaac agcccaagat ggtgaggaag aagaaaatga gaaagctctt caaaggaatc	420
taaagacagc aagacatcat ctaaagatga caaaggaagt acaagtagta ctagtggtag	480
cagtggaagc tcaactaaaa atatctgggt tagtggactt tcatctaata ccaaagctgc	540
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tgctcgaagt cctggggcaa aatgctatgg cattgttaact atg tct tca agc aca	655
Met Ser Ser Ser Thr	
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gag gtg tcc agg tgt att gca cat ctt cat cgc act gag ctg cat gga	703
Glu Val Ser Arg Cys Ile Ala His Leu His Arg Thr Glu Leu His Gly	
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cag ctg att tct gtt gaa aaa gta aaa ggt gat ccc tct aag aaa gaa	751
Gln Leu Ile Ser Val Glu Lys Val Lys Gly Asp Pro Ser Lys Lys Glu	
25 30 35	
atg aag aaa gaa aat gat gaa aag agt agt tca aga agt tct gga gat	799
Met Lys Lys Glu Asn Asp Glu Lys Ser Ser Ser Arg Ser Ser Gly Asp	
40 45 50	
aaa aaa aat acg agt gat aga agt agc aag aca caa gcc tct gtc aaa	847
Lys Lys Asn Thr Ser Asp Arg Ser Ser Lys Thr Gln Ala Ser Val Lys	
55 60 65	
aaa gaa gag aaa aga tcg tct gag aaa tct gaa aaa aaa gaa agc aag	895
Lys Glu Glu Lys Arg Ser Ser Glu Lys Ser Glu Lys Lys Glu Ser Lys	
70 75 80 85	

gat act aag aaa ata gaa ggt aaa gat gag aag aat gat aat gga gca 943
 Asp Thr Lys Lys Ile Glu Gly Lys Asp Glu Lys Asn Asp Asn Gly Ala
 90 95 100
 agt ggc caa aca tca gaa tcg att aaa aaa agt gaa gaa aag aag cga 991
 Ser Gly Gln Thr Ser Glu Ser Ile Lys Lys Ser Glu Glu Lys Lys Arg
 105 110 115
 ata agt tcc aag agt cca gga cat atg gta ata cta gac caa act aaa 1039
 Ile Ser Ser Lys Ser Pro Gly His Met Val Ile Leu Asp Gln Thr Lys
 120 125 130
 gga gat cat tgt aga cca tca aga aga gga aga tat gag aaa att cat 1087
 Gly Asp His Cys Arg Pro Ser Arg Arg Gly Arg Tyr Glu Lys Ile His
 135 140 145
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 Gly Arg Ser Lys Glu Lys Glu Arg Ala Ser Leu Asp Lys Lys Arg Asp
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 aaa gac tac aga agg aaa gag atc ttg cct ttt gaa aag atg aag gaa 1183
 Lys Asp Tyr Arg Arg Lys Glu Ile Leu Pro Phe Glu Lys Met Lys Glu
 170 175 180
 caa agg ttg aga gaa cat tta gtt cgt ttt gaa agg ctg cga cga gca 1231
 Gln Arg Leu Arg Glu His Leu Val Arg Phe Glu Arg Leu Arg Arg Ala
 185 190 195
 atg gaa ctt cga aga cga aga gag att gca gag aga gag cgt cga gag 1279
 Met Glu Leu Arg Arg Arg Arg Glu Ile Ala Glu Arg Glu Arg Arg Glu
 200 205 210
 cga gaa cgc att aga ata att cgt gaa cgg gaa gaa cgg gaa cgc tta 1327
 Arg Glu Arg Ile Arg Ile Ile Arg Glu Arg Glu Glu Arg Glu Arg Leu
 215 220 225

cag aga gag aga gag cgc cta gaa att gaa agg caa aaa cta gag aga 1375
 Gln Arg Glu Arg Glu Arg Leu Glu Ile Glu Arg Gln Lys Leu Glu Arg
 230 235 240 245
 gag aga atg gaa cgc gaa cgc ttg gaa agg gaa cgc att cgt att gaa 1423
 Glu Arg Met Glu Arg Glu Arg Leu Glu Arg Glu Arg Ile Arg Ile Glu
 250 255 260
 cag gaa cgt cgt aag gaa gct gaa cgg att gct cga gaa aga gag gaa 1471
 Gln Glu Arg Arg Lys Glu Ala Glu Arg Ile Ala Arg Glu Arg Glu Glu
 265 270 275
 ctc aga agg caa caa cag cag ctt cgt tat gaa caa gaa aaa agg aat 1519
 Leu Arg Arg Gln Gln Gln Gln Leu Arg Tyr Glu Gln Glu Lys Arg Asn
 280 285 290
 tcc ttg aaa cgc cca cgt gat gta gat cat agg cga gat gat cct tac 1567
 Ser Leu Lys Arg Pro Arg Asp Val Asp His Arg Arg Asp Asp Pro Tyr
 295 300 305
 tgg agc gag aat aaa aag ttg tct cta gat aca gat gca cga ttt ggc 1615
 Trp Ser Glu Asn Lys Lys Leu Ser Leu Asp Thr Asp Ala Arg Phe Gly
 310 315 320 325
 cat gga tcc gac tac tct cgc caa cag aac aga ttt aat gac ttt gat 1663
 His Gly Ser Asp Tyr Ser Arg Gln Gln Asn Arg Phe Asn Asp Phe Asp
 330 335 340
 cac cga gag agg ggc agg ttt cct gag agt tca gca gta cag tct tca 1711
 His Arg Glu Arg Gly Arg Phe Pro Glu Ser Ser Ala Val Gln Ser Ser
 345 350 355
 tct ttt gaa agg cgg gat cgc ttt gtt ggt caa agt gag ggg aaa aaa 1759
 Ser Phe Glu Arg Arg Asp Arg Phe Val Gly Gln Ser Glu Gly Lys Lys
 360 365 370

gca cga cct act gca cga agg gaa gat cca agc ttc gaa aga tat ccc 1807
 Ala Arg Pro Thr Ala Arg Arg Glu Asp Pro Ser Phe Glu Arg Tyr Pro
 375 380 385
 aaa aat ttc agt gac tcc aga aga aat gag cct cca cca cca aga aat 1855
 Lys Asn Phe Ser Asp Ser Arg Arg Asn Glu Pro Pro Pro Pro Arg Asn
 390 395 400 405
 gaa ctt aga gaa tca gac agg cga gaa gta cga ggg gag cga gac gaa 1903
 Glu Leu Arg Glu Ser Asp Arg Arg Glu Val Arg Gly Glu Arg Asp Glu
 410 415 420
 agg aga acg gtg att att cat gac agg cct gat atc act cat cct aga 1951
 Arg Arg Thr Val Ile Ile His Asp Arg Pro Asp Ile Thr His Pro Arg
 425 430 435
 cat cct cga gag gca ggg ccc aat cct tcc aga ccc acc agc tgg aaa 1999
 His Pro Arg Glu Ala Gly Pro Asn Pro Ser Arg Pro Thr Ser Trp Lys
 440 445 450
 agt gaa gga agc atg tcc act gac aaa cgg gaa aca aga gtt gaa agg 2047
 Ser Glu Gly Ser Met Ser Thr Asp Lys Arg Glu Thr Arg Val Glu Arg
 455 460 465
 cca gaa cga tct ggg aga gaa gta tca ggg cac agt gtg aga ggc gct 2095
 Pro Glu Arg Ser Gly Arg Glu Val Ser Gly His Ser Val Arg Gly Ala
 470 475 480 485
 ccc cct ggg aat cgt agc agc gct tcg ggg tac ggg agc aga gag gga 2143
 Pro Pro Gly Asn Arg Ser Ser Ala Ser Gly Tyr Gly Ser Arg Glu Gly
 490 495 500
 gac aga gga gtc atc aca gac cga gga ggt gga tca cag cac tat cct 2191
 Asp Arg Gly Val Ile Thr Asp Arg Gly Gly Gly Ser Gln His Tyr Pro
 505 510 515

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gag gag cga cat gtg gtt gaa cgc cat gga cgg gac aca agc gga cca 2239
 Glu Glu Arg His Val Val Glu Arg His Gly Arg Asp Thr Ser Gly Pro
 520 525 530
 agg aaa gag tgg cat ggt cca ccc tct caa ggg cct agc tat cat gat 2287
 Arg Lys Glu Trp His Gly Pro Pro Ser Gln Gly Pro Ser Tyr His Asp
 535 540 545
 acg agg cga atg ggt gac ggc cgg gca gga gca ggc atg ata acc caa 2335
 Thr Arg Arg Met Gly Asp Gly Arg Ala Gly Ala Gly Met Ile Thr Gln
 550 555 560 565
 cat tca agt aac gca tcc cca att aat aga att gta caa atc agt ggc 2383
 His Ser Ser Asn Ala Ser Pro Ile Asn Arg Ile Val Gln Ile Ser Gly
 570 575 580
 aat tcc atg cca aga gga agt ggc tcc gga ttt aag cca ttt aag ggt 2431
 Asn Ser Met Pro Arg Gly Ser Gly Ser Gly Phe Lys Pro Phe Lys Gly
 585 590 595
 gga cct ccg cga cga ttc tgaaaatgag ctctctgccca aggttttaag 2479
 Gly Pro Pro Arg Arg Phe
 600
 ataattttatt gaaatctcct gtaaaccttta cttgactact tatgaagagg acctctgact 2539
 tgcttgagag ttctgtcaga cttttctttt taaaaattta acatgattgc ttttctcaat 2599
 tttggagaag atgtttaaat agttctgttg taacttttaa tagttttgtg tatcattcaa 2659
 ctttttttct tgcagcaccg aggcacattt gaaaagatgg aattgaagtc gttttgttta 2719
 acgctgtgtg aatataaaga gtagtttgca gctgtgtggt agtggtttta tttgcagcct 2779
 tagctctgtg gtgtctggct ctagagttac ttctttttac caagcatttt cagcctccat 2839
 tttgaaggct gtctacactt aagaagtctt agctgtctaa tttttagaga ataagattgt 2899
 tcattgcatt tctgagtatt atgtaacctt tttttgcaga aggtactgtt acattaagtg 2959
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tat

3022

<210> 158

<211> 603

<212> PRT

<213> Homo sapiens

<400> 158

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Thr Glu Leu His Gly Gln Leu Ile Ser Val Glu Lys Val Lys Gly Asp
20 25 30
Pro Ser Lys Lys Glu Met Lys Lys Glu Asn Asp Glu Lys Ser Ser Ser
35 40 45
Arg Ser Ser Gly Asp Lys Lys Asn Thr Ser Asp Arg Ser Ser Lys Thr
50 55 60
Gln Ala Ser Val Lys Lys Glu Glu Lys Arg Ser Ser Glu Lys Ser Glu
65 70 75 80
Lys Lys Glu Ser Lys Asp Thr Lys Lys Ile Glu Gly Lys Asp Glu Lys
85 90 95
Asn Asp Asn Gly Ala Ser Gly Gln Thr Ser Glu Ser Ile Lys Lys Ser
100 105 110
Glu Glu Lys Lys Arg Ile Ser Ser Lys Ser Pro Gly His Met Val Ile
115 120 125
Leu Asp Gln Thr Lys Gly Asp His Cys Arg Pro Ser Arg Arg Gly Arg
130 135 140
Tyr Glu Lys Ile His Gly Arg Ser Lys Glu Lys Glu Arg Ala Ser Leu
145 150 155 160

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Asp Lys Lys Arg Asp Lys Asp Tyr Arg Arg Lys Glu Ile Leu Pro Phe
165 170 175
Glu Lys Met Lys Glu Gln Arg Leu Arg Glu His Leu Val Arg Phe Glu
180 185 190
Arg Leu Arg Arg Ala Met Glu Leu Arg Arg Arg Arg Glu Ile Ala Glu
195 200 205
Arg Glu Arg Arg Glu Arg Glu Arg Ile Arg Ile Ile Arg Glu Arg Glu
210 215 220
Glu Arg Glu Arg Leu Gln Arg Glu Arg Glu Arg Leu Glu Ile Glu Arg
225 230 235 240
Gln Lys Leu Glu Arg Glu Arg Met Glu Arg Glu Arg Leu Glu Arg Glu
245 250 255
Arg Ile Arg Ile Glu Gln Glu Arg Arg Lys Glu Ala Glu Arg Ile Ala
260 265 270
Arg Glu Arg Glu Glu Leu Arg Arg Gln Gln Gln Gln Leu Arg Tyr Glu
275 280 285
Gln Glu Lys Arg Asn Ser Leu Lys Arg Pro Arg Asp Val Asp His Arg
290 295 300
Arg Asp Asp Pro Tyr Trp Ser Glu Asn Lys Lys Leu Ser Leu Asp Thr
305 310 315 320
Asp Ala Arg Phe Gly His Gly Ser Asp Tyr Ser Arg Gln Gln Asn Arg
325 330 335
Phe Asn Asp Phe Asp His Arg Glu Arg Gly Arg Phe Pro Glu Ser Ser
340 345 350
Ala Val Gln Ser Ser Ser Phe Glu Arg Arg Asp Arg Phe Val Gly Gln
355 360 365
Ser Glu Gly Lys Lys Ala Arg Pro Thr Ala Arg Arg Glu Asp Pro Ser

370 375 380
Phe Glu Arg Tyr Pro Lys Asn Phe Ser Asp Ser Arg Arg Asn Glu Pro
385 390 395 400
Pro Pro Pro Arg Asn Glu Leu Arg Glu Ser Asp Arg Arg Glu Val Arg
405 410 415
Gly Glu Arg Asp Glu Arg Arg Thr Val Ile Ile His Asp Arg Pro Asp
420 425 430
Ile Thr His Pro Arg His Pro Arg Glu Ala Gly Pro Asn Pro Ser Arg
435 440 445
Pro Thr Ser Trp Lys Ser Glu Gly Ser Met Ser Thr Asp Lys Arg Glu
450 455 460
Thr Arg Val Glu Arg Pro Glu Arg Ser Gly Arg Glu Val Ser Gly His
465 470 475 480
Ser Val Arg Gly Ala Pro Pro Gly Asn Arg Ser Ser Ala Ser Gly Tyr
485 490 495
Gly Ser Arg Glu Gly Asp Arg Gly Val Ile Thr Asp Arg Gly Gly Gly
500 505 510
Ser Gln His Tyr Pro Glu Glu Arg His Val Val Glu Arg His Gly Arg
515 520 525
Asp Thr Ser Gly Pro Arg Lys Glu Trp His Gly Pro Pro Ser Gln Gly
530 535 540
Pro Ser Tyr His Asp Thr Arg Arg Met Gly Asp Gly Arg Ala Gly Ala
545 550 555 560
Gly Met Ile Thr Gln His Ser Ser Asn Ala Ser Pro Ile Asn Arg Ile
565 570 575
Val Gln Ile Ser Gly Asn Ser Met Pro Arg Gly Ser Gly Ser Gly Phe
580 585 590

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Lys Pro Phe Lys Gly Gly Pro Pro Arg Arg Phe

595

600

<210> 159

<211> 3389

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (240).. (2744)

<223>

<400> 159

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 ttcatcttcc ctgcgccatc ttgtattat ttctaattta ttttgatgt caaaaggcac 120
 tgatgaagat attttctctg gagtctcctt ctttctaacc cggtctctcc gatgtgaacc 180
 gagccgtcgt ccgcccgcgc ccgcccgcgc cgccgcccgc gcccgcccgc cagcccacc 239
 atg tct cgc cgc aag caa ggc aaa ccc cag cac tta agc aaa cgg gaa 287
 Met Ser Arg Arg Lys Gln Gly Lys Pro Gln His Leu Ser Lys Arg Glu
 1 5 10 15
 ttc tcg ccc gag cct ctt gaa gcc att ctt aca gat gat gaa cca gac 335
 Phe Ser Pro Glu Pro Leu Glu Ala Ile Leu Thr Asp Asp Glu Pro Asp
 20 25 30
 cac ggc ccg ttg gga gct cca gaa ggg gat cat gac ctc ctc acc tgt 383
 His Gly Pro Leu Gly Ala Pro Glu Gly Asp His Asp Leu Leu Thr Cys
 35 40 45
 ggg cag tgc cag atg aac ttc cca ttg ggg gac att ctt att ttt atc 431
 Gly Gln Cys Gln Met Asn Phe Pro Leu Gly Asp Ile Leu Ile Phe Ile

50	55	60	
gag cac aaa cgg aaa caa tgc aat ggc agc ctc tgc tta gaa aaa gct			479
Glu His Lys Arg Lys Gln Cys Asn Gly Ser Leu Cys Leu Glu Lys Ala			
65	70	75	80
gtg gat aag cca cct tcc cct tca cca atc gag atg aaa aaa gca tcc			527
Val Asp Lys Pro Pro Ser Pro Ser Pro Ile Glu Met Lys Lys Ala Ser			
85	90	95	
aat ccc gtg gag gtt ggc atc cag gtc acg cca gag gat gac gat tgt			575
Asn Pro Val Glu Val Gly Ile Gln Val Thr Pro Glu Asp Asp Asp Cys			
100	105	110	
tta tca acg tca tct aga gga att tgc ccc aaa cag gaa cac ata gca			623
Leu Ser Thr Ser Ser Arg Gly Ile Cys Pro Lys Gln Glu His Ile Ala			
115	120	125	
gat aaa ctt ctg cac tgg agg ggc ctc tcc tcc cct cgt tct gca cat			671
Asp Lys Leu Leu His Trp Arg Gly Leu Ser Ser Pro Arg Ser Ala His			
130	135	140	
gga gct cta atc ccc acg cct ggg atg agt gca gaa tat gcc ccg cag			719
Gly Ala Leu Ile Pro Thr Pro Gly Met Ser Ala Glu Tyr Ala Pro Gln			
145	150	155	160
ggt att tgt aaa gat gag ccc agc agc tac aca tgt aca act tgt aaa			767
Gly Ile Cys Lys Asp Glu Pro Ser Ser Tyr Thr Cys Thr Thr Cys Lys			
165	170	175	
cag cca ttc acc agt gca tgg ttt ctc ttg caa cac gca cag aac act			815
Gln Pro Phe Thr Ser Ala Trp Phe Leu Leu Gln His Ala Gln Asn Thr			
180	185	190	
cat gga tta aga atc tac tta gaa agc gaa cac gga agt ccc ctg acc			863
His Gly Leu Arg Ile Tyr Leu Glu Ser Glu His Gly Ser Pro Leu Thr			

195	200	205	
ccg cgg gtt ggt atc cct tca gga cta ggt gca gaa tgt cct tcc cag			911
Pro Arg Val Gly Ile Pro Ser Gly Leu Gly Ala Glu Cys Pro Ser Gln			
210	215	220	
cca cct ctc cat ggg att cat att gca gac aat aac ccc ttt aac ctg			959
Pro Pro Leu His Gly Ile His Ile Ala Asp Asn Asn Pro Phe Asn Leu			
225	230	235	240
cta aga ata cca gga tca gta tcg aga gag gct tcc ggc ctg gca gaa			1007
Leu Arg Ile Pro Gly Ser Val Ser Arg Glu Ala Ser Gly Leu Ala Glu			
245	250	255	
ggg cgc ttt cca ccc act ccc ccc ctg ttt agt cca cca ccg aga cat			1055
Gly Arg Phe Pro Pro Thr Pro Pro Leu Phe Ser Pro Pro Pro Arg His			
260	265	270	
cac ttg gac ccc cac cgc ata gag cgc ctg ggg gcg gaa gag atg gcc			1103
His Leu Asp Pro His Arg Ile Glu Arg Leu Gly Ala Glu Glu Met Ala			
275	280	285	
ctg gcc acc cat cac ccg agt gcc ttt gac agg gtg ctg cgg ttg aat			1151
Leu Ala Thr His His Pro Ser Ala Phe Asp Arg Val Leu Arg Leu Asn			
290	295	300	
cca atg gct atg gag cct ccc gcc atg gat ttc tct agg aga ctt aga			1199
Pro Met Ala Met Glu Pro Pro Ala Met Asp Phe Ser Arg Arg Leu Arg			
305	310	315	320
gag ctg gca ggg aac acg tct agc cca ccg ctg tcc cca ggc cgg ccc			1247
Glu Leu Ala Gly Asn Thr Ser Ser Pro Pro Leu Ser Pro Gly Arg Pro			
325	330	335	
agc cct atg caa agg tta ctg caa cca ttc cag cca ggt agc aag ccg			1295
Ser Pro Met Gln Arg Leu Leu Gln Pro Phe Gln Pro Gly Ser Lys Pro			

340	345	350	
ccc ttc ctg gcg acg ccc ccc ctc cct cct ctg caa tcc gcc cct cct			1343
Pro Phe Leu Ala Thr Pro Pro Leu Pro Pro Leu Gln Ser Ala Pro Pro			
355	360	365	
ccc tcc cag ccc ccg gtc aag tcc aag tca tgc gag ttc tgc ggc aag			1391
Pro Ser Gln Pro Pro Val Lys Ser Lys Ser Cys Glu Phe Cys Gly Lys			
370	375	380	
acg ttc aaa ttt cag agc aac ctg gtg gtg cac cgg cgc agc cac acg			1439
Thr Phe Lys Phe Gln Ser Asn Leu Val Val His Arg Arg Ser His Thr			
385	390	395	400
ggc gag aag ccc tac aag tgc aac ctg tgc gac cac gcg tgc acc cag			1487
Gly Glu Lys Pro Tyr Lys Cys Asn Leu Cys Asp His Ala Cys Thr Gln			
405	410	415	
gcc agc aag ctg aag cgc cac atg aag acg cac atg cac aaa tcg tcc			1535
Ala Ser Lys Leu Lys Arg His Met Lys Thr His Met His Lys Ser Ser			
420	425	430	
ccc atg acg gtc aag tcc gac gac ggt ctc tcc acc gcc agc tcc ccg			1583
Pro Met Thr Val Lys Ser Asp Asp Gly Leu Ser Thr Ala Ser Ser Pro			
435	440	445	
gaa ccc ggc acc agc gac ttg gtg ggc agc gcc agc agc gcg ctc aag			1631
Glu Pro Gly Thr Ser Asp Leu Val Gly Ser Ala Ser Ser Ala Leu Lys			
450	455	460	
tcc gtg gtg gcc aag ttc aag agc gag aac gac ccc aac ctg atc ccg			1679
Ser Val Val Ala Lys Phe Lys Ser Glu Asn Asp Pro Asn Leu Ile Pro			
465	470	475	480
gag aac ggg gac gag gag gaa gag gag gac gag gag gaa gag gaa gaa			1727
Glu Asn Gly Asp Glu Glu Glu Glu Glu Asp Asp Glu Glu Glu Glu Glu			

485	490	495	
gag gag gaa gag gag gag gag gag ctg acg gag agc gag agg gtg gac			1775
Glu Glu Glu Glu Glu Glu Glu Glu Leu Thr Glu Ser Glu Arg Val Asp			
500	505	510	
tac ggc ttc ggg ctg agc ctg gag gcg gcg cgc cac cac gag aac agc			1823
Tyr Gly Phe Gly Leu Ser Leu Glu Ala Ala Arg His His Glu Asn Ser			
515	520	525	
tcg cgg ggc gcg gtc gtg ggc gtg ggc gac gag agc cgc gcc ctg ccc			1871
Ser Arg Gly Ala Val Val Gly Val Gly Asp Glu Ser Arg Ala Leu Pro			
530	535	540	
gac gtc atg cag ggc atg gtg ctc agc tcc atg cag cac ttc agc gag			1919
Asp Val Met Gln Gly Met Val Leu Ser Ser Met Gln His Phe Ser Glu			
545	550	555	560
gcc ttc cac cag gtc ctg ggc gag aag cat aag cgc ggc cac ctg gcc			1967
Ala Phe His Gln Val Leu Gly Glu Lys His Lys Arg Gly His Leu Ala			
565	570	575	
gag gcc gag ggc cac agg gac act tgc gac gaa gac tcg gtg gcc ggc			2015
Glu Ala Glu Gly His Arg Asp Thr Cys Asp Glu Asp Ser Val Ala Gly			
580	585	590	
gag tcg gac cgc ata gac gat ggc act gtt aat ggc cgc ggc tgc tcc			2063
Glu Ser Asp Arg Ile Asp Asp Gly Thr Val Asn Gly Arg Gly Cys Ser			
595	600	605	
ccg ggc gag tcg gcc tcg ggg ggc ctg tcc aaa aag ctg ctg ctg ggc			2111
Pro Gly Glu Ser Ala Ser Gly Gly Leu Ser Lys Lys Leu Leu Leu Gly			
610	615	620	
agc ccc agc tcg ctg agc ccc ttc tct aag cgc atc aag ctc gag aag			2159
Ser Pro Ser Ser Leu Ser Pro Phe Ser Lys Arg Ile Lys Leu Glu Lys			

625	630	635	640	
gag ttc gac ctg ccc ccg gcc gcg atg ccc aac acg gag aac gtg tac				2207
Glu Phe Asp Leu Pro Pro Ala Ala Met Pro Asn Thr Glu Asn Val Tyr				
645	650	655		
tcg cag tgg ctc gcc ggc tac gcg gcc tcc agg cag ctc aaa gat ccc				2255
Ser Gln Trp Leu Ala Gly Tyr Ala Ala Ser Arg Gln Leu Lys Asp Pro				
660	665	670		
ttc ctt agc ttc gga gac tcc aga caa tcg cct ttt gcc tcc tcg tcg				2303
Phe Leu Ser Phe Gly Asp Ser Arg Gln Ser Pro Phe Ala Ser Ser Ser				
675	680	685		
gag cac tcc tcg gag aac ggg agc ttg cgc ttc tcc aca ccg ccc ggg				2351
Glu His Ser Ser Glu Asn Gly Ser Leu Arg Phe Ser Thr Pro Pro Gly				
690	695	700		
gag ctg gac gga ggg atc tcg ggg cgc agc ggc acg gga agt gga ggg				2399
Glu Leu Asp Gly Gly Ile Ser Gly Arg Ser Gly Thr Gly Ser Gly Gly				
705	710	715	720	
agc acg ccc cat att agt ggt ccg ggc ccg ggc agg ccc agc tca aaa				2447
Ser Thr Pro His Ile Ser Gly Pro Gly Pro Gly Arg Pro Ser Ser Lys				
725	730	735		
gag ggc aga cgc agc gac act tgt gag tac tgt ggg aaa gtc ttc aag				2495
Glu Gly Arg Arg Ser Asp Thr Cys Glu Tyr Cys Gly Lys Val Phe Lys				
740	745	750		
aac tgt agc aat ctc act gtc cac agg aga agc cac acg ggc gaa agg				2543
Asn Cys Ser Asn Leu Thr Val His Arg Arg Ser His Thr Gly Glu Arg				
755	760	765		
cct tat aaa tgc gag ctg tgc aac tat gcc tgt gcc cag agt agc aag				2591
Pro Tyr Lys Cys Glu Leu Cys Asn Tyr Ala Cys Ala Gln Ser Ser Lys				

770	775	780	
ctc acc agg cac atg aaa acg cat ggc cag gtg ggg aag gac gtt tac			2639
Leu Thr Arg His Met Lys Thr His Gly Gln Val Gly Lys Asp Val Tyr			
785	790	795	800
aaa tgt gaa att tgt aag atg cct ttt agc gtg tac agt acc ctg gag			2687
Lys Cys Glu Ile Cys Lys Met Pro Phe Ser Val Tyr Ser Thr Leu Glu			
	805	810	815
aaa cac atg aaa aaa tgg cac agt gat cga gtg ttg aat aat gat ata			2735
Lys His Met Lys Lys Trp His Ser Asp Arg Val Leu Asn Asn Asp Ile			
	820	825	830
aaa act gaa tagaggtata ttaatacccc tccctcactc ccacctgaca			2784
Lys Thr Glu			
	835		
cccccttttt caccactccc ctccccatc gccctccagc cccactccct gtaggatttt			2844
tttctagtcc catgtgattt aaacaaacaa acaacaaac agaagtaacg aagctaagaa			2904
tatgagagtg cttgtcacca gcacacctgt tttttttctt tttctttttc ttttttcttt			2964
ttcttttttt tttttttttc ctttatgttc tcaccgtttg aatgcatgat ctgtatgggg			3024
caatactatt gcattttacg caaactttga gcctttctct tgtgcaataa tttacatgtt			3084
gtgtatgttt ttttttaaac ttagacagca tgtatggat gttatggcta ttttaaattg			3144
tcctaattc gttgctgagc aaacatgttg ctgtttccag ttccgttctg agagaaaaag			3204
agagagagag agaaaaagac catgctgcat acattctgta atacatatca tgtacagttt			3264
tattttataa cgtgaggagg aaaaacagtc tttggattaa ccctctatag acagaataga			3324
tagcactgaa aaaaaatctc tatgagctaa atgtctgtct ctaaagggtt aaatgtatca			3384
attgg			3389

<210> 160

<211> 835

<212> PRT

<213> Homo sapiens

<400> 160

Met Ser Arg Arg Lys Gln Gly Lys Pro Gln His Leu Ser Lys Arg Glu
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 Phe Ser Pro Glu Pro Leu Glu Ala Ile Leu Thr Asp Asp Glu Pro Asp
 20 25 30
 His Gly Pro Leu Gly Ala Pro Glu Gly Asp His Asp Leu Leu Thr Cys
 35 40 45
 Gly Gln Cys Gln Met Asn Phe Pro Leu Gly Asp Ile Leu Ile Phe Ile
 50 55 60
 Glu His Lys Arg Lys Gln Cys Asn Gly Ser Leu Cys Leu Glu Lys Ala
 65 70 75 80
 Val Asp Lys Pro Pro Ser Pro Ser Pro Ile Glu Met Lys Lys Ala Ser
 85 90 95
 Asn Pro Val Glu Val Gly Ile Gln Val Thr Pro Glu Asp Asp Asp Cys
 100 105 110
 Leu Ser Thr Ser Ser Arg Gly Ile Cys Pro Lys Gln Glu His Ile Ala
 115 120 125
 Asp Lys Leu Leu His Trp Arg Gly Leu Ser Ser Pro Arg Ser Ala His
 130 135 140
 Gly Ala Leu Ile Pro Thr Pro Gly Met Ser Ala Glu Tyr Ala Pro Gln
 145 150 155 160
 Gly Ile Cys Lys Asp Glu Pro Ser Ser Tyr Thr Cys Thr Thr Cys Lys
 165 170 175
 Gln Pro Phe Thr Ser Ala Trp Phe Leu Leu Gln His Ala Gln Asn Thr
 180 185 190

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His Gly Leu Arg Ile Tyr Leu Glu Ser Glu His Gly Ser Pro Leu Thr
195 200 205

Pro Arg Val Gly Ile Pro Ser Gly Leu Gly Ala Glu Cys Pro Ser Gln
210 215 220

Pro Pro Leu His Gly Ile His Ile Ala Asp Asn Asn Pro Phe Asn Leu
225 230 235 240

Leu Arg Ile Pro Gly Ser Val Ser Arg Glu Ala Ser Gly Leu Ala Glu
245 250 255

Gly Arg Phe Pro Pro Thr Pro Pro Leu Phe Ser Pro Pro Pro Arg His
260 265 270

His Leu Asp Pro His Arg Ile Glu Arg Leu Gly Ala Glu Glu Met Ala
275 280 285

Leu Ala Thr His His Pro Ser Ala Phe Asp Arg Val Leu Arg Leu Asn
290 295 300

Pro Met Ala Met Glu Pro Pro Ala Met Asp Phe Ser Arg Arg Leu Arg
305 310 315 320

Glu Leu Ala Gly Asn Thr Ser Ser Pro Pro Leu Ser Pro Gly Arg Pro
325 330 335

Ser Pro Met Gln Arg Leu Leu Gln Pro Phe Gln Pro Gly Ser Lys Pro
340 345 350

Pro Phe Leu Ala Thr Pro Pro Leu Pro Pro Leu Gln Ser Ala Pro Pro
355 360 365

Pro Ser Gln Pro Pro Val Lys Ser Lys Ser Cys Glu Phe Cys Gly Lys
370 375 380

Thr Phe Lys Phe Gln Ser Asn Leu Val Val His Arg Arg Ser His Thr
385 390 395 400

Gly Glu Lys Pro Tyr Lys Cys Asn Leu Cys Asp His Ala Cys Thr Gln

405 410 415
Ala Ser Lys Leu Lys Arg His Met Lys Thr His Met His Lys Ser Ser
420 425 430
Pro Met Thr Val Lys Ser Asp Asp Gly Leu Ser Thr Ala Ser Ser Pro
435 440 445
Glu Pro Gly Thr Ser Asp Leu Val Gly Ser Ala Ser Ser Ala Leu Lys
450 455 460
Ser Val Val Ala Lys Phe Lys Ser Glu Asn Asp Pro Asn Leu Ile Pro
465 470 475 480
Glu Asn Gly Asp Glu Glu Glu Glu Glu Asp Asp Glu Glu Glu Glu Glu
485 490 495
Glu Glu Glu Glu Glu Glu Glu Glu Leu Thr Glu Ser Glu Arg Val Asp
500 505 510
Tyr Gly Phe Gly Leu Ser Leu Glu Ala Ala Arg His His Glu Asn Ser
515 520 525
Ser Arg Gly Ala Val Val Gly Val Gly Asp Glu Ser Arg Ala Leu Pro
530 535 540
Asp Val Met Gln Gly Met Val Leu Ser Ser Met Gln His Phe Ser Glu
545 550 555 560
Ala Phe His Gln Val Leu Gly Glu Lys His Lys Arg Gly His Leu Ala
565 570 575
Glu Ala Glu Gly His Arg Asp Thr Cys Asp Glu Asp Ser Val Ala Gly
580 585 590
Glu Ser Asp Arg Ile Asp Asp Gly Thr Val Asn Gly Arg Gly Cys Ser
595 600 605
Pro Gly Glu Ser Ala Ser Gly Gly Leu Ser Lys Lys Leu Leu Leu Gly
610 615 620

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Ser Pro Ser Ser Leu Ser Pro Phe Ser Lys Arg Ile Lys Leu Glu Lys
625 630 635 640
Glu Phe Asp Leu Pro Pro Ala Ala Met Pro Asn Thr Glu Asn Val Tyr
 645 650 655
Ser Gln Trp Leu Ala Gly Tyr Ala Ala Ser Arg Gln Leu Lys Asp Pro
 660 665 670
Phe Leu Ser Phe Gly Asp Ser Arg Gln Ser Pro Phe Ala Ser Ser Ser
 675 680 685
Glu His Ser Ser Glu Asn Gly Ser Leu Arg Phe Ser Thr Pro Pro Gly
 690 695 700
Glu Leu Asp Gly Gly Ile Ser Gly Arg Ser Gly Thr Gly Ser Gly Gly
705 710 715 720
Ser Thr Pro His Ile Ser Gly Pro Gly Pro Gly Arg Pro Ser Ser Lys
 725 730 735
Glu Gly Arg Arg Ser Asp Thr Cys Glu Tyr Cys Gly Lys Val Phe Lys
 740 745 750
Asn Cys Ser Asn Leu Thr Val His Arg Arg Ser His Thr Gly Glu Arg
 755 760 765
Pro Tyr Lys Cys Glu Leu Cys Asn Tyr Ala Cys Ala Gln Ser Ser Lys
 770 775 780
Leu Thr Arg His Met Lys Thr His Gly Gln Val Gly Lys Asp Val Tyr
785 790 795 800
Lys Cys Glu Ile Cys Lys Met Pro Phe Ser Val Tyr Ser Thr Leu Glu
 805 810 815
Lys His Met Lys Lys Trp His Ser Asp Arg Val Leu Asn Asn Asp Ile
 820 825 830
Lys Thr Glu

835

<210> 161

<211> 2864

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (129).. (2447)

<223>

<400> 161

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atgtgaaccg agccgtcgtc cgcccgccgc cgccgcgcgc gccgcgcgcg cccgccccgc 120

agcccacc atg tct cgc cgc aag caa ggc aaa ccc cag cac tta agc aaa 170

Met Ser Arg Arg Lys Gln Gly Lys Pro Gln His Leu Ser Lys

1

5

10

cgg gaa ttc tcg ccc gag cct ctt gaa gcc att ctt aca gat gat gaa 218

Arg Glu Phe Ser Pro Glu Pro Leu Glu Ala Ile Leu Thr Asp Asp Glu

15

20

25

30

cca gac cac ggc ccg ttg gga gct cca gaa ggg gat cat gac ctc ctc 266

Pro Asp His Gly Pro Leu Gly Ala Pro Glu Gly Asp His Asp Leu Leu

35

40

45

acc tgt ggg cag tgc cag atg aac ttc cca ttg ggg gac att ctt att 314

Thr Cys Gly Gln Cys Gln Met Asn Phe Pro Leu Gly Asp Ile Leu Ile

50

55

60

ttt atc gag cac aaa cgg aaa caa tgc aat ggc agc ctc tgc tta gaa 362

Phe Ile Glu His Lys Arg Lys Gln Cys Asn Gly Ser Leu Cys Leu Glu

539/617

65	70	75	
aaa gct gtg gat aag cca cct tcc cct tca cca atc gag atg aaa aaa			410
Lys Ala Val Asp Lys Pro Pro Ser Pro Ser Pro Ile Glu Met Lys Lys			
80	85	90	
gca tcc aat ccc gtg gag gtt ggc atc cag gtc acg cca gag gat gac			458
Ala Ser Asn Pro Val Glu Val Gly Ile Gln Val Thr Pro Glu Asp Asp			
95	100	105	110
gat tgt tta tca acg tca tct aga gga att tgc ccc aaa cag gaa cac			506
Asp Cys Leu Ser Thr Ser Ser Arg Gly Ile Cys Pro Lys Gln Glu His			
115	120	125	
ata gca gat aaa ctt ctg cac tgg agg ggc ctc tcc tcc cct cgt tct			554
Ile Ala Asp Lys Leu Leu His Trp Arg Gly Leu Ser Ser Pro Arg Ser			
130	135	140	
gca cat gga gct cta atc ccc acg cct ggg atg agt gca gaa tat gcc			602
Ala His Gly Ala Leu Ile Pro Thr Pro Gly Met Ser Ala Glu Tyr Ala			
145	150	155	
ccg cag ggt att tgt aaa gat gag ccc agc agc tac aca tgt aca act			650
Pro Gln Gly Ile Cys Lys Asp Glu Pro Ser Ser Tyr Thr Cys Thr Thr			
160	165	170	
tgc aaa cag cca ttc acc agt gca tgg ttt ctc ttg caa cac gca cag			698
Cys Lys Gln Pro Phe Thr Ser Ala Trp Phe Leu Leu Gln His Ala Gln			
175	180	185	190
aac act cat gga tta aga atc tac tta gaa agc gaa cac gga agt ccc			746
Asn Thr His Gly Leu Arg Ile Tyr Leu Glu Ser Glu His Gly Ser Pro			
195	200	205	
ctg acc ccg cgg gtt ggt atc cct tca gga cta ggt gca gaa tgt cct			794
Leu Thr Pro Arg Val Gly Ile Pro Ser Gly Leu Gly Ala Glu Cys Pro			

210	215	220	
tcc cag cca cct ctc cat ggg att cat att gca gac aat aac ccc ttt			842
Ser Gln Pro Pro Leu His Gly Ile His Ile Ala Asp Asn Asn Pro Phe			
225	230	235	
aac ctg cta aga ata cca gga tca gta tcg aga gag gct tcc ggc ctg			890
Asn Leu Leu Arg Ile Pro Gly Ser Val Ser Arg Glu Ala Ser Gly Leu			
240	245	250	
gca gaa ggg cgc ttt cca ccc act ccc ccc ctg ttt agt cca cca ccg			938
Ala Glu Gly Arg Phe Pro Pro Thr Pro Pro Leu Phe Ser Pro Pro Pro			
255	260	265	270
aga cat cac ttg gac ccc cac cgc ata gag cgc ctg ggg gcg gaa gag			986
Arg His His Leu Asp Pro His Arg Ile Glu Arg Leu Gly Ala Glu Glu			
275	280	285	
atg gcc ctg gcc acc cat cac ccg agt gcc ttt gac agg gtg ctg cgg			1034
Met Ala Leu Ala Thr His His Pro Ser Ala Phe Asp Arg Val Leu Arg			
290	295	300	
ttg aat cca atg gct atg gag cct ccc gcc atg gat ttc tct agg aga			1082
Leu Asn Pro Met Ala Met Glu Pro Pro Ala Met Asp Phe Ser Arg Arg			
305	310	315	
ctt aga gag ctg gca ggg aac acg tct agc cca ccg ctg tcc cca ggc			1130
Leu Arg Glu Leu Ala Gly Asn Thr Ser Ser Pro Pro Leu Ser Pro Gly			
320	325	330	
cgg ccc agc cct atg caa agg tta ctg caa cca ttc cag cca ggt agc			1178
Arg Pro Ser Pro Met Gln Arg Leu Leu Gln Pro Phe Gln Pro Gly Ser			
335	340	345	350
aag ccg ccc ttc ctg gcg acg ccc ccc etc cct cct ctg caa tcc gcc			1226
Lys Pro Pro Phe Leu Ala Thr Pro Pro Leu Pro Pro Leu Gln Ser Ala			

355	360	365	
cct cct ccc tcc cag ccc ccg gtc aag tcc aag tca tgc gag ttc tgc			1274
Pro Pro Pro Ser Gln Pro Pro Val Lys Ser Lys Ser Cys Glu Phe Cys			
370	375	380	
ggc aag acg ttc aaa ttt cag agc aac ctg gtg gtg cac cgg cgc agc			1322
Gly Lys Thr Phe Lys Phe Gln Ser Asn Leu Val Val His Arg Arg Ser			
385	390	395	
cac acg ggc gag aag ccc tac aag tgc aac ctg tgc gac cac gcg tgc			1370
His Thr Gly Glu Lys Pro Tyr Lys Cys Asn Leu Cys Asp His Ala Cys			
400	405	410	
acc cag gcc agc aag ctg aag cgc cac atg aag acg cac atg cac aaa			1418
Thr Gln Ala Ser Lys Leu Lys Arg His Met Lys Thr His Met His Lys			
415	420	425	430
tcg tcc ccc atg acg gtc aag tcc gac gac ggt ctc tcc acc gcc agc			1466
Ser Ser Pro Met Thr Val Lys Ser Asp Asp Gly Leu Ser Thr Ala Ser			
435	440	445	
tcc ccg gaa ccc ggc acc agc gac ttg gtg ggc agc gcc agc agc gcg			1514
Ser Pro Glu Pro Gly Thr Ser Asp Leu Val Gly Ser Ala Ser Ser Ala			
450	455	460	
ctc aag tcc gtg gtg gcc aag ttc aag agc gag aac gac ccc aac ctg			1562
Leu Lys Ser Val Val Ala Lys Phe Lys Ser Glu Asn Asp Pro Asn Leu			
465	470	475	
atc ccg gag aac ggg gac gag gag gaa gag gag gac gac gag gaa gag			1610
Ile Pro Glu Asn Gly Asp Glu Glu Glu Glu Glu Asp Asp Glu Glu Glu			
480	485	490	
gaa gaa gag gag gaa gag gag gag gag ctg acg gag agc gag agg			1658
Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Leu Thr Glu Ser Glu Arg			

495	500	505	510	
gtg gac tac ggc ttc ggg ctg agc ctg gag gcg gcg cgc cac cac gag				1706
Val Asp Tyr Gly Phe Gly Leu Ser Leu Glu Ala Ala Arg His His Glu				
515	520	525		
aac agc tcg cgg ggc gcg gtc gtg ggc gtg ggc gac gag agc cgc gcc				1754
Asn Ser Ser Arg Gly Ala Val Val Gly Val Gly Asp Glu Ser Arg Ala				
530	535	540		
ctg ccc gac gtc atg cag ggc atg gtg ctc agc tcc atg cag cac ttc				1802
Leu Pro Asp Val Met Gln Gly Met Val Leu Ser Ser Met Gln His Phe				
545	550	555		
agc gag gcc ttc cac cag gtc ctg ggc gag aag cat aag cgc ggc cac				1850
Ser Glu Ala Phe His Gln Val Leu Gly Glu Lys His Lys Arg Gly His				
560	565	570		
ctg gcc gag gcc gag ggc cac agg gac act tgc gac gaa gac tcg gtg				1898
Leu Ala Glu Ala Glu Gly His Arg Asp Thr Cys Asp Glu Asp Ser Val				
575	580	585	590	
gcc ggc gag tcg gac cgc ata gac gat ggc act gtt aat ggc cgc ggc				1946
Ala Gly Glu Ser Asp Arg Ile Asp Asp Gly Thr Val Asn Gly Arg Gly				
595	600	605		
tgc tcc ccg ggc gag tcg gcc tcg ggg ggc ctg tcc aaa aag ctg ctg				1994
Cys Ser Pro Gly Glu Ser Ala Ser Gly Gly Leu Ser Lys Lys Leu Leu				
610	615	620		
ctg ggc agc ccc agc tcg ctg agc ccc ttc tct aag cgc atc aag ctc				2042
Leu Gly Ser Pro Ser Ser Leu Ser Pro Phe Ser Lys Arg Ile Lys Leu				
625	630	635		
gag aag gag ttc gac ctg ccc ccg gcc gcg atg ccc aac acg gag aac				2090
Glu Lys Glu Phe Asp Leu Pro Pro Ala Ala Met Pro Asn Thr Glu Asn				

640	645	650	
gtg tac tcg cag tgg ctc gcc ggc tac gcg gcc tcc agg cag ctc aaa			2138
Val Tyr Ser Gln Trp Leu Ala Gly Tyr Ala Ala Ser Arg Gln Leu Lys			
655	660	665	670
gat ccc ttc ctt agc ttc gga gac tcc aga caa tcg cct ttt gcc tcc			2186
Asp Pro Phe Leu Ser Phe Gly Asp Ser Arg Gln Ser Pro Phe Ala Ser			
675	680	685	
tcg tcg gag cac tcc tcg gag aac ggg agc ttg cgc ttc tcc aca ccg			2234
Ser Ser Glu His Ser Ser Glu Asn Gly Ser Leu Arg Phe Ser Thr Pro			
690	695	700	
ccc ggg gag ctg gac gga ggg atc tcg ggg cgc agc ggc acg gga agt			2282
Pro Gly Glu Leu Asp Gly Gly Ile Ser Gly Arg Ser Gly Thr Gly Ser			
705	710	715	
gga ggg agc acg ccc cat att agt ggt ccg ggc ccg ggc agg ccc agc			2330
Gly Gly Ser Thr Pro His Ile Ser Gly Pro Gly Pro Gly Arg Pro Ser			
720	725	730	
tca aaa gag ggc aga cgc agc gac act tgt tct tca cac acc ccc att			2378
Ser Lys Glu Gly Arg Arg Ser Asp Thr Cys Ser Ser His Thr Pro Ile			
735	740	745	750
cgg cgt agt acc cag aga gct caa gat gtg tgg cag ttt tcg gat gga			2426
Arg Arg Ser Thr Gln Arg Ala Gln Asp Val Trp Gln Phe Ser Asp Gly			
755	760	765	
agc tcg aga gcc ctt aag ttc tgagaaaatt tgaagccccc aggggtgggg			2477
Ser Ser Arg Ala Leu Lys Phe			
770			
tggacgcgtg ccgccagtc gacgtcagcg tggctgtgca tctgtctagt ttgtgatgtt			2537
ttctgacagt agcctccaag aagccgttgt gcgaagacag agtcctgcag agtccttcca			2597

gcctaggcct gcagcgccat tttatttata ttttttaata aaaagtaaaa acaaaaaaac 2657
 agaccacat tggaacagtg aatcagtccc atagagaggg cccgtggacc atcgctgtca 2717
 tgagtgatgc cctggccctt ctgaaaccag ccaacctaata tacctgtatt gtggaaatgc 2777
 gcatgagtcc ccaaccctt gtttctatac attctatgtt gtcttttaaa aagtgtgctt 2837
 aacattgaca ataaatgttg gagcttt 2864

<210> 162

<211> 773

<212> PRT

<213> Homo sapiens

<400> 162

Met Ser Arg Arg Lys Gln Gly Lys Pro Gln His Leu Ser Lys Arg Glu
 1 5 10 15
 Phe Ser Pro Glu Pro Leu Glu Ala Ile Leu Thr Asp Asp Glu Pro Asp
 20 25 30
 His Gly Pro Leu Gly Ala Pro Glu Gly Asp His Asp Leu Leu Thr Cys
 35 40 45
 Gly Gln Cys Gln Met Asn Phe Pro Leu Gly Asp Ile Leu Ile Phe Ile
 50 55 60
 Glu His Lys Arg Lys Gln Cys Asn Gly Ser Leu Cys Leu Glu Lys Ala
 65 70 75 80
 Val Asp Lys Pro Pro Ser Pro Ser Pro Ile Glu Met Lys Lys Ala Ser
 85 90 95
 Asn Pro Val Glu Val Gly Ile Gln Val Thr Pro Glu Asp Asp Asp Cys
 100 105 110
 Leu Ser Thr Ser Ser Arg Gly Ile Cys Pro Lys Gln Glu His Ile Ala
 115 120 125

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Asp Lys Leu Leu His Trp Arg Gly Leu Ser Ser Pro Arg Ser Ala His
 130 135 140
 Gly Ala Leu Ile Pro Thr Pro Gly Met Ser Ala Glu Tyr Ala Pro Gln
 145 150 155 160
 Gly Ile Cys Lys Asp Glu Pro Ser Ser Tyr Thr Cys Thr Thr Cys Lys
 165 170 175
 Gln Pro Phe Thr Ser Ala Trp Phe Leu Leu Gln His Ala Gln Asn Thr
 180 185 190
 His Gly Leu Arg Ile Tyr Leu Glu Ser Glu His Gly Ser Pro Leu Thr
 195 200 205
 Pro Arg Val Gly Ile Pro Ser Gly Leu Gly Ala Glu Cys Pro Ser Gln
 210 215 220
 Pro Pro Leu His Gly Ile His Ile Ala Asp Asn Asn Pro Phe Asn Leu
 225 230 235 240
 Leu Arg Ile Pro Gly Ser Val Ser Arg Glu Ala Ser Gly Leu Ala Glu
 245 250 255
 Gly Arg Phe Pro Pro Thr Pro Pro Leu Phe Ser Pro Pro Pro Arg His
 260 265 270
 His Leu Asp Pro His Arg Ile Glu Arg Leu Gly Ala Glu Glu Met Ala
 275 280 285
 Leu Ala Thr His His Pro Ser Ala Phe Asp Arg Val Leu Arg Leu Asn
 290 295 300
 Pro Met Ala Met Glu Pro Pro Ala Met Asp Phe Ser Arg Arg Leu Arg
 305 310 315 320
 Glu Leu Ala Gly Asn Thr Ser Ser Pro Pro Leu Ser Pro Gly Arg Pro
 325 330 335
 Ser Pro Met Gln Arg Leu Leu Gln Pro Phe Gln Pro Gly Ser Lys Pro

340	345	350
Pro Phe Leu Ala Thr Pro Pro Leu Pro Pro Leu Gln Ser Ala Pro Pro		
355	360	365
Pro Ser Gln Pro Pro Val Lys Ser Lys Ser Cys Glu Phe Cys Gly Lys		
370	375	380
Thr Phe Lys Phe Gln Ser Asn Leu Val Val His Arg Arg Ser His Thr		
385	390	395
		400
Gly Glu Lys Pro Tyr Lys Cys Asn Leu Cys Asp His Ala Cys Thr Gln		
405	410	415
Ala Ser Lys Leu Lys Arg His Met Lys Thr His Met His Lys Ser Ser		
420	425	430
Pro Met Thr Val Lys Ser Asp Asp Gly Leu Ser Thr Ala Ser Ser Pro		
435	440	445
Glu Pro Gly Thr Ser Asp Leu Val Gly Ser Ala Ser Ser Ala Leu Lys		
450	455	460
Ser Val Val Ala Lys Phe Lys Ser Glu Asn Asp Pro Asn Leu Ile Pro		
465	470	475
		480
Glu Asn Gly Asp Glu Glu Glu Glu Glu Asp Asp Glu Glu Glu Glu Glu		
485	490	495
Glu Glu Glu Glu Glu Glu Glu Glu Leu Thr Glu Ser Glu Arg Val Asp		
500	505	510
Tyr Gly Phe Gly Leu Ser Leu Glu Ala Ala Arg His His Glu Asn Ser		
515	520	525
Ser Arg Gly Ala Val Val Gly Val Gly Asp Glu Ser Arg Ala Leu Pro		
530	535	540
Asp Val Met Gln Gly Met Val Leu Ser Ser Met Gln His Phe Ser Glu		
545	550	555
		560

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Ala Phe His Gln Val Leu Gly Glu Lys His Lys Arg Gly His Leu Ala

565

570

575

Glu Ala Glu Gly His Arg Asp Thr Cys Asp Glu Asp Ser Val Ala Gly

580

585

590

Glu Ser Asp Arg Ile Asp Asp Gly Thr Val Asn Gly Arg Gly Cys Ser

595

600

605

Pro Gly Glu Ser Ala Ser Gly Gly Leu Ser Lys Lys Leu Leu Leu Gly

610

615

620

Ser Pro Ser Ser Leu Ser Pro Phe Ser Lys Arg Ile Lys Leu Glu Lys

625

630

635

640

Glu Phe Asp Leu Pro Pro Ala Ala Met Pro Asn Thr Glu Asn Val Tyr

645

650

655

Ser Gln Trp Leu Ala Gly Tyr Ala Ala Ser Arg Gln Leu Lys Asp Pro

660

665

670

Phe Leu Ser Phe Gly Asp Ser Arg Gln Ser Pro Phe Ala Ser Ser Ser

675

680

685

Glu His Ser Ser Glu Asn Gly Ser Leu Arg Phe Ser Thr Pro Pro Gly

690

695

700

Glu Leu Asp Gly Gly Ile Ser Gly Arg Ser Gly Thr Gly Ser Gly Gly

705

710

715

720

Ser Thr Pro His Ile Ser Gly Pro Gly Pro Gly Arg Pro Ser Ser Lys

725

730

735

Glu Gly Arg Arg Ser Asp Thr Cys Ser Ser His Thr Pro Ile Arg Arg

740

745

750

Ser Thr Gln Arg Ala Gln Asp Val Trp Gln Phe Ser Asp Gly Ser Ser

755

760

765

Arg Ala Leu Lys Phe

548/617

770

<210> 163

<211> 1636

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (34).. (918)

<223>

<400> 163

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Met Phe Ser Ile Asn Pro Leu

1

5

gag aac ctg aag gtg tac atc agc agt cgg cct ccc ctg gtg gtc ttc 102

Glu Asn Leu Lys Val Tyr Ile Ser Ser Arg Pro Pro Leu Val Val Phe

10

15

20

atg atc agc gta agc gcc atg gcc ata gct ttc ctg acc ctg ggc tac 150

Met Ile Ser Val Ser Ala Met Ala Ile Ala Phe Leu Thr Leu Gly Tyr

25

30

35

ttc ttc aaa atc aag gag att aaa tcc cca gaa atg gca gag gat tgg 198

Phe Phe Lys Ile Lys Glu Ile Lys Ser Pro Glu Met Ala Glu Asp Trp

40

45

50

55

aat act ttt ctg cta cgg ttc aat gat ttg gac ttg tgt gta tca gag 246

Asn Thr Phe Leu Leu Arg Phe Asn Asp Leu Asp Leu Cys Val Ser Glu

60

65

70

aat gaa acc ctc aag cat ctc aca aac gac acc aca act ccg gaa agt 294

549/617

Asn Glu Thr Leu Lys His Leu Thr Asn Asp Thr Thr Thr Pro Glu Ser	
75 80 85	
aca atg acc agc ggg cag gcc cga gct tcc acc cag tcc ccc cag gcc	342
Thr Met Thr Ser Gly Gln Ala Arg Ala Ser Thr Gln Ser Pro Gln Ala	
90 95 100	
ctg gag gac tgc ggc ccg gtg aat atc tca gtc tca atc acc cta acc	390
Leu Glu Asp Ser Gly Pro Val Asn Ile Ser Val Ser Ile Thr Leu Thr	
105 110 115	
ctg gac cca ctg aaa ccc ttc gga ggg tat tcc cgc aac gtc acc cat	438
Leu Asp Pro Leu Lys Pro Phe Gly Gly Tyr Ser Arg Asn Val Thr His	
120 125 130 135	
ctg tac tca acc atc tta ggg cat cag att gga ctt tca ggc agg gaa	486
Leu Tyr Ser Thr Ile Leu Gly His Gln Ile Gly Leu Ser Gly Arg Glu	
140 145 150	
gcc cac gag gag ata aac atc acc ttc acc ctg cct aca gcg tgg agc	534
Ala His Glu Glu Ile Asn Ile Thr Phe Thr Leu Pro Thr Ala Trp Ser	
155 160 165	
tca gat gac tgc gcc ctc cac ggt cac tgt gag cag gtg gta ttc aca	582
Ser Asp Asp Cys Ala Leu His Gly His Cys Glu Gln Val Val Phe Thr	
170 175 180	
gcc tgc atg acc ctc acg gcc agc cct ggg gtg ttc ccc gtc act gta	630
Ala Cys Met Thr Leu Thr Ala Ser Pro Gly Val Phe Pro Val Thr Val	
185 190 195	
cag cca ccg cac tgt gtt cct gac acg tac agc aac gcc acg ctc tgg	678
Gln Pro Pro His Cys Val Pro Asp Thr Tyr Ser Asn Ala Thr Leu Trp	
200 205 210 215	
tac aag atc ttc aca act gcc aga gat gcc aac aca aaa tac gcc caa	726

Tyr Lys Ile Phe Thr Thr Ala Arg Asp Ala Asn Thr Lys Tyr Ala Gln
 220 225 230
 gat tac aat cct ttc tgg tgt tat aag ggg gcc att gga aaa gtc tat 774
 Asp Tyr Asn Pro Phe Trp Cys Tyr Lys Gly Ala Ile Gly Lys Val Tyr
 235 240 245
 cat gct tta aat ccc aag ctt aca gtg att gtt cca gat gat gct ttc 822
 His Ala Leu Asn Pro Lys Leu Thr Val Ile Val Pro Asp Asp Ala Phe
 250 255 260
 att gga ttt gga gga aat gtg atc agg caa caa gtc aag gat aac gcc 870
 Ile Gly Phe Gly Gly Asn Val Ile Arg Gln Gln Val Lys Asp Asn Ala
 265 270 275
 aaa tgg tat atc act gat ttt gta gag ctg ctg gga gaa ctg gaa gaa 918
 Lys Trp Tyr Ile Thr Asp Phe Val Glu Leu Leu Gly Glu Leu Glu Glu
 280 285 290 295
 taacatccat tgcgtacag ctccaaacaa cttcagatga atttttacaa gttatacaga 978
 ttgatactgt ttgcttacag ttgcctatta caacttgcta tagaaagttg gtacaaatga 1038
 tctgtacttt aaactacagt taggaatcct agaagattgc tttttttttt tttttaactg 1098
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 agaatcttgc tctgttgccc aggetggagt gcagtggcgc ggtctcggct cactgcaagc 1218
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 caattaaaca cctttactct tagaaatacg gattcggcag ccttcagtga atattgggtt 1578
 ctcttttgta tgtcaataaa agtttatccg tatgtcagaa cggatttgtg gaattttc 1636

<210> 164

<211> 295

<212> PRT

<213> Homo sapiens

<400> 164

Met Phe Ser Ile Asn Pro Leu Glu Asn Leu Lys Val Tyr Ile Ser Ser

1 5 10 15

Arg Pro Pro Leu Val Val Phe Met Ile Ser Val Ser Ala Met Ala Ile

20 25 30

Ala Phe Leu Thr Leu Gly Tyr Phe Phe Lys Ile Lys Glu Ile Lys Ser

35 40 45

Pro Glu Met Ala Glu Asp Trp Asn Thr Phe Leu Leu Arg Phe Asn Asp

50 55 60

Leu Asp Leu Cys Val Ser Glu Asn Glu Thr Leu Lys His Leu Thr Asn

65 70 75 80

Asp Thr Thr Thr Pro Glu Ser Thr Met Thr Ser Gly Gln Ala Arg Ala

85 90 95

Ser Thr Gln Ser Pro Gln Ala Leu Glu Asp Ser Gly Pro Val Asn Ile

100 105 110

Ser Val Ser Ile Thr Leu Thr Leu Asp Pro Leu Lys Pro Phe Gly Gly

115 120 125

Tyr Ser Arg Asn Val Thr His Leu Tyr Ser Thr Ile Leu Gly His Gln

130 135 140

Ile Gly Leu Ser Gly Arg Glu Ala His Glu Glu Ile Asn Ile Thr Phe

145 150 155 160

Thr Leu Pro Thr Ala Trp Ser Ser Asp Asp Cys Ala Leu His Gly His

165 170 175

552/617

Cys Glu Gln Val Val Phe Thr Ala Cys Met Thr Leu Thr Ala Ser Pro
 180 185 190
 Gly Val Phe Pro Val Thr Val Gln Pro Pro His Cys Val Pro Asp Thr
 195 200 205
 Tyr Ser Asn Ala Thr Leu Trp Tyr Lys Ile Phe Thr Thr Ala Arg Asp
 210 215 220
 Ala Asn Thr Lys Tyr Ala Gln Asp Tyr Asn Pro Phe Trp Cys Tyr Lys
 225 230 235 240
 Gly Ala Ile Gly Lys Val Tyr His Ala Leu Asn Pro Lys Leu Thr Val
 245 250 255
 Ile Val Pro Asp Asp Ala Phe Ile Gly Phe Gly Gly Asn Val Ile Arg
 260 265 270
 Gln Gln Val Lys Asp Asn Ala Lys Trp Tyr Ile Thr Asp Phe Val Glu
 275 280 285
 Leu Leu Gly Glu Leu Glu Glu
 290 295

<210> 165

<211> 1902

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (246).. (1187)

<223>

<400> 165

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 ctcgggcccc ccacgcgccg ccacgagtga gcccagcgcg accgcgggcg tccgccgagc 180
 agctggcccc gctgggcccc gggcgcgcgag ctgcccgcgcg gggcggggtg gagctgatca 240
 gaata atg ttc agc atc aac ccc ctg gag aac ctg aag gtg tac atc agc 290
 Met Phe Ser Ile Asn Pro Leu Glu Asn Leu Lys Val Tyr Ile Ser
 1 5 10 15
 agt cgg cct ccc ctg gtg gtc ttc atg atc agc gta agc gcc atg gcc 338
 Ser Arg Pro Pro Leu Val Val Phe Met Ile Ser Val Ser Ala Met Ala
 20 25 30
 ata get ttc ctg acc ctg ggc tac ttc ttc aaa atc aag gag att aaa 386
 Ile Ala Phe Leu Thr Leu Gly Tyr Phe Phe Lys Ile Lys Glu Ile Lys
 35 40 45
 tcc cca gaa atg gca gag gat tgg aat act ttt ctg cta cgg ttc aat 434
 Ser Pro Glu Met Ala Glu Asp Trp Asn Thr Phe Leu Leu Arg Phe Asn
 50 55 60
 gat ttg gac ttg tgt gta tca gag aat gaa acc ctc aag cat ctc aca 482
 Asp Leu Asp Leu Cys Val Ser Glu Asn Glu Thr Leu Lys His Leu Thr
 65 70 75
 aac gac acc aca act ccg gaa agt aca atg acc agc ggg cag gcc cga 530
 Asn Asp Thr Thr Thr Pro Glu Ser Thr Met Thr Ser Gly Gln Ala Arg
 80 85 90 95
 gct tcc acc cag tcc ccc cag gcc ctg gag gac tcg ggc ccg gtg aat 578
 Ala Ser Thr Gln Ser Pro Gln Ala Leu Glu Asp Ser Gly Pro Val Asn
 100 105 110
 atc tca gtc tca atc acc cta acc ctg gac cca ctg aaa ccc ttc gga 626
 Ile Ser Val Ser Ile Thr Leu Thr Leu Asp Pro Leu Lys Pro Phe Gly
 115 120 125

ggg tat tcc cgc aac gtc acc cat ctg tac tca acc atc tta ggg cat 674
 Gly Tyr Ser Arg Asn Val Thr His Leu Tyr Ser Thr Ile Leu Gly His
 130 135 140
 cag att gga ctt tca ggc agg gaa gcc cac gag gag ata aac atc acc 722
 Gln Ile Gly Leu Ser Gly Arg Glu Ala His Glu Glu Ile Asn Ile Thr
 145 150 155
 ttc acc ctg cct aca gcg tgg agc tca gat gac tgc gcc ctc cac ggt 770
 Phe Thr Leu Pro Thr Ala Trp Ser Ser Asp Asp Cys Ala Leu His Gly
 160 165 170 175
 cac tgt gag cag gtg gta ttc aca gcc tgc atg acc ctc acg gcc agc 818
 His Cys Glu Gln Val Val Phe Thr Ala Cys Met Thr Leu Thr Ala Ser
 180 185 190
 cct ggg gtg ttc ccc gtc act gta cag cca ccg cac tgt gtt cct gac 866
 Pro Gly Val Phe Pro Val Thr Val Gln Pro Pro His Cys Val Pro Asp
 195 200 205
 acg tac agc aac gcc acg ctc tgg tac aag atc ttc aca act gcc aga 914
 Thr Tyr Ser Asn Ala Thr Leu Trp Tyr Lys Ile Phe Thr Thr Ala Arg
 210 215 220
 gat gcc aac aca aaa tac gcc caa gat tac aat cct ttc tgg tgt tat 962
 Asp Ala Asn Thr Lys Tyr Ala Gln Asp Tyr Asn Pro Phe Trp Cys Tyr
 225 230 235
 aag ggg gcc att gga aaa gtc tat cat gct tta aat ccc aag ctt aca 1010
 Lys Gly Ala Ile Gly Lys Val Tyr His Ala Leu Asn Pro Lys Leu Thr
 240 245 250 255
 gtg att gtt cca gat gat gac cgt tca tta ata aat ttg cat ctc atg 1058
 Val Ile Val Pro Asp Asp Asp Arg Ser Leu Ile Asn Leu His Leu Met
 260 265 270

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cac acc agt tac ttc ctc ttt gtg atg gtg ata aca atg ttt tgc tat 1106
 His Thr Ser Tyr Phe Leu Phe Val Met Val Ile Thr Met Phe Cys Tyr
 275 280 285
 gct gtt atc aag ggc aga cct agc aaa ttg cgt cag agc aat cct gaa 1154
 Ala Val Ile Lys Gly Arg Pro Ser Lys Leu Arg Gln Ser Asn Pro Glu
 290 295 300
 ttt tgt ccc gag aag gtg gct ttg gct gaa gcc taattccaca gtccttggt 1207
 Phe Cys Pro Glu Lys Val Ala Leu Ala Glu Ala
 305 310
 ttttgagaga gactgagaga accataatcc ttgcctgctg aaccagcct gggcctggat 1267
 gctctgtgaa tacattatct tgcgatgttg ggtattcca gccaaagaca tttcaagtgc 1327
 ctgtaactga tttgtacata ttataaaaa tctattcaga aattggtcca ataatgcacg 1387
 tgctttgcc tgggtacagc cagagccctt caaccacc ttggacttga ggacctacct 1447
 gatgggacgt ttccacgtgt ctctagagaa ggattcctgg atctagctgg tcacgacgat 1507
 gttttcacca aggtcacagg agcattgcgt cgctgatggg gttgaagttt ggtttggttc 1567
 ttgtttcagc ccaatatgta gagaacattt gaaacagtct gcaccttga tacggtattg 1627
 catttccaaa gccaccaatc cattttgttg attttatgtg tctgtggctt aataatcata 1687
 gtaacaacaa taataccttt ttctccattt tgcttgcagg aaacatacct taagtttttt 1747
 ttgttttggt ttgttttttt tgttttttgt tttcctttat gaagaaaaaa taaaatagtc 1807
 acattttaat actaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaccacgc gtccgccac 1867
 gcgtccgcgg acgcgtgggc ggacgcacgc gtccg 1902

<210> 166

<211> 314

<212> PRT

<213> Homo sapiens

<400> 166

Met Phe Ser Ile Asn Pro Leu Glu Asn Leu Lys Val Tyr Ile Ser Ser
 1 5 10 15
 Arg Pro Pro Leu Val Val Phe Met Ile Ser Val Ser Ala Met Ala Ile
 20 25 30
 Ala Phe Leu Thr Leu Gly Tyr Phe Phe Lys Ile Lys Glu Ile Lys Ser
 35 40 45
 Pro Glu Met Ala Glu Asp Trp Asn Thr Phe Leu Leu Arg Phe Asn Asp
 50 55 60
 Leu Asp Leu Cys Val Ser Glu Asn Glu Thr Leu Lys His Leu Thr Asn
 65 70 75 80
 Asp Thr Thr Thr Pro Glu Ser Thr Met Thr Ser Gly Gln Ala Arg Ala
 85 90 95
 Ser Thr Gln Ser Pro Gln Ala Leu Glu Asp Ser Gly Pro Val Asn Ile
 100 105 110
 Ser Val Ser Ile Thr Leu Thr Leu Asp Pro Leu Lys Pro Phe Gly Gly
 115 120 125
 Tyr Ser Arg Asn Val Thr His Leu Tyr Ser Thr Ile Leu Gly His Gln
 130 135 140
 Ile Gly Leu Ser Gly Arg Glu Ala His Glu Glu Ile Asn Ile Thr Phe
 145 150 155 160
 Thr Leu Pro Thr Ala Trp Ser Ser Asp Asp Cys Ala Leu His Gly His
 165 170 175
 Cys Glu Gln Val Val Phe Thr Ala Cys Met Thr Leu Thr Ala Ser Pro
 180 185 190
 Gly Val Phe Pro Val Thr Val Gln Pro Pro His Cys Val Pro Asp Thr
 195 200 205
 Tyr Ser Asn Ala Thr Leu Trp Tyr Lys Ile Phe Thr Thr Ala Arg Asp

210 215 220
 Ala Asn Thr Lys Tyr Ala Gln Asp Tyr Asn Pro Phe Trp Cys Tyr Lys
 225 230 235 240
 Gly Ala Ile Gly Lys Val Tyr His Ala Leu Asn Pro Lys Leu Thr Val
 245 250 255
 Ile Val Pro Asp Asp Asp Arg Ser Leu Ile Asn Leu His Leu Met His
 260 265 270
 Thr Ser Tyr Phe Leu Phe Val Met Val Ile Thr Met Phe Cys Tyr Ala
 275 280 285
 Val Ile Lys Gly Arg Pro Ser Lys Leu Arg Gln Ser Asn Pro Glu Phe
 290 295 300
 Cys Pro Glu Lys Val Ala Leu Ala Glu Ala
 305 310

<210> 167

<211> 1768

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (232)..(1227)

<223>

<400> 167

aggcggcggc accgcgcggg acggagcttg gctgttggtc ggtgggttcc cgtgcggcgg 60
 cggccaagga ggaggagaca cagttggagc agctccgtgg gctgactggg gcgaggcctc 120
 agcagcgcga gcttgagtgc ggccgagcct gcggcgcctt cccctgcggg tggggacgag 180
 cgggccccgc ggcgtcatcg gcggcgagga gccgccgcgc ctgcgcctag c atg tcg 237

Met Ser

1

gaa gcg ggc gag gag cag ccc atg gag acg acg ggc gcc acc gag aac	285
Glu Ala Gly Glu Glu Gln Pro Met Glu Thr Thr Gly Ala Thr Glu Asn	
5 10 15	
gga cat gag gcc gtc ccc gaa ggc gag tcg ccg gcc ggg gct ggc acg	333
Gly His Glu Ala Val Pro Glu Gly Glu Ser Pro Ala Gly Ala Gly Thr	
20 25 30	
ggc gcc gcg gcg ggg gct gga ggc gcg acc gcg gcg ccc ccg agc ggg	381
Gly Ala Ala Ala Gly Ala Gly Gly Ala Thr Ala Ala Pro Pro Ser Gly	
35 40 45 50	
aat cag aac ggc gcc gag ggc gac cag atc aac gcc agc aag aac gag	429
Asn Gln Asn Gly Ala Glu Gly Asp Gln Ile Asn Ala Ser Lys Asn Glu	
55 60 65	
gag gac gcg gga aaa atg ttc gtt ggt ggc ctg agc tgg gat act agc	477
Glu Asp Ala Gly Lys Met Phe Val Gly Gly Leu Ser Trp Asp Thr Ser	
70 75 80	
aaa aaa gat tta aaa gac tat ttt act aaa ttt gga gag gtc gtt gac	525
Lys Lys Asp Leu Lys Asp Tyr Phe Thr Lys Phe Gly Glu Val Val Asp	
85 90 95	
tgt aca ata aaa atg gat ccc aac act gga cgg tca aga ggg ttt ggg	573
Cys Thr Ile Lys Met Asp Pro Asn Thr Gly Arg Ser Arg Gly Phe Gly	
100 105 110	
ttt atc ctg ttc aaa gat gca gcc agt gtg gag aag gtc cta gac cag	621
Phe Ile Leu Phe Lys Asp Ala Ala Ser Val Glu Lys Val Leu Asp Gln	
115 120 125 130	
aag gag cac agg ctg gat ggc cgt gtc att gac cct aaa aag gcc atg	669

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Lys Glu His Arg Leu Asp Gly Arg Val Ile Asp Pro Lys Lys Ala Met
 135 140 145
 gct atg aag aag gac ccg gtg aag aaa atc ttc gtt ggg ggt ctg aat 717
 Ala Met Lys Lys Asp Pro Val Lys Lys Ile Phe Val Gly Gly Leu Asn
 150 155 160
 cct gaa gcc act gag gaa aag atc agg gag tac ttt ggc gag ttt ggg 765
 Pro Glu Ala Thr Glu Glu Lys Ile Arg Glu Tyr Phe Gly Glu Phe Gly
 165 170 175
 gag att gag gcc att gaa ttg cca atg gat cca aag ttg aac aaa aga 813
 Glu Ile Glu Ala Ile Glu Leu Pro Met Asp Pro Lys Leu Asn Lys Arg
 180 185 190
 cga ggt ttt gtg ttt atc acc ttt aaa gaa gaa gaa ccc gtg aag aag 861
 Arg Gly Phe Val Phe Ile Thr Phe Lys Glu Glu Glu Pro Val Lys Lys
 195 200 205 210
 gtt ctg gag aaa aag ttc cat act gtc agt gga agc aag tgt gag atc 909
 Val Leu Glu Lys Lys Phe His Thr Val Ser Gly Ser Lys Cys Glu Ile
 215 220 225
 aag gtg gcc cag ccc aaa gaa gtc tat cag cag cag cag tat ggc tct 957
 Lys Val Ala Gln Pro Lys Glu Val Tyr Gln Gln Gln Gln Tyr Gly Ser
 230 235 240
 ggg ggc cgt gga aac cgc aac cga ggg aac cga ggc agc gga ggt ggt 1005
 Gly Gly Arg Gly Asn Arg Asn Arg Gly Asn Arg Gly Ser Gly Gly Gly
 245 250 255
 ggt gga ggt gga ggt cag agt cag agt tgg aat cag ggc tac ggc aac 1053
 Gly Gly Gly Gly Gly Gln Ser Gln Ser Trp Asn Gln Gly Tyr Gly Asn
 260 265 270
 tac tgg aac cag ggc tac ggc tac cag cag ggc tac ggg cct ggc tat 1101

Tyr Trp Asn Gln Gly Tyr Gly Tyr Gln Gln Gly Tyr Gly Pro Gly Tyr
 275 280 285 290
 ggc ggc tac gac tac tcg ccc tat ggc tat tac ggc tac ggc ccc ggc 1149
 Gly Gly Tyr Asp Tyr Ser Pro Tyr Gly Tyr Tyr Gly Tyr Gly Pro Gly
 295 300 305
 tac gac tac agt cag ggt agt aca aac tac ggc aag agc cag cga cgt 1197
 Tyr Asp Tyr Ser Gln Gly Ser Thr Asn Tyr Gly Lys Ser Gln Arg Arg
 310 315 320
 ggt ggc cat cag aat aac tac aag cca tac tgaggcggca gcaggagcga 1247
 Gly Gly His Gln Asn Asn Tyr Lys Pro Tyr
 325 330
 ccaactgatac gcacacatgc tttgtttgga tatggagtga acacaattat gtaccaaatt 1307
 taacttggca aactttctat tgcctgtccc atgtgcatct tatttaaaat ttcccccatg 1367
 gaaatcactc tcctgttgac tatttcaga gctctaggtg tttaggcagc gtgtggtgtc 1427
 tgagaggcca tagcgccatc atgggctgat ttttattacc aggtcccca gaagcaggtg 1487
 ggaggctctg ctctctgtg ccgctctgca gcctggacct gtggaccctg gttgtaaaga 1547
 gtaaattgta tcttaggaaa ccagtgtcac ctttttttca ctttttaatt ttatattatt 1607
 tgcgtcatac atttctgtg acggaagtgt taattttact gtactttttg gtaccttttg 1667
 ggaatctaata gtattgtaag gtattttaca cgtgtcctga ttttgccaca acctggatat 1727
 tgaagctatc caagcttttg aaataaaatt taaaaacccc c 1768

<210> 168

<211> 332

<212> PRT

<213> Homo sapiens

<400> 168

Met Ser Glu Ala Gly Glu Glu Gln Pro Met Glu Thr Thr Gly Ala Thr

1 5 10 15
Glu Asn Gly His Glu Ala Val Pro Glu Gly Glu Ser Pro Ala Gly Ala
20 25 30
Gly Thr Gly Ala Ala Ala Gly Ala Gly Gly Ala Thr Ala Ala Pro Pro
35 40 45
Ser Gly Asn Gln Asn Gly Ala Glu Gly Asp Gln Ile Asn Ala Ser Lys
50 55 60
Asn Glu Glu Asp Ala Gly Lys Met Phe Val Gly Gly Leu Ser Trp Asp
65 70 75 80
Thr Ser Lys Lys Asp Leu Lys Asp Tyr Phe Thr Lys Phe Gly Glu Val
85 90 95
Val Asp Cys Thr Ile Lys Met Asp Pro Asn Thr Gly Arg Ser Arg Gly
100 105 110
Phe Gly Phe Ile Leu Phe Lys Asp Ala Ala Ser Val Glu Lys Val Leu
115 120 125
Asp Gln Lys Glu His Arg Leu Asp Gly Arg Val Ile Asp Pro Lys Lys
130 135 140
Ala Met Ala Met Lys Lys Asp Pro Val Lys Lys Ile Phe Val Gly Gly
145 150 155 160
Leu Asn Pro Glu Ala Thr Glu Glu Lys Ile Arg Glu Tyr Phe Gly Glu
165 170 175
Phe Gly Glu Ile Glu Ala Ile Glu Leu Pro Met Asp Pro Lys Leu Asn
180 185 190
Lys Arg Arg Gly Phe Val Phe Ile Thr Phe Lys Glu Glu Glu Pro Val
195 200 205
Lys Lys Val Leu Glu Lys Lys Phe His Thr Val Ser Gly Ser Lys Cys
210 215 220

Glu Ile Lys Val Ala Gln Pro Lys Glu Val Tyr Gln Gln Gln Gln Tyr
 225 230 235 240
 Gly Ser Gly Gly Arg Gly Asn Arg Asn Arg Gly Asn Arg Gly Ser Gly
 245 250 255
 Gly Gly Gly Gly Gly Gly Gly Gln Ser Gln Ser Trp Asn Gln Gly Tyr
 260 265 270
 Gly Asn Tyr Trp Asn Gln Gly Tyr Gly Tyr Gln Gln Gly Tyr Gly Pro
 275 280 285
 Gly Tyr Gly Gly Tyr Asp Tyr Ser Pro Tyr Gly Tyr Tyr Gly Tyr Gly
 290 295 300
 Pro Gly Tyr Asp Tyr Ser Gln Gly Ser Thr Asn Tyr Gly Lys Ser Gln
 305 310 315 320
 Arg Arg Gly Gly His Gln Asn Asn Tyr Lys Pro Tyr
 325 330

<210> 169

<211> 1647

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (234)..(1088)

<223>

<400> 169

ggcaacgaggg gcaccgcgcg ggacggagct tggtgttgg tcggtgggtt cccgtgcggc 60
 ggcgcccaag gaggaggaga cacagttgga gcagctccgt gggctgactg gggcgaggcc 120
 tcagcagcgc gagcttgagt gggccgagc ctgcggcgcc ttcccctgcg ggtggggacg 180

agcgggcccc gcggcgatcat cggcggcgag gagccgccgc gcctcggcct agc atg 236
 Met
 1
 tcg gaa gcg ggc gag gag cag ccc atg gag acg acg ggc gcc acc gag 284
 Ser Glu Ala Gly Glu Glu Gln Pro Met Glu Thr Thr Gly Ala Thr Glu
 5 10 15
 aac gga cat gag gcc gtc ccc gaa ggc gag tcg ccg gcc ggg gct ggc 332
 Asn Gly His Glu Ala Val Pro Glu Gly Glu Ser Pro Ala Gly Ala Gly
 20 25 30
 acg ggc gcc gcg gcg ggg gct gga ggc gcg acc gcg gcg ccc ccg agc 380
 Thr Gly Ala Ala Ala Gly Ala Gly Gly Ala Thr Ala Ala Pro Pro Ser
 35 40 45
 ggg aat cag aac ggc gcc gag ggc gac cag atc aac gcc agc aag aac 428
 Gly Asn Gln Asn Gly Ala Glu Gly Asp Gln Ile Asn Ala Ser Lys Asn
 50 55 60 65
 gag gag gac gcg gga aaa atg ttc gtt ggt ggc ctg agc tgg gat act 476
 Glu Glu Asp Ala Gly Lys Met Phe Val Gly Gly Leu Ser Trp Asp Thr
 70 75 80
 agc aaa aaa gat tta aaa gac tat ttt act aaa ttt gga gag gtc gtt 524
 Ser Lys Lys Asp Leu Lys Asp Tyr Phe Thr Lys Phe Gly Glu Val Val
 85 90 95
 gac tgt aca ata aaa atg gat ccc aac act gga cgg tca aga ggg ttt 572
 Asp Cys Thr Ile Lys Met Asp Pro Asn Thr Gly Arg Ser Arg Gly Phe
 100 105 110
 ggg ttt atc ctg ttc aaa gat gca gcc agt gtg gag aag gtc cta gac 620
 Gly Phe Ile Leu Phe Lys Asp Ala Ala Ser Val Glu Lys Val Leu Asp
 115 120 125

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cag aag gag cac agg ctg gat ggc cgt gtc att gac cct aaa aag gcc	668
Gln Lys Glu His Arg Leu Asp Gly Arg Val Ile Asp Pro Lys Lys Ala	
130 135 140 145	
atg gct atg aag aag gac ccg gtg aag aaa atc ttc gtt ggg ggt ctg	716
Met Ala Met Lys Lys Asp Pro Val Lys Lys Ile Phe Val Gly Gly Leu	
150 155 160	
aat cct gaa gcc act gag gaa aag atc agg gag tac ttt ggc gag ttt	764
Asn Pro Glu Ala Thr Glu Glu Lys Ile Arg Glu Tyr Phe Gly Glu Phe	
165 170 175	
ggg gag att gag gcc att gaa ttg cca atg gat cca aag ttg aac aaa	812
Gly Glu Ile Glu Ala Ile Glu Leu Pro Met Asp Pro Lys Leu Asn Lys	
180 185 190	
aga cga ggt ttt gtg ttt atc acc ttt aaa gaa gaa gaa ccc gtg aag	860
Arg Arg Gly Phe Val Phe Ile Thr Phe Lys Glu Glu Glu Pro Val Lys	
195 200 205	
aag gtt ctg gag aaa aag ttc cat act gtc agt gga agc aag tgt gag	908
Lys Val Leu Glu Lys Lys Phe His Thr Val Ser Gly Ser Lys Cys Glu	
210 215 220 225	
atc aag gtg gcc cag ccc aaa gaa gtc tat cag cag cag cag tat ggc	956
Ile Lys Val Ala Gln Pro Lys Glu Val Tyr Gln Gln Gln Gln Tyr Gly	
230 235 240	
tct ggg ggc cgt gga aac cgc aac cga ggg aac cga ggc agc gga ggt	1004
Ser Gly Gly Arg Gly Asn Arg Asn Arg Gly Asn Arg Gly Ser Gly Gly	
245 250 255	
ggt ggt gga ggt gga ggt cag ggt agt aca aac tac ggc aag agc cag	1052
Gly Gly Gly Gly Gly Gly Gln Gly Ser Thr Asn Tyr Gly Lys Ser Gln	
260 265 270	

cga cgt ggt ggc cat cag aat aac tac aag cca tac tgaggcggca 1098
 Arg Arg Gly Gly His Gln Asn Asn Tyr Lys Pro Tyr
 275 280 285
 gcaggagcga ccaactgac gcacacatgc tttgtttgga tatggagtga acacaattat 1158
 gtaccaaatt taacttggca aactttctat tgcctgtccc atgtgcatct tatttaaaat 1218
 ttcccccatg gaaatcactc tcctgttgac tatttccaga gctctagggtg tttaggcagc 1278
 gtgtggtgtc tgagaggcca tagcgccatc atgggctgat ttttattacc aggtccccc 1338
 gaagcaggtg ggaggctctg ctctctgctg ccgctctgca gcctggacct gtggaccctg 1398
 gttgtaaaga gtaaattgta tcttaggaaa ccagtgtcac ctttttttca cttttaatt 1458
 ttatattatt tgcgtcatat atttctgta acggaagtgt taattttact gtactttttg 1518
 gtaccttttg ggaatctaata gtattgtaag gtattttaca cgtgtcctga ttttgccaca 1578
 acctggatat tgaagctatc caagcttttg aaataaaatt taaaaacccc caaaaaaaaaa 1638
 aaaaaaaaaa 1647

<210> 170

<211> 285

<212> PRT

<213> Homo sapiens

<400> 170

Met Ser Glu Ala Gly Glu Glu Gln Pro Met Glu Thr Thr Gly Ala Thr
 1 5 10 15
 Glu Asn Gly His Glu Ala Val Pro Glu Gly Glu Ser Pro Ala Gly Ala
 20 25 30
 Gly Thr Gly Ala Ala Ala Gly Ala Gly Gly Ala Thr Ala Ala Pro Pro
 35 40 45
 Ser Gly Asn Gln Asn Gly Ala Glu Gly Asp Gln Ile Asn Ala Ser Lys
 50 55 60

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Asn Glu Glu Asp Ala Gly Lys Met Phe Val Gly Gly Leu Ser Trp Asp
 65 70 75 80
 Thr Ser Lys Lys Asp Leu Lys Asp Tyr Phe Thr Lys Phe Gly Glu Val
 85 90 95
 Val Asp Cys Thr Ile Lys Met Asp Pro Asn Thr Gly Arg Ser Arg Gly
 100 105 110
 Phe Gly Phe Ile Leu Phe Lys Asp Ala Ala Ser Val Glu Lys Val Leu
 115 120 125
 Asp Gln Lys Glu His Arg Leu Asp Gly Arg Val Ile Asp Pro Lys Lys
 130 135 140
 Ala Met Ala Met Lys Lys Asp Pro Val Lys Lys Ile Phe Val Gly Gly
 145 150 155 160
 Leu Asn Pro Glu Ala Thr Glu Glu Lys Ile Arg Glu Tyr Phe Gly Glu
 165 170 175
 Phe Gly Glu Ile Glu Ala Ile Glu Leu Pro Met Asp Pro Lys Leu Asn
 180 185 190
 Lys Arg Arg Gly Phe Val Phe Ile Thr Phe Lys Glu Glu Glu Pro Val
 195 200 205
 Lys Lys Val Leu Glu Lys Lys Phe His Thr Val Ser Gly Ser Lys Cys
 210 215 220
 Glu Ile Lys Val Ala Gln Pro Lys Glu Val Tyr Gln Gln Gln Gln Tyr
 225 230 235 240
 Gly Ser Gly Gly Arg Gly Asn Arg Asn Arg Gly Asn Arg Gly Ser Gly
 245 250 255
 Gly Gly Gly Gly Gly Gly Gly Gln Gly Ser Thr Asn Tyr Gly Lys Ser
 260 265 270
 Gln Arg Arg Gly Gly His Gln Asn Asn Tyr Lys Pro Tyr

275

280

285

<210> 171

<211> 2144

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (87)..(1853)

<223>

<400> 171

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gggcctccgc gccgcggccg ttagtc atg tcg gat tct gga agt tac ggt cag 113

Met Ser Asp Ser Gly Ser Tyr Gly Gln

1

5

tct ggg ggt gag cag caa agt tat tct acc tat gga aat cca ggc agc 161

Ser Gly Gly Glu Gln Gln Ser Tyr Ser Thr Tyr Gly Asn Pro Gly Ser

10 15 20 25

caa ggc tat gga caa gca tca caa agc tat tct ggc tat ggg caa acg 209

Gln Gly Tyr Gly Gln Ala Ser Gln Ser Tyr Ser Gly Tyr Gly Gln Thr

30

35

40

act gat tcc tct tat gga cag aac tac agc ggt tac tcc agt tat gga 257

Thr Asp Ser Ser Tyr Gly Gln Asn Tyr Ser Gly Tyr Ser Ser Tyr Gly

45

50

55

caa agt tat tca cag tcc tat ggt ggt tat gag aat caa aag cag agc 305

Gln Ser Tyr Ser Gln Ser Tyr Gly Gly Tyr Glu Asn Gln Lys Gln Ser

60

65

70

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tca tat agc cag caa cca tat aat aac cag gga cag cag caa aac atg	353
Ser Tyr Ser Gln Gln Pro Tyr Asn Asn Gln Gly Gln Gln Gln Asn Met	
75 80 85	
gaa tca tca gga agc caa ggt gga aga gca cct tcc tat gac cag cca	401
Glu Ser Ser Gly Ser Gln Gly Gly Arg Ala Pro Ser Tyr Asp Gln Pro	
90 95 100 105	
gac tat ggt caa caa cat tca tat gac cag cag tca ggc tat gat caa	449
Asp Tyr Gly Gln Gln His Ser Tyr Asp Gln Gln Ser Gly Tyr Asp Gln	
110 115 120	
cat caa ggc tca tat gat gag cag tca aat tat gat cag cag cac gat	497
His Gln Gly Ser Tyr Asp Glu Gln Ser Asn Tyr Asp Gln Gln His Asp	
125 130 135	
tcc tat agt caa aac cag cag tcc tat cat tca caa agg gaa aac tac	545
Ser Tyr Ser Gln Asn Gln Gln Ser Tyr His Ser Gln Arg Glu Asn Tyr	
140 145 150	
agc cac cac aca caa gat gac cgt cgt gat gtg agt agg tat gga gaa	593
Ser His His Thr Gln Asp Asp Arg Arg Asp Val Ser Arg Tyr Gly Glu	
155 160 165	
gat aat aga gga tat ggc ggg tca cag gga gga ggt aga ggg cgt ggg	641
Asp Asn Arg Gly Tyr Gly Gly Ser Gln Gly Gly Gly Arg Gly Arg Gly	
170 175 180 185	
gga tat gac aag gat gga aga ggt cct atg aca gga tca agt ggt ggt	689
Gly Tyr Asp Lys Asp Gly Arg Gly Pro Met Thr Gly Ser Ser Gly Gly	
190 195 200	
gac cgc ggt ggc ttc aaa aat ttt ggt ggt cac agg gat tat gga ccc	737
Asp Arg Gly Gly Phe Lys Asn Phe Gly Gly His Arg Asp Tyr Gly Pro	
205 210 215	

569/617

aga aca gat gct gat tca gaa tct gat aat tca gat aac aac aca atc	785
Arg Thr Asp Ala Asp Ser Glu Ser Asp Asn Ser Asp Asn Asn Thr Ile	
220 225 230	
ttt gtg caa gga ctt ggg gag ggt gtg tct aca gat caa gtt ggg gag	833
Phe Val Gln Gly Leu Gly Glu Gly Val Ser Thr Asp Gln Val Gly Glu	
235 240 245	
ttc ttt aaa caa ata gga att atc aag aca aat aag aag acc gga aaa	881
Phe Phe Lys Gln Ile Gly Ile Ile Lys Thr Asn Lys Lys Thr Gly Lys	
250 255 260 265	
cca atg ata aat ctt tat aca gac aag gac aca gga aag cca aag ggg	929
Pro Met Ile Asn Leu Tyr Thr Asp Lys Asp Thr Gly Lys Pro Lys Gly	
270 275 280	
gag gca aca gtg tca ttt gat gac cct cct tca gct aag gca gcc att	977
Glu Ala Thr Val Ser Phe Asp Asp Pro Pro Ser Ala Lys Ala Ala Ile	
285 290 295	
gac tgg ttt gat gga aaa gaa ttc cat ggc aac atc att aaa gtg tcc	1025
Asp Trp Phe Asp Gly Lys Glu Phe His Gly Asn Ile Ile Lys Val Ser	
300 305 310	
ttt gcc act aga aga cct gaa ttc atg aga gga ggt gga agt gga ggt	1073
Phe Ala Thr Arg Arg Pro Glu Phe Met Arg Gly Gly Gly Ser Gly Gly	
315 320 325	
ggg cgg cga ggc cgt gga gga tat aga ggt cgt gga ggc ttt caa ggg	1121
Gly Arg Arg Gly Arg Gly Gly Tyr Arg Gly Arg Gly Gly Phe Gln Gly	
330 335 340 345	
aga ggt gga gac ccc aaa agt ggg gat tgg gtt tgc cct aat ccg tca	1169
Arg Gly Gly Asp Pro Lys Ser Gly Asp Trp Val Cys Pro Asn Pro Ser	
350 355 360	

tgc gga aat atg aac ttt gct cga agg aat tcc tgc aat cag tgc aat	1217
Cys Gly Asn Met Asn Phe Ala Arg Arg Asn Ser Cys Asn Gln Cys Asn	
365 370 375	
gag cct aga cca gag gac tct cgt ccc tca gga gga gat ttc cgg ggg	1265
Glu Pro Arg Pro Glu Asp Ser Arg Pro Ser Gly Gly Asp Phe Arg Gly	
380 385 390	
aga ggc tac ggt gga gag agg ggc tac aga ggt cgt ggg ggc aga ggt	1313
Arg Gly Tyr Gly Gly Glu Arg Gly Tyr Arg Gly Arg Gly Gly Arg Gly	
395 400 405	
gga gac cga ggc ggc tat ggt gga gac aga agt ggg ggt ggc tat ggt	1361
Gly Asp Arg Gly Gly Tyr Gly Gly Asp Arg Ser Gly Gly Gly Tyr Gly	
410 415 420 425	
gga gac aga agc agc ggt ggt ggc tac agc gga gat aga agt ggg ggc	1409
Gly Asp Arg Ser Ser Gly Gly Gly Tyr Ser Gly Asp Arg Ser Gly Gly	
430 435 440	
ggc tat ggt gga gac aga agt ggg ggt ggc tat ggt ggg gac aga ggc	1457
Gly Tyr Gly Gly Asp Arg Ser Gly Gly Gly Tyr Gly Gly Asp Arg Gly	
445 450 455	
ggc ggc tat ggt ggg gac aga gga ggc ggc tat gga gga gac cga gga	1505
Gly Gly Tyr Gly Gly Asp Arg Gly Gly Gly Tyr Gly Gly Asp Arg Gly	
460 465 470	
ggt ggc tat gga gga gac cga ggt ggc tat gga gga gac cga ggt gga	1553
Gly Gly Tyr Gly Gly Asp Arg Gly Gly Tyr Gly Gly Asp Arg Gly Gly	
475 480 485	
ggc tat ggt gga gac cga gga ggc tat gga gga gat cga gga ggt tac	1601
Gly Tyr Gly Gly Asp Arg Gly Gly Tyr Gly Gly Asp Arg Gly Gly Tyr	
490 495 500 505	

gga gga gat cga gga ggt tat gga gga gat cga gga ggc tat gga gga 1649
 Gly Gly Asp Arg Gly Gly Tyr Gly Gly Asp Arg Gly Gly Tyr Gly Gly

510

515

520

gac aga agc cgg ggg ggc tat gga gga gac cgt ggt ggt ggc agt ggc 1697
 Asp Arg Ser Arg Gly Gly Tyr Gly Gly Asp Arg Gly Gly Gly Ser Gly

525

530

535

tac ggt gga gac cga agt gga ggc tat gga gga gac agg agt ggt ggc 1745
 Tyr Gly Gly Asp Arg Ser Gly Gly Tyr Gly Gly Asp Arg Ser Gly Gly

540

545

550

ggc tat gga gga gac cga ggt ggg ggc tac gga gga gac cga ggt ggc 1793
 Gly Tyr Gly Gly Asp Arg Gly Gly Gly Tyr Gly Gly Asp Arg Gly Gly

555

560

565

tat gga ggc aaa atg gga gga aga aac gac tac aga aat gat cag cgc 1841
 Tyr Gly Gly Lys Met Gly Gly Arg Asn Asp Tyr Arg Asn Asp Gln Arg

570

575

580

585

aac cga cca tac tgatgactgt tttgaatgtt cctttgtctc tgacatgac 1893
 Asn Arg Pro Tyr

catagtga aa ttgccagagt ttgcctgct gctttcctcg tggcctcttc ttgggtagtg 1953

aaattaagt acatttgat tttatttgg gtgggagggc tgggacagtt tttcctctag 2013

aatgtctgt tgagatttcc cccttagtt tccaaccttc tccccaaccc ttggagctaa 2073

atgcgttgta aaatattgcc aaaatgaaaa gtgttttgta atactgcaat aaaggctgct 2133

tgtttttg g 2144

<210> 172

<211> 589

<212> PRT

<213> Homo sapiens

<400> 172

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Met Ser Asp Ser Gly Ser Tyr Gly Gln Ser Gly Gly Glu Gln Gln Ser
1           5           10           15
Tyr Ser Thr Tyr Gly Asn Pro Gly Ser Gln Gly Tyr Gly Gln Ala Ser
           20           25           30
Gln Ser Tyr Ser Gly Tyr Gly Gln Thr Thr Asp Ser Ser Tyr Gly Gln
           35           40           45
Asn Tyr Ser Gly Tyr Ser Ser Tyr Gly Gln Ser Tyr Ser Gln Ser Tyr
           50           55           60
Gly Gly Tyr Glu Asn Gln Lys Gln Ser Ser Tyr Ser Gln Gln Pro Tyr
65           70           75           80
Asn Asn Gln Gly Gln Gln Gln Asn Met Glu Ser Ser Gly Ser Gln Gly
           85           90           95
Gly Arg Ala Pro Ser Tyr Asp Gln Pro Asp Tyr Gly Gln Gln His Ser
           100          105          110
Tyr Asp Gln Gln Ser Gly Tyr Asp Gln His Gln Gly Ser Tyr Asp Glu
           115          120          125
Gln Ser Asn Tyr Asp Gln Gln His Asp Ser Tyr Ser Gln Asn Gln Gln
           130          135          140
Ser Tyr His Ser Gln Arg Glu Asn Tyr Ser His His Thr Gln Asp Asp
145          150          155          160
Arg Arg Asp Val Ser Arg Tyr Gly Glu Asp Asn Arg Gly Tyr Gly Gly
           165          170          175
Ser Gln Gly Gly Gly Arg Gly Arg Gly Gly Tyr Asp Lys Asp Gly Arg
           180          185          190
Gly Pro Met Thr Gly Ser Ser Gly Gly Asp Arg Gly Gly Phe Lys Asn

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573/617

195 200 205
Phe Gly Gly His Arg Asp Tyr Gly Pro Arg Thr Asp Ala Asp Ser Glu
210 215 220
Ser Asp Asn Ser Asp Asn Asn Thr Ile Phe Val Gln Gly Leu Gly Glu
225 230 235 240
Gly Val Ser Thr Asp Gln Val Gly Glu Phe Phe Lys Gln Ile Gly Ile
245 250 255
Ile Lys Thr Asn Lys Lys Thr Gly Lys Pro Met Ile Asn Leu Tyr Thr
260 265 270
Asp Lys Asp Thr Gly Lys Pro Lys Gly Glu Ala Thr Val Ser Phe Asp
275 280 285
Asp Pro Pro Ser Ala Lys Ala Ala Ile Asp Trp Phe Asp Gly Lys Glu
290 295 300
Phe His Gly Asn Ile Ile Lys Val Ser Phe Ala Thr Arg Arg Pro Glu
305 310 315 320
Phe Met Arg Gly Gly Gly Ser Gly Gly Gly Arg Arg Gly Arg Gly Gly
325 330 335
Tyr Arg Gly Arg Gly Gly Phe Gln Gly Arg Gly Gly Asp Pro Lys Ser
340 345 350
Gly Asp Trp Val Cys Pro Asn Pro Ser Cys Gly Asn Met Asn Phe Ala
355 360 365
Arg Arg Asn Ser Cys Asn Gln Cys Asn Glu Pro Arg Pro Glu Asp Ser
370 375 380
Arg Pro Ser Gly Gly Asp Phe Arg Gly Arg Gly Tyr Gly Gly Glu Arg
385 390 395 400
Gly Tyr Arg Gly Arg Gly Gly Arg Gly Gly Asp Arg Gly Gly Tyr Gly
405 410 415

Gly Asp Arg Ser Gly Gly Gly Tyr Gly Gly Asp Arg Ser Ser Gly Gly
420 425 430
Gly Tyr Ser Gly Asp Arg Ser Gly Gly Gly Tyr Gly Gly Asp Arg Ser
435 440 445
Gly Gly Gly Tyr Gly Gly Asp Arg Gly Gly Gly Tyr Gly Gly Asp Arg
450 455 460
Gly Gly Gly Tyr Gly Gly Asp Arg Gly Gly Gly Tyr Gly Gly Asp Arg
465 470 475 480
Gly Gly Tyr Gly Gly Asp Arg Gly Gly Gly Tyr Gly Gly Asp Arg Gly
485 490 495
Gly Tyr Gly Gly Asp Arg Gly Gly Tyr Gly Gly Asp Arg Gly Gly Tyr
500 505 510
Gly Gly Asp Arg Gly Gly Tyr Gly Gly Asp Arg Ser Arg Gly Gly Tyr
515 520 525
Gly Gly Asp Arg Gly Gly Gly Ser Gly Tyr Gly Gly Asp Arg Ser Gly
530 535 540
Gly Tyr Gly Gly Asp Arg Ser Gly Gly Gly Tyr Gly Gly Asp Arg Gly
545 550 555 560
Gly Gly Tyr Gly Gly Asp Arg Gly Gly Tyr Gly Gly Lys Met Gly Gly
565 570 575
Arg Asn Asp Tyr Arg Asn Asp Gln Arg Asn Arg Pro Tyr
580 585

<210> 173

<211> 2153

<212> DNA

<213> Homo sapiens

575/617

<220>

<221> CDS

<222> (87).. (1862)

<223>

<400> 173

agtacagctc cggccgccgc gccgcctggc ttctgtattc gttgttctcg gcgggctgtg 60

gggcctccgc gccgcggccg ttagtc atg tcg gat tct gga agt tac ggt cag 113

Met Ser Asp Ser Gly Ser Tyr Gly Gln

1

5

tct ggg ggt gag cag caa agt tat tct acc tat gga aat cca ggc agc 161

Ser Gly Gly Glu Gln Gln Ser Tyr Ser Thr Tyr Gly Asn Pro Gly Ser

10 15 20 25

caa ggc tat gga caa gca tca caa agc tat tct ggc tat ggg caa acg 209

Gln Gly Tyr Gly Gln Ala Ser Gln Ser Tyr Ser Gly Tyr Gly Gln Thr

30

35

40

act gat tcc tct tat gga cag aac tac agc ggt tac tcc agt tat gga 257

Thr Asp Ser Ser Tyr Gly Gln Asn Tyr Ser Gly Tyr Ser Ser Tyr Gly

45

50

55

caa agt cag tca ggt tat tca cag tcc tat ggt ggt tat gag aat caa 305

Gln Ser Gln Ser Gly Tyr Ser Gln Ser Tyr Gly Gly Tyr Glu Asn Gln

60

65

70

aag cag agc tca tat agc cag caa cca tat aat aac cag gga cag cag 353

Lys Gln Ser Ser Tyr Ser Gln Gln Pro Tyr Asn Asn Gln Gly Gln Gln

75

80

85

caa aac atg gaa tca tca gga agc caa ggt gga aga gca cct tcc tat 401

Gln Asn Met Glu Ser Ser Gly Ser Gln Gly Gly Arg Ala Pro Ser Tyr

90

95

100

105

576/617

gac cag cca gac tat ggt caa caa gat tca tat gac cag cag tca ggc 449
 Asp Gln Pro Asp Tyr Gly Gln Gln Asp Ser Tyr Asp Gln Gln Ser Gly
 110 115 120
 tat gat caa cat caa ggc tca tat gat gag cag tca aat tat gat cag 497
 Tyr Asp Gln His Gln Gly Ser Tyr Asp Glu Gln Ser Asn Tyr Asp Gln
 125 130 135
 cag cat gat tcc tat agt caa aac cag cag tcc tat cat tca caa agg 545
 Gln His Asp Ser Tyr Ser Gln Asn Gln Gln Ser Tyr His Ser Gln Arg
 140 145 150
 gaa aac tac agc cac cac aca caa gat gac cgt cgt gat gtg agt agg 593
 Glu Asn Tyr Ser His His Thr Gln Asp Asp Arg Arg Asp Val Ser Arg
 155 160 165
 tat gga gaa gat aat aga gga tat ggc ggg tca cag gga gga ggt aga 641
 Tyr Gly Glu Asp Asn Arg Gly Tyr Gly Gly Ser Gln Gly Gly Gly Arg
 170 175 180 185
 ggg cgt ggg gga tat gac aag gat gga aga ggt cct atg aca gga tca 689
 Gly Arg Gly Gly Tyr Asp Lys Asp Gly Arg Gly Pro Met Thr Gly Ser
 190 195 200
 agt ggt ggt gac cgc ggt ggc ttc aaa aat ttt ggt ggt cac agg gat 737
 Ser Gly Gly Asp Arg Gly Gly Phe Lys Asn Phe Gly Gly His Arg Asp
 205 210 215
 tat gga ccc aga aca gat gct gat tca gaa tct gat aat tca gat aac 785
 Tyr Gly Pro Arg Thr Asp Ala Asp Ser Glu Ser Asp Asn Ser Asp Asn
 220 225 230
 aac aca atc ttt gtg caa gga ctt ggg gag ggt gtg tct aca gat caa 833
 Asn Thr Ile Phe Val Gln Gly Leu Gly Glu Gly Val Ser Thr Asp Gln
 235 240 245

578/617

ttc cgg ggg aga ggc tac ggt gga gag agg ggc tac aga ggt cgt ggg 1313
 Phe Arg Gly Arg Gly Tyr Gly Gly Glu Arg Gly Tyr Arg Gly Arg Gly
 395 400 405
 ggc aga ggt gga gac cga ggc ggc tat ggt gga gac aga agt ggg ggt 1361
 Gly Arg Gly Gly Asp Arg Gly Gly Tyr Gly Gly Asp Arg Ser Gly Gly
 410 415 420 425
 ggc tat ggt ggg gac aga agc agc ggt ggt ggc tac agc gga gat aga 1409
 Gly Tyr Gly Gly Asp Arg Ser Ser Gly Gly Gly Tyr Ser Gly Asp Arg
 430 435 440
 agt ggg ggc ggc tat ggt gga gac aga agt ggg ggt ggc tat ggt ggg 1457
 Ser Gly Gly Gly Tyr Gly Gly Asp Arg Ser Gly Gly Gly Tyr Gly Gly
 445 450 455
 gac aga ggc ggc ggc tat ggt ggg gac aga gga ggc ggc tat gga gga 1505
 Asp Arg Gly Gly Gly Tyr Gly Gly Asp Arg Gly Gly Gly Tyr Gly Gly
 460 465 470
 gac cga gga ggt ggc tat gga gga gat cga ggt ggc tat gga gga gac 1553
 Asp Arg Gly Gly Gly Tyr Gly Gly Asp Arg Gly Gly Tyr Gly Gly Asp
 475 480 485
 cga ggt gga ggc tat ggt gga gac cga gga ggc tat gga gga gat cga 1601
 Arg Gly Gly Gly Tyr Gly Gly Asp Arg Gly Gly Tyr Gly Gly Asp Arg
 490 495 500 505
 gga ggt tac gga gga gat cga gga ggt tat gga gga gat cga gga ggc 1649
 Gly Gly Tyr Gly Gly Asp Arg Gly Gly Tyr Gly Gly Asp Arg Gly Gly
 510 515 520
 tat gga gga gac aga agc cgg ggg ggc tat gga gga gac cgt ggt ggt 1697
 Tyr Gly Gly Asp Arg Ser Arg Gly Gly Tyr Gly Gly Asp Arg Gly Gly
 525 530 535

ggc agt ggc tac ggt gga gac cga agt gga ggc tat gga gga gac agg 1745
 Gly Ser Gly Tyr Gly Gly Asp Arg Ser Gly Gly Tyr Gly Gly Asp Arg
 540 545 550
 agt ggt ggc ggc tat gga gga gac cga ggt ggg ggc tac gga gga gac 1793
 Ser Gly Gly Gly Tyr Gly Gly Asp Arg Gly Gly Gly Tyr Gly Gly Asp
 555 560 565
 cga ggt ggc tat gga ggc aaa atg gga gga aga aac gac tac aga aat 1841
 Arg Gly Gly Tyr Gly Gly Lys Met Gly Gly Arg Asn Asp Tyr Arg Asn
 570 575 580 585
 gat cag cgc aac cga cca tac tgatgactgt ttgaatgttc ctttgtctct 1892
 Asp Gln Arg Asn Arg Pro Tyr
 590
 gacatgatcc atagtgaat tgccagagtt ttgcctgctg ctttcctcgt ggccctcttct 1952
 tgggtagtga aattaagtga catttggatt tttatttggg tgggagggt gggacagttt 2012
 ttcttctaga aatgtctgtt gagatttccc ctttagttt ccaaccttct cccaaccct 2072
 tggagctaaa tgcgttgtaa aatattgcca aaatgaaaag tgttttgtaa tactgcaata 2132
 aaaggctgct tgtttttgtg g 2153

<210> 174

<211> 592

<212> PRT

<213> Homo sapiens

<400> 174

Met Ser Asp Ser Gly Ser Tyr Gly Gln Ser Gly Gly Glu Gln Gln Ser
 1 5 10 15
 Tyr Ser Thr Tyr Gly Asn Pro Gly Ser Gln Gly Tyr Gly Gln Ala Ser
 20 25 30

580/617

Gln Ser Tyr Ser Gly Tyr Gly Gln Thr Thr Asp Ser Ser Tyr Gly Gln
35 40 45
Asn Tyr Ser Gly Tyr Ser Ser Tyr Gly Gln Ser Gln Ser Gly Tyr Ser
50 55 60
Gln Ser Tyr Gly Gly Tyr Glu Asn Gln Lys Gln Ser Ser Tyr Ser Gln
65 70 75 80
Gln Pro Tyr Asn Asn Gln Gly Gln Gln Gln Asn Met Glu Ser Ser Gly
85 90 95
Ser Gln Gly Gly Arg Ala Pro Ser Tyr Asp Gln Pro Asp Tyr Gly Gln
100 105 110
Gln Asp Ser Tyr Asp Gln Gln Ser Gly Tyr Asp Gln His Gln Gly Ser
115 120 125
Tyr Asp Glu Gln Ser Asn Tyr Asp Gln Gln His Asp Ser Tyr Ser Gln
130 135 140
Asn Gln Gln Ser Tyr His Ser Gln Arg Glu Asn Tyr Ser His His Thr
145 150 155 160
Gln Asp Asp Arg Arg Asp Val Ser Arg Tyr Gly Glu Asp Asn Arg Gly
165 170 175
Tyr Gly Gly Ser Gln Gly Gly Gly Arg Gly Arg Gly Gly Tyr Asp Lys
180 185 190
Asp Gly Arg Gly Pro Met Thr Gly Ser Ser Gly Gly Asp Arg Gly Gly
195 200 205
Phe Lys Asn Phe Gly Gly His Arg Asp Tyr Gly Pro Arg Thr Asp Ala
210 215 220
Asp Ser Glu Ser Asp Asn Ser Asp Asn Asn Thr Ile Phe Val Gln Gly
225 230 235 240
Leu Gly Glu Gly Val Ser Thr Asp Gln Val Gly Glu Phe Phe Lys Gln

245	250	255
Ile Gly Ile Ile Lys Thr Asn Lys Lys Thr Gly Lys Pro Met Ile Asn		
260	265	270
Leu Tyr Thr Asp Lys Asp Thr Gly Lys Pro Lys Gly Glu Ala Thr Val		
275	280	285
Ser Phe Asp Asp Pro Pro Ser Ala Lys Ala Ala Ile Asp Trp Phe Asp		
290	295	300
Gly Lys Glu Phe His Gly Asn Ile Ile Lys Val Ser Phe Ala Thr Arg		
305	310	315
Arg Pro Glu Phe Met Arg Gly Gly Gly Ser Gly Gly Gly Arg Arg Gly		
325	330	335
Arg Gly Gly Tyr Arg Gly Arg Gly Gly Phe Gln Gly Arg Gly Gly Asp		
340	345	350
Pro Lys Ser Gly Asp Trp Val Cys Pro Asn Pro Ser Cys Gly Asn Met		
355	360	365
Asn Phe Ala Arg Arg Asn Ser Cys Asn Gln Cys Asn Glu Pro Arg Pro		
370	375	380
Glu Asp Ser Arg Pro Ser Gly Gly Asp Phe Arg Gly Arg Gly Tyr Gly		
385	390	395
Gly Glu Arg Gly Tyr Arg Gly Arg Gly Gly Arg Gly Gly Asp Arg Gly		
405	410	415
Gly Tyr Gly Gly Asp Arg Ser Gly Gly Gly Tyr Gly Gly Asp Arg Ser		
420	425	430
Ser Gly Gly Gly Tyr Ser Gly Asp Arg Ser Gly Gly Gly Tyr Gly Gly		
435	440	445
Asp Arg Ser Gly Gly Gly Tyr Gly Gly Asp Arg Gly Gly Gly Tyr Gly		
450	455	460

582/617

Gly Asp Arg Gly Gly Gly Tyr Gly Gly Asp Arg Gly Gly Gly Tyr Gly
 465 470 475 480
 Gly Asp Arg Gly Gly Tyr Gly Gly Asp Arg Gly Gly Gly Tyr Gly Gly
 485 490 495
 Asp Arg Gly Gly Tyr Gly Gly Asp Arg Gly Gly Tyr Gly Gly Asp Arg
 500 505 510
 Gly Gly Tyr Gly Gly Asp Arg Gly Gly Tyr Gly Gly Asp Arg Ser Arg
 515 520 525
 Gly Gly Tyr Gly Gly Asp Arg Gly Gly Gly Ser Gly Tyr Gly Gly Asp
 530 535 540
 Arg Ser Gly Gly Tyr Gly Gly Asp Arg Ser Gly Gly Gly Tyr Gly Gly
 545 550 555 560
 Asp Arg Gly Gly Gly Tyr Gly Gly Asp Arg Gly Gly Tyr Gly Gly Lys
 565 570 575
 Met Gly Gly Arg Asn Asp Tyr Arg Asn Asp Gln Arg Asn Arg Pro Tyr
 580 585 590

<210> 175

<211> 1987

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (271).. (1095)

<223>

<400> 175

ctcccagcgc ggtaacgcggt gccttttgag ctccttgctc acgctccgtc ccggtgggaa 60

cggccgcgcg ctccccgcag gtggatcatcc gccgcctgcc tccgggcctc accaaggagc 120
 agctggagga gcagctgcgc ccgctgccag cacacgacta cttcgagttc ttcgccgccg 180
 acctgagatc cagaatataa gaagttttta gaaacctact gtgtggagga agagaagacc 240
 agtgccaacc ctgagactct gctgggggag atg gag gcg aag aca aga gag ctc 294
 Met Glu Ala Lys Thr Arg Glu Leu
 1 5
 att gct aga aga acc aca cct ctt ttg gaa tat att aaa aat aga aaa 342
 Ile Ala Arg Arg Thr Thr Pro Leu Leu Glu Tyr Ile Lys Asn Arg Lys
 10 15 20
 tta gaa aag cag aga att cga gaa gag aag cga gaa gaa cgg agg agg 390
 Leu Glu Lys Gln Arg Ile Arg Glu Glu Lys Arg Glu Glu Arg Arg Arg
 25 30 35 40
 aga gag tta gaa aag aaa cgt ttg cgg gaa gag gaa aaa aga aga aga 438
 Arg Glu Leu Glu Lys Lys Arg Leu Arg Glu Glu Glu Lys Arg Arg Arg
 45 50 55
 aga gaa gaa gaa aga tgc aaa aaa aaa gag gca gat aaa cag aag aaa 486
 Arg Glu Glu Glu Arg Cys Lys Lys Lys Glu Ala Asp Lys Gln Lys Lys
 60 65 70
 att gca gag aaa gaa gta agg att aag ctt ctt aag aaa cca gaa aag 534
 Ile Ala Glu Lys Glu Val Arg Ile Lys Leu Leu Lys Lys Pro Glu Lys
 75 80 85
 gga gag gaa cca acc aca gag aaa cca aaa gaa aga gga gag gag att 582
 Gly Glu Glu Pro Thr Thr Glu Lys Pro Lys Glu Arg Gly Glu Glu Ile
 90 95 100
 gat act gga ggt ggc aag cag gaa tcc tgt gcc ccc ggt gca gtc gta 630
 Asp Thr Gly Gly Gly Lys Gln Glu Ser Cys Ala Pro Gly Ala Val Val
 105 110 115 120

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aaa gcc agg ccc atg gaa ggc tcg ctg gag gag ccc cag gag acg tca      678
Lys Ala Arg Pro Met Glu Gly Ser Leu Glu Glu Pro Gln Glu Thr Ser
          125              130              135

cac agc ggc agt gat aaa gag cac agg gat gtg gag aga tct caa gaa      726
His Ser Gly Ser Asp Lys Glu His Arg Asp Val Glu Arg Ser Gln Glu
          140              145              150

caa gaa tct gaa gca caa aga tac cat gtg gat gac ggc agg agg cac      774
Gln Glu Ser Glu Ala Gln Arg Tyr His Val Asp Asp Gly Arg Arg His
          155              160              165

aga gct cac cac gag cct gaa cgg ctt tcc aga agg agt gag gat gag      822
Arg Ala His His Glu Pro Glu Arg Leu Ser Arg Arg Ser Glu Asp Glu
          170              175              180

cag aga tgg ggg aaa gga cct ggc caa gac aga ggg aag aag ggg agc      870
Gln Arg Trp Gly Lys Gly Pro Gly Gln Asp Arg Gly Lys Lys Gly Ser
          185              190              195              200

cag gac agc ggg gct ccg ggg gag gcc atg gag aga ctg gga aga gcg      918
Gln Asp Ser Gly Ala Pro Gly Glu Ala Met Glu Arg Leu Gly Arg Ala
          205              210              215

cag agg tgt gac gac agt cca gca ccc aga aaa gag cga ctg gca aac      966
Gln Arg Cys Asp Asp Ser Pro Ala Pro Arg Lys Glu Arg Leu Ala Asn
          220              225              230

aag gac cgg cca gcc ttg cag ctg tat gat cca gga gct cgc ttc cga     1014
Lys Asp Arg Pro Ala Leu Gln Leu Tyr Asp Pro Gly Ala Arg Phe Arg
          235              240              245

gcg cga gag tgt ggc gga aac agg agg atc tgc aag gca gaa ggt tcg     1062
Ala Arg Glu Cys Gly Gly Asn Arg Arg Ile Cys Lys Ala Glu Gly Ser
          250              255              260

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585/617

ggg act ggt cct gag aag agg gaa gag gca gag tgagtcactg cacgcacctg 1115
 Gly Thr Gly Pro Glu Lys Arg Glu Glu Ala Glu
 265 270 275
 gcctccatgg acgagcaagg gcatcccaga aacgtgtaaa tgaccccgag tgtgactggg 1175
 aaggagaact tattccttac caggaaactg gaagctaaaa atacagaggg tgacgtagaa 1235
 acacgcagaa accattctaa agaaagtagt gatcttgtat taaattgagc agaattctca 1295
 cagattttac cattcctggt ataaactagt atttgttggt tagccaaaac agaaaatgat 1355
 ttccactgga cagtagaaaa atatgtgtaa aatagggag aaagttagta ttggatcagt 1415
 gtgagtcctg aagcactttc agtgctgtga gaacgacatc cactttgggt ttcattcggt 1475
 tgtaagcaga ggagctgtca gtcactcgtg cttctcgggt gcctctgagc catggtgtcg 1535
 agtgaagagt agttcttggt tgttacaacc ttgtgagtc agccatgcc gcaaagcgtg 1595
 ctgtgtttta gtcctggtag gaatatttat cagagttcac actatataaa acccaacagc 1655
 ttcaactatt gccctttcaa cagttttgcc actgaccgga tagaaacgt ttcagtctct 1715
 ggatggatgt gtttgtggt tgtaaccatt acggtttaaa ccatggttta agaatttggc 1775
 caaataacag aaattttgtt cgggaaggga taaactagat atagcataca gagcctgttt 1835
 ttgagtttta gatactttat ttgtaaataa cttaaaatag ctttctgaaa ccgtgcattc 1895
 tgtagtttct tcctttcagt gaaattgcta aatgtcaatg tatttttggc actgcgattt 1955
 taaccattta ttaaataaaa atttgttaa ag 1987

<210> 176

<211> 275

<212> PRT

<213> Homo sapiens

<400> 176

Met Glu Ala Lys Thr Arg Glu Leu Ile Ala Arg Arg Thr Thr Pro Leu

1 5 10 15

Leu Glu Tyr Ile Lys Asn Arg Lys Leu Glu Lys Gln Arg Ile Arg Glu

20	25	30
Glu Lys Arg Glu Glu Arg Arg Arg Arg Glu Leu Glu Lys Lys Arg Leu		
35	40	45
Arg Glu Glu Glu Lys Arg Arg Arg Arg Glu Glu Glu Arg Cys Lys Lys		
50	55	60
Lys Glu Ala Asp Lys Gln Lys Lys Ile Ala Glu Lys Glu Val Arg Ile		
65	70	75
Lys Leu Leu Lys Lys Pro Glu Lys Gly Glu Glu Pro Thr Thr Glu Lys		
85	90	95
Pro Lys Glu Arg Gly Glu Glu Ile Asp Thr Gly Gly Gly Lys Gln Glu		
100	105	110
Ser Cys Ala Pro Gly Ala Val Val Lys Ala Arg Pro Met Glu Gly Ser		
115	120	125
Leu Glu Glu Pro Gln Glu Thr Ser His Ser Gly Ser Asp Lys Glu His		
130	135	140
Arg Asp Val Glu Arg Ser Gln Glu Gln Glu Ser Glu Ala Gln Arg Tyr		
145	150	155
His Val Asp Asp Gly Arg Arg His Arg Ala His His Glu Pro Glu Arg		
165	170	175
Leu Ser Arg Arg Ser Glu Asp Glu Gln Arg Trp Gly Lys Gly Pro Gly		
180	185	190
Gln Asp Arg Gly Lys Lys Gly Ser Gln Asp Ser Gly Ala Pro Gly Glu		
195	200	205
Ala Met Glu Arg Leu Gly Arg Ala Gln Arg Cys Asp Asp Ser Pro Ala		
210	215	220
Pro Arg Lys Glu Arg Leu Ala Asn Lys Asp Arg Pro Ala Leu Gln Leu		
225	230	235
240		

Tyr Asp Pro Gly Ala Arg Phe Arg Ala Arg Glu Cys Gly Gly Asn Arg

245

250

255

Arg Ile Cys Lys Ala Glu Gly Ser Gly Thr Gly Pro Glu Lys Arg Glu

260

265

270

Glu Ala Glu

275

<210> 177

<211> 1663

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (57).. (1484)

<223>

<400> 177

agctctcgcg aggttttcgtc gggggctggc ggctgcggct cggcggagag tgcggc atg 59

Met

1

cgc tcg gaa aag gag ggg gcc gga ggc ctt cgg gcg gcc gtt gcc gcg 107

Arg Ser Glu Lys Glu Gly Ala Gly Gly Leu Arg Ala Ala Val Ala Ala

5

10

15

cgg ggc ccg agc ggg agg gag aag ctg tcg gcc cta gaa gtg cag ttc 155

Arg Gly Pro Ser Gly Arg Glu Lys Leu Ser Ala Leu Glu Val Gln Phe

20

25

30

cac cgc gac tcg cag cag cag gag gct gag acg ccg cca act tcg tcc 203

His Arg Asp Ser Gln Gln Gln Glu Ala Glu Thr Pro Pro Thr Ser Ser

588/617

35	40	45	
tcc ggt tgc ggg ggc ggt gcg ggc aaa cct cgc gag gag aag agg acg	251		
Ser Gly Cys Gly Gly Gly Ala Gly Lys Pro Arg Glu Glu Lys Arg Thr			
50	55	60	65
gcc ctg agc aag gtg gtc atc cgc cgc ctg cct ccg ggc ctc acc aag	299		
Ala Leu Ser Lys Val Val Ile Arg Arg Leu Pro Pro Gly Leu Thr Lys			
70	75	80	
gag cag ctg gag gag cag ctg cgc ccg ctg cca gca cac gac tac ttc	347		
Glu Gln Leu Glu Glu Gln Leu Arg Pro Leu Pro Ala His Asp Tyr Phe			
85	90	95	
gag ttc ttc gcc gcc gac ctg agt ctt tat cct cat ctc tac tca aga	395		
Glu Phe Phe Ala Ala Asp Leu Ser Leu Tyr Pro His Leu Tyr Ser Arg			
100	105	110	
gca tac att aat ttt agg aat cct gat gac atc ctt ctt ttt aga gat	443		
Ala Tyr Ile Asn Phe Arg Asn Pro Asp Asp Ile Leu Leu Phe Arg Asp			
115	120	125	
cgt ttt gat gga tat atc ttc ctt gac agc aaa ggc cta gaa tat cct	491		
Arg Phe Asp Gly Tyr Ile Phe Leu Asp Ser Lys Gly Leu Glu Tyr Pro			
130	135	140	145
gca gtg gta gag ttt gct cca ttc cag aag ata gcc aaa aag aag ctg	539		
Ala Val Val Glu Phe Ala Pro Phe Gln Lys Ile Ala Lys Lys Lys Leu			
150	155	160	
aga aaa aaa gat gcc aag act gga agc atc gaa gat gat cca gaa tat	587		
Arg Lys Lys Asp Ala Lys Thr Gly Ser Ile Glu Asp Asp Pro Glu Tyr			
165	170	175	
aag aag ttt tta gaa acc tac tgt gtg gag gaa gag aag acc agt gcc	635		
Lys Lys Phe Leu Glu Thr Tyr Cys Val Glu Glu Glu Lys Thr Ser Ala			

180	185	190	
aac cct gag act ctg ctg ggg gag atg gag gcg aag aca aga gag ctc			683
Asn Pro Glu Thr Leu Leu Gly Glu Met Glu Ala Lys Thr Arg Glu Leu			
195	200	205	
att gct aga aga acc aca cct ctt ttg gaa tat att aaa aat aga aaa			731
Ile Ala Arg Arg Thr Thr Pro Leu Leu Glu Tyr Ile Lys Asn Arg Lys			
210	215	220	225
tta gaa aag cag aga att cga gaa gag aag cga gaa gaa cgg agg agg			779
Leu Glu Lys Gln Arg Ile Arg Glu Glu Lys Arg Glu Glu Arg Arg Arg			
230	235	240	
aga gag tta gaa aag aaa cgt ttg cgg gaa gag gaa aaa aga aga aga			827
Arg Glu Leu Glu Lys Lys Arg Leu Arg Glu Glu Glu Lys Arg Arg Arg			
245	250	255	
aga gaa gaa gaa aga tgc aaa aaa gag aca gat aaa cag aag aaa			875
Arg Glu Glu Glu Arg Cys Lys Lys Lys Glu Thr Asp Lys Gln Lys Lys			
260	265	270	
att gca gag aaa gaa gta agg att aag ctt ctt aag aaa cca gaa aag			923
Ile Ala Glu Lys Glu Val Arg Ile Lys Leu Leu Lys Lys Pro Glu Lys			
275	280	285	
gga gag gaa cca acc aca gag aaa cca aaa gaa aga gga gag gag att			971
Gly Glu Glu Pro Thr Thr Glu Lys Pro Lys Glu Arg Gly Glu Glu Ile			
290	295	300	305
gat act gga ggt ggc aag cag gaa tcc tgt gcc ccc ggt gca gtc gta			1019
Asp Thr Gly Gly Gly Lys Gln Glu Ser Cys Ala Pro Gly Ala Val Val			
310	315	320	
aaa gcc agg ccc atg gaa ggc tcg ctg gag gag ccc cag gag acg tca			1067
Lys Ala Arg Pro Met Glu Gly Ser Leu Glu Glu Pro Gln Glu Thr Ser			

325	330	335	
cac agc ggc agt gat aaa gag cac agg gat gtg gag aga tct caa gaa			1115
His Ser Gly Ser Asp Lys Glu His Arg Asp Val Glu Arg Ser Gln Glu			
340	345	350	
caa gaa tct gaa gca caa aga tac cat gtg gat gac ggc agg agg cac			1163
Gln Glu Ser Glu Ala Gln Arg Tyr His Val Asp Asp Gly Arg Arg His			
355	360	365	
aga gct cac cac gag cct gaa cgg ctt tcc aga agg agt gag gat gag			1211
Arg Ala His His Glu Pro Glu Arg Leu Ser Arg Arg Ser Glu Asp Glu			
370	375	380	385
cag aga tgg ggg aaa gga cct ggc caa gac aga ggg aag aag ggg agc			1259
Gln Arg Trp Gly Lys Gly Pro Gly Gln Asp Arg Gly Lys Lys Gly Ser			
390	395	400	
cag gac agc ggg gct ccg ggg gag gcc atg gag aga ctg gga aga gcg			1307
Gln Asp Ser Gly Ala Pro Gly Glu Ala Met Glu Arg Leu Gly Arg Ala			
405	410	415	
cag agg tgt gac gac agt cca gca ccc aga aaa gag cga ctg gca aac			1355
Gln Arg Cys Asp Asp Ser Pro Ala Pro Arg Lys Glu Arg Leu Ala Asn			
420	425	430	
aag gac cgg cca gcc ttg cag ctg tat gat cca gga gct cgc ttc cga			1403
Lys Asp Arg Pro Ala Leu Gln Leu Tyr Asp Pro Gly Ala Arg Phe Arg			
435	440	445	
gcg cga gag tgt ggc gga aac agg agg atc tgc aag gca gaa ggt tcg			1451
Ala Arg Glu Cys Gly Gly Asn Arg Arg Ile Cys Lys Ala Glu Gly Ser			
450	455	460	465
ggg act ggt cct gag aag agg gaa gag gca gag tgagtcactg cacgcacctg			1504
Gly Thr Gly Pro Glu Lys Arg Glu Glu Ala Glu			

470

475

gcctccatgg acgagcaagg gcatcccaga aacgtgtaaa tgaccccgag tgtgactggg 1564
 aaggagaact tattccttac caggaaactg gaagctaaaa atacagaggg tgacgtagaa 1624
 acacgcagaa accattctaa agaaagtagt gatcttgta 1663

<210> 178

<211> 476

<212> PRT

<213> Homo sapiens

<400> 178

Met Arg Ser Glu Lys Glu Gly Ala Gly Gly Leu Arg Ala Ala Val Ala

1 5 10 15

Ala Arg Gly Pro Ser Gly Arg Glu Lys Leu Ser Ala Leu Glu Val Gln

20 25 30

Phe His Arg Asp Ser Gln Gln Gln Glu Ala Glu Thr Pro Pro Thr Ser

35 40 45

Ser Ser Gly Cys Gly Gly Gly Ala Gly Lys Pro Arg Glu Glu Lys Arg

50 55 60

Thr Ala Leu Ser Lys Val Val Ile Arg Arg Leu Pro Pro Gly Leu Thr

65 70 75 80

Lys Glu Gln Leu Glu Glu Gln Leu Arg Pro Leu Pro Ala His Asp Tyr

85 90 95

Phe Glu Phe Phe Ala Ala Asp Leu Ser Leu Tyr Pro His Leu Tyr Ser

100 105 110

Arg Ala Tyr Ile Asn Phe Arg Asn Pro Asp Asp Ile Leu Leu Phe Arg

115 120 125

Asp Arg Phe Asp Gly Tyr Ile Phe Leu Asp Ser Lys Gly Leu Glu Tyr

592/617

130 135 140
Pro Ala Val Val Glu Phe Ala Pro Phe Gln Lys Ile Ala Lys Lys Lys
145 150 155 160
Leu Arg Lys Lys Asp Ala Lys Thr Gly Ser Ile Glu Asp Asp Pro Glu
165 170 175
Tyr Lys Lys Phe Leu Glu Thr Tyr Cys Val Glu Glu Glu Lys Thr Ser
180 185 190
Ala Asn Pro Glu Thr Leu Leu Gly Glu Met Glu Ala Lys Thr Arg Glu
195 200 205
Leu Ile Ala Arg Arg Thr Thr Pro Leu Leu Glu Tyr Ile Lys Asn Arg
210 215 220
Lys Leu Glu Lys Gln Arg Ile Arg Glu Glu Lys Arg Glu Glu Arg Arg
225 230 235 240
Arg Arg Glu Leu Glu Lys Lys Arg Leu Arg Glu Glu Glu Lys Arg Arg
245 250 255
Arg Arg Glu Glu Glu Arg Cys Lys Lys Lys Glu Thr Asp Lys Gln Lys
260 265 270
Lys Ile Ala Glu Lys Glu Val Arg Ile Lys Leu Leu Lys Lys Pro Glu
275 280 285
Lys Gly Glu Glu Pro Thr Thr Glu Lys Pro Lys Glu Arg Gly Glu Glu
290 295 300
Ile Asp Thr Gly Gly Gly Lys Gln Glu Ser Cys Ala Pro Gly Ala Val
305 310 315 320
Val Lys Ala Arg Pro Met Glu Gly Ser Leu Glu Glu Pro Gln Glu Thr
325 330 335
Ser His Ser Gly Ser Asp Lys Glu His Arg Asp Val Glu Arg Ser Gln
340 345 350

Glu Gln Glu Ser Glu Ala Gln Arg Tyr His Val Asp Asp Gly Arg Arg
355 360 365
His Arg Ala His His Glu Pro Glu Arg Leu Ser Arg Arg Ser Glu Asp
370 375 380
Glu Gln Arg Trp Gly Lys Gly Pro Gly Gln Asp Arg Gly Lys Lys Gly
385 390 395 400
Ser Gln Asp Ser Gly Ala Pro Gly Glu Ala Met Glu Arg Leu Gly Arg
405 410 415
Ala Gln Arg Cys Asp Asp Ser Pro Ala Pro Arg Lys Glu Arg Leu Ala
420 425 430
Asn Lys Asp Arg Pro Ala Leu Gln Leu Tyr Asp Pro Gly Ala Arg Phe
435 440 445
Arg Ala Arg Glu Cys Gly Gly Asn Arg Arg Ile Cys Lys Ala Glu Gly
450 455 460
Ser Gly Thr Gly Pro Glu Lys Arg Glu Glu Ala Glu
465 470 475

<210> 179

<211> 2241

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (21).. (1349)

<223>

<400> 179

gagagagagg agagtgcggc atg cgc tcg gaa aag gag ggg gcc gga ggc ctt 53

Met Arg Ser Glu Lys Glu Gly Ala Gly Gly Leu

1	5	10	
cgg gcg gcc gtt gcc gcg cgg ggc ccg agc ggg agg gag aag ctg tcg			101
Arg Ala Ala Val Ala Ala Arg Gly Pro Ser Gly Arg Glu Lys Leu Ser			
15	20	25	
gcc cta gaa gtg cag ttc cac cgc gac tcg cag cag cag gag gct gag			149
Ala Leu Glu Val Gln Phe His Arg Asp Ser Gln Gln Gln Glu Ala Glu			
30	35	40	
acg ccg cca act tcg tcc tcc ggt tgc ggg ggc ggt gcg ggc aaa cct			197
Thr Pro Pro Thr Ser Ser Ser Gly Cys Gly Gly Gly Ala Gly Lys Pro			
45	50	55	
cgc gag gag aag agg acg gcc ctg agc aag gtg gtc atc cgc cgc ctg			245
Arg Glu Glu Lys Arg Thr Ala Leu Ser Lys Val Val Ile Arg Arg Leu			
60	65	70	75
cct ccg ggc ctc acc aag gag cag ctg gag gag cag ctg cgc ccg ctg			293
Pro Pro Gly Leu Thr Lys Glu Gln Leu Glu Glu Gln Leu Arg Pro Leu			
80	85	90	
cca gca cac gac tac ttc gag ttc ttc gcc gcc gac ctg agt ctt tat			341
Pro Ala His Asp Tyr Phe Glu Phe Phe Ala Ala Asp Leu Ser Leu Tyr			
95	100	105	
cct cat ctc tac tca aga gca tac att aat ttt agg aat cct gat gac			389
Pro His Leu Tyr Ser Arg Ala Tyr Ile Asn Phe Arg Asn Pro Asp Asp			
110	115	120	
atc ctt ctt ttt aga gat cgt ttt gat gga tat atc ttc ctt gac agc			437
Ile Leu Leu Phe Arg Asp Arg Phe Asp Gly Tyr Ile Phe Leu Asp Ser			
125	130	135	
aaa gat cca gaa tat aag aag ttt tta gaa acc tac tgt gtg gag gaa			485

Lys Asp Pro Glu Tyr Lys Lys Phe Leu Glu Thr Tyr Cys Val Glu Glu
 140 145 150 155
 gag aag acc agt gcc aac cct gag act ctg ctg ggg gag atg gag gcg 533
 Glu Lys Thr Ser Ala Asn Pro Glu Thr Leu Leu Gly Glu Met Glu Ala
 160 165 170
 aag aca aga gag ctc att gct aga aga acc aca cct ctt ttg gaa tat 581
 Lys Thr Arg Glu Leu Ile Ala Arg Arg Thr Thr Pro Leu Leu Glu Tyr
 175 180 185
 att aaa aat aga aaa tta gaa aag cag aga att cga gaa gag aag cga 629
 Ile Lys Asn Arg Lys Leu Glu Lys Gln Arg Ile Arg Glu Glu Lys Arg
 190 195 200
 gaa gaa cgg agg agg aga gag tta gaa aag aaa cgt ttg cgg gaa gag 677
 Glu Glu Arg Arg Arg Arg Glu Leu Glu Lys Lys Arg Leu Arg Glu Glu
 205 210 215
 gaa aaa aga aga aga aga gaa gaa gaa aga tgc aaa aaa gag aca 725
 Glu Lys Arg Arg Arg Arg Glu Glu Glu Arg Cys Lys Lys Lys Glu Thr
 220 225 230 235
 gat aaa cag aag aaa att gca gag aaa gaa gta agg att aag ctt ctt 773
 Asp Lys Gln Lys Lys Ile Ala Glu Lys Glu Val Arg Ile Lys Leu Leu
 240 245 250
 aag aaa cca gaa aag gga gag gaa cca acc aca gag aaa cca aaa gaa 821
 Lys Lys Pro Glu Lys Gly Glu Glu Pro Thr Thr Glu Lys Pro Lys Glu
 255 260 265
 aga gga gag gag att gat act gga ggt ggc aag cag gaa tcc tgt gcc 869
 Arg Gly Glu Glu Ile Asp Thr Gly Gly Gly Lys Gln Glu Ser Cys Ala
 270 275 280
 ccc ggt gca gtc gta aaa gcc agg ccc atg gaa ggc tcg ctg gag gag 917

Pro Gly Ala Val Val Lys Ala Arg Pro Met Glu Gly Ser Leu Glu Glu
 285 290 295
 ccc cag gag acg tca cac agc ggc agt gat aaa gag cac agg gat gtg 965
 Pro Gln Glu Thr Ser His Ser Gly Ser Asp Lys Glu His Arg Asp Val
 300 305 310 315
 gag aga tct caa gaa caa gaa tct gaa gca caa aga tac cat gtg gat 1013
 Glu Arg Ser Gln Glu Gln Glu Ser Glu Ala Gln Arg Tyr His Val Asp
 320 325 330
 gac ggc agg agg cac aga gct cac cac gag cct gaa cgg ctt tcc aga 1061
 Asp Gly Arg Arg His Arg Ala His His Glu Pro Glu Arg Leu Ser Arg
 335 340 345
 agg agt gag gat gag cag aga tgg ggg aaa gga cct ggc caa gac aga 1109
 Arg Ser Glu Asp Glu Gln Arg Trp Gly Lys Gly Pro Gly Gln Asp Arg
 350 355 360
 ggg aag aag ggg agc cag gac agc ggg gct ccg ggg gag gcc atg gag 1157
 Gly Lys Lys Gly Ser Gln Asp Ser Gly Ala Pro Gly Glu Ala Met Glu
 365 370 375
 aga ctg gga aga gcg cag agg tgt gac gac agt cca gca ccc aga aaa 1205
 Arg Leu Gly Arg Ala Gln Arg Cys Asp Asp Ser Pro Ala Pro Arg Lys
 380 385 390 395
 gag cga ctg gca aac aag gac cgg cca gcc ttg cag ctg tat gat cca 1253
 Glu Arg Leu Ala Asn Lys Asp Arg Pro Ala Leu Gln Leu Tyr Asp Pro
 400 405 410
 gga gct cgc ttc cga gcg cga gag tgt ggc gga aac agg agg atc tgc 1301
 Gly Ala Arg Phe Arg Ala Arg Glu Cys Gly Gly Asn Arg Arg Ile Cys
 415 420 425
 aag gca gaa ggt tcg ggg act ggt cct gag aag agg gaa gag gca gag 1349

Lys Ala Glu Gly Ser Gly Thr Gly Pro Glu Lys Arg Glu Glu Ala Glu

430

435

440

tgagtcactg cacgcacctg gcctccatgg acgagcaagg gcatcccaga aacgtgtaaa 1409
 tgaccccgag tgtgactggg aaggagaact tattccttac caggaaactg gaagctaaaa 1469
 atacagaggg tgacgtàgaa acacgcagaa accattctaa agaaagtagt gatcttgat 1529
 taaattgagc agaattctca cagattttac cattcctggt ataaactagt atttgttggt 1589
 tagccaaaac agaaaatgat ttccactgga cagtagaaaa atatgtgtaa aataggaag 1649
 aaagttagta ttggatcagt gtgagtcctg aagcactttc agtgcgtgta gaacgacatc 1709
 cactttgggt ttcattcggt tgtaagcaga ggagctgtca gtcactcgtg cttctcggtg 1769
 gcctctgagc catggtgtcg agtgaagagt agttcttggt tgttacaacc tttgtgagtc 1829
 agccatgccc gcaaagcgtg ctgtgtttta gtctggttag gaatatattat cagagttcac 1889
 actatataaa acccaacagc ttcaactatt gccctttcaa cagttttgcc actgaccgga 1949
 tagaaacggt ttcagtctct ggatggatgt gtttgtggtt tgtaaccatt acggtttaa 2009
 ccatggttta agaatttgcc caaataacag aaattttggt cggaaggga taaactagat 2069
 atagcataca gagcctgttt ttgagtttta gatactttat ttgtaaataa cttaaaatag 2129
 cttttgaaa ccgtgcattc tgtagtttct tcctttcagt gaaattgcta aatgtcaatg 2189
 tatttttggc cctgcgattt taaccattta ttaaataaaa attttgtaa ag 2241

<210> 180

<211> 443

<212> PRT

<213> Homo sapiens

<400> 180

Met Arg Ser Glu Lys Glu Gly Ala Gly Gly Leu Arg Ala Ala Val Ala

1

5

10

15

Ala Arg Gly Pro Ser Gly Arg Glu Lys Leu Ser Ala Leu Glu Val Gln

20

25

30

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Phe His Arg Asp Ser Gln Gln Gln Glu Ala Glu Thr Pro Pro Thr Ser
 35 40 45
 Ser Ser Gly Cys Gly Gly Gly Ala Gly Lys Pro Arg Glu Glu Lys Arg
 50 55 60
 Thr Ala Leu Ser Lys Val Val Ile Arg Arg Leu Pro Pro Gly Leu Thr
 65 70 75 80
 Lys Glu Gln Leu Glu Glu Gln Leu Arg Pro Leu Pro Ala His Asp Tyr
 85 90 95
 Phe Glu Phe Phe Ala Ala Asp Leu Ser Leu Tyr Pro His Leu Tyr Ser
 100 105 110
 Arg Ala Tyr Ile Asn Phe Arg Asn Pro Asp Asp Ile Leu Leu Phe Arg
 115 120 125
 Asp Arg Phe Asp Gly Tyr Ile Phe Leu Asp Ser Lys Asp Pro Glu Tyr
 130 135 140
 Lys Lys Phe Leu Glu Thr Tyr Cys Val Glu Glu Glu Lys Thr Ser Ala
 145 150 155 160
 Asn Pro Glu Thr Leu Leu Gly Glu Met Glu Ala Lys Thr Arg Glu Leu
 165 170 175
 Ile Ala Arg Arg Thr Thr Pro Leu Leu Glu Tyr Ile Lys Asn Arg Lys
 180 185 190
 Leu Glu Lys Gln Arg Ile Arg Glu Glu Lys Arg Glu Glu Arg Arg Arg
 195 200 205
 Arg Glu Leu Glu Lys Lys Arg Leu Arg Glu Glu Glu Lys Arg Arg Arg
 210 215 220
 Arg Glu Glu Glu Arg Cys Lys Lys Lys Glu Thr Asp Lys Gln Lys Lys
 225 230 235 240
 Ile Ala Glu Lys Glu Val Arg Ile Lys Leu Leu Lys Lys Pro Glu Lys

245 250 255
Gly Glu Glu Pro Thr Thr Glu Lys Pro Lys Glu Arg Gly Glu Glu Ile
260 265 270
Asp Thr Gly Gly Gly Lys Gln Glu Ser Cys Ala Pro Gly Ala Val Val
275 280 285
Lys Ala Arg Pro Met Glu Gly Ser Leu Glu Glu Pro Gln Glu Thr Ser
290 295 300
His Ser Gly Ser Asp Lys Glu His Arg Asp Val Glu Arg Ser Gln Glu
305 310 315 320
Gln Glu Ser Glu Ala Gln Arg Tyr His Val Asp Asp Gly Arg Arg His
325 330 335
Arg Ala His His Glu Pro Glu Arg Leu Ser Arg Arg Ser Glu Asp Glu
340 345 350
Gln Arg Trp Gly Lys Gly Pro Gly Gln Asp Arg Gly Lys Lys Gly Ser
355 360 365
Gln Asp Ser Gly Ala Pro Gly Glu Ala Met Glu Arg Leu Gly Arg Ala
370 375 380
Gln Arg Cys Asp Asp Ser Pro Ala Pro Arg Lys Glu Arg Leu Ala Asn
385 390 395 400
Lys Asp Arg Pro Ala Leu Gln Leu Tyr Asp Pro Gly Ala Arg Phe Arg
405 410 415
Ala Arg Glu Cys Gly Gly Asn Arg Arg Ile Cys Lys Ala Glu Gly Ser
420 425 430
Gly Thr Gly Pro Glu Lys Arg Glu Glu Ala Glu
435 440

<210> 181

600/617

<211> 1764

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (155).. (1762)

<223>

<400> 181

aaaaacgggc agcttgggac gcaccccgga gaccgctgag ttcctgggtg aggacctgct 60

gcaggtagaa cagcggctgg agccggccaa gcgggcagcc cacaacatcc acaagcggct 120

gcaggcctgt ctgcagggcc agagcggggc agac atg gac aag cgg gtg aag aag 175

Met Asp Lys Arg Val Lys Lys

1

5

ctt ccc ctc atg gct ctg tcc acc acg atg gct gag agc ttc aag gag 223

Leu Pro Leu Met Ala Leu Ser Thr Thr Met Ala Glu Ser Phe Lys Glu

10

15

20

ctg gac cct gat tcc agc atg ggg aag gcc ttg gag atg agc tgt gcc 271

Leu Asp Pro Asp Ser Ser Met Gly Lys Ala Leu Glu Met Ser Cys Ala

25

30

35

atc cag aat cag ctg gcc cgc atc ctg gcc gag ttt gag atg acc ctg 319

Ile Gln Asn Gln Leu Ala Arg Ile Leu Ala Glu Phe Glu Met Thr Leu

40

45

50

55

gag agg gac gtc ctg cag cca ctc agc agg ctg agt gag gag gag ctg 367

Glu Arg Asp Val Leu Gln Pro Leu Ser Arg Leu Ser Glu Glu Glu Leu

60

65

70

cca gcc atc ctc aaa cac aag aaa agc ctc cag aag ctc gtg tcc gac 415

Pro Ala Ile Leu Lys His Lys Lys Ser Leu Gln Lys Leu Val Ser Asp

601/617

75	80	85	
tgg aac aca ctc aag agc agg ctc agt cag gca acc aag aat tca ggc			463
Trp Asn Thr Leu Lys Ser Arg Leu Ser Gln Ala Thr Lys Asn Ser Gly			
90	95	100	
agc agt caa ggc cta gga ggc agc ccg ggt agt cac agc cat acg acc			511
Ser Ser Gln Gly Leu Gly Gly Ser Pro Gly Ser His Ser His Thr Thr			
105	110	115	
atg gcc aac aag gtg gag acg ctg aag gag gag gag gag ctg aag			559
Met Ala Asn Lys Val Glu Thr Leu Lys Glu Glu Glu Glu Glu Leu Lys			
120	125	130	135
agg aaa gtg gag caa tgc agg gac gag tac ttg gct gac ctg tac cac			607
Arg Lys Val Glu Gln Cys Arg Asp Glu Tyr Leu Ala Asp Leu Tyr His			
140	145	150	
ttt gtt acc aag gag gac tcc tat gcc aac tac ttc att cgt ctc ctg			655
Phe Val Thr Lys Glu Asp Ser Tyr Ala Asn Tyr Phe Ile Arg Leu Leu			
155	160	165	
gag att cag gcc gat tac cat cgc agg tca ctg agc tcg ctg gac aca			703
Glu Ile Gln Ala Asp Tyr His Arg Arg Ser Leu Ser Ser Leu Asp Thr			
170	175	180	
gcc ctg gct gag ctg agg gag aac cac ggc caa gca gac cac tcc cct			751
Ala Leu Ala Glu Leu Arg Glu Asn His Gly Gln Ala Asp His Ser Pro			
185	190	195	
tcg atg aca gcc acc cac ttc ccc agg gtg tat ggg gtg tcg ctg gca			799
Ser Met Thr Ala Thr His Phe Pro Arg Val Tyr Gly Val Ser Leu Ala			
200	205	210	215
acc cac ctg caa gag ctg ggc cgg gag att gcc ctg ccc atc gag gcc			847
Thr His Leu Gln Glu Leu Gly Arg Glu Ile Ala Leu Pro Ile Glu Ala			

220	225	230	
tgc gtc atg atg ctg ctt tct gag ggc atg aag gaa gag ggt ctc ttc			895
Cys Val Met Met Leu Leu Ser Glu Gly Met Lys Glu Glu Gly Leu Phe			
235	240	245	
cgt ctg gct gct ggg gcc tcg gtg ctg aag cgt ctc aag cag aca atg			943
Arg Leu Ala Ala Gly Ala Ser Val Leu Lys Arg Leu Lys Gln Thr Met			
250	255	260	
gcc tcg gac ccc cac agc ctg gag gag ttc tgc tcc gac ccg cac gct			991
Ala Ser Asp Pro His Ser Leu Glu Glu Phe Cys Ser Asp Pro His Ala			
265	270	275	
gtg gca ggt gcc ctc aag tcc tat ctg cgg gag ctg cca gag cct ctg			1039
Val Ala Gly Ala Leu Lys Ser Tyr Leu Arg Glu Leu Pro Glu Pro Leu			
280	285	290	295
atg acc ttc gac ctc tat gat gac tgg atg agg gca gcc agc ctg aag			1087
Met Thr Phe Asp Leu Tyr Asp Asp Trp Met Arg Ala Ala Ser Leu Lys			
300	305	310	
gag cca ggg gcc cgg ctg cag gcc ctc caa gag gtg tgc agc cgc cta			1135
Glu Pro Gly Ala Arg Leu Gln Ala Leu Gln Glu Val Cys Ser Arg Leu			
315	320	325	
ccc ccc gag aac ctc agc aac ctc agg tac ctg atg aag ttc ctg gca			1183
Pro Pro Glu Asn Leu Ser Asn Leu Arg Tyr Leu Met Lys Phe Leu Ala			
330	335	340	
cgg ctg gcc gag gag cag gag gtg aac aag atg aca ccc agc aac atc			1231
Arg Leu Ala Glu Glu Gln Glu Val Asn Lys Met Thr Pro Ser Asn Ile			
345	350	355	
gcc ata gtc ctg gga ccc aac ttg ctg tgg cca cct gag aaa gaa ggg			1279
Ala Ile Val Leu Gly Pro Asn Leu Leu Trp Pro Pro Glu Lys Glu Gly			

360	365	370	375	
gac cag gcc cag ctg gat gca gcc tcc gtg tct tcc atc cag gtg gtg				1327
Asp Gln Ala Gln Leu Asp Ala Ala Ser Val Ser Ser Ile Gln Val Val				
380	385	390		
ggc gtc gtc gag gcg ctg atc cag agc gca gac acc ctc ttc cct gga				1375
Gly Val Val Glu Ala Leu Ile Gln Ser Ala Asp Thr Leu Phe Pro Gly				
395	400	405		
gac atc aac ttc aac gtg tca ggc ctc ttc tca gct gtt acc ctc cag				1423
Asp Ile Asn Phe Asn Val Ser Gly Leu Phe Ser Ala Val Thr Leu Gln				
410	415	420		
gac aca gtc agt gac agg ctg gcc tct gag gaa ctt ccg tcc act gcc				1471
Asp Thr Val Ser Asp Arg Leu Ala Ser Glu Glu Leu Pro Ser Thr Ala				
425	430	435		
gtg ccc acc cca gcc acc acc ccg gct ccg gct ccg gct cca gct cca				1519
Val Pro Thr Pro Ala Thr Thr Pro Ala Pro Ala Pro Ala Pro				
440	445	450	455	
gct ccg gcc cca gcc ttg gct tca gca gct acc aag gaa agg aca gag				1567
Ala Pro Ala Pro Ala Leu Ala Ser Ala Ala Thr Lys Glu Arg Thr Glu				
460	465	470		
tct gag gtg cct ccc aga cca gcc tcc ccc aag gtc acc agg agt ccc				1615
Ser Glu Val Pro Pro Arg Pro Ala Ser Pro Lys Val Thr Arg Ser Pro				
475	480	485		
ccg gag aca gct gcc cca gtg gag gac atg gct cgg agg agt cct agg				1663
Pro Glu Thr Ala Ala Pro Val Glu Asp Met Ala Arg Arg Ser Pro Arg				
490	495	500		
gga gcc acc gga agg aag gag agg ttt gcc tgc tcc tac ggg act gat				1711
Gly Ala Thr Gly Arg Lys Glu Arg Phe Ala Cys Ser Tyr Gly Thr Asp				

505	510	515	
tct tct ctt gtc gac atg ttt ttt gta agg ctg gta aat aaa tta ttt	1759		
Ser Ser Leu Val Asp Met Phe Phe Val Arg Leu Val Asn Lys Leu Phe			
520	525	530	535
tgg ac			1764
Trp			

<210> 182

<211> 536

<212> PRT

<213> Homo sapiens

<400> 182

Met Asp Lys Arg Val Lys Lys Leu Pro Leu Met Ala Leu Ser Thr Thr

1 5 10 15

Met Ala Glu Ser Phe Lys Glu Leu Asp Pro Asp Ser Ser Met Gly Lys

20 25 30

Ala Leu Glu Met Ser Cys Ala Ile Gln Asn Gln Leu Ala Arg Ile Leu

35 40 45

Ala Glu Phe Glu Met Thr Leu Glu Arg Asp Val Leu Gln Pro Leu Ser

50 55 60

Arg Leu Ser Glu Glu Glu Leu Pro Ala Ile Leu Lys His Lys Lys Ser

65 70 75 80

Leu Gln Lys Leu Val Ser Asp Trp Asn Thr Leu Lys Ser Arg Leu Ser

85 90 95

Gln Ala Thr Lys Asn Ser Gly Ser Ser Gln Gly Leu Gly Gly Ser Pro

100 105 110

Gly Ser His Ser His Thr Thr Met Ala Asn Lys Val Glu Thr Leu Lys

605/617

115 120 125
Glu Glu Glu Glu Glu Leu Lys Arg Lys Val Glu Gln Cys Arg Asp Glu
130 135 140
Tyr Leu Ala Asp Leu Tyr His Phe Val Thr Lys Glu Asp Ser Tyr Ala
145 150 155 160
Asn Tyr Phe Ile Arg Leu Leu Glu Ile Gln Ala Asp Tyr His Arg Arg
165 170 175
Ser Leu Ser Ser Leu Asp Thr Ala Leu Ala Glu Leu Arg Glu Asn His
180 185 190
Gly Gln Ala Asp His Ser Pro Ser Met Thr Ala Thr His Phe Pro Arg
195 200 205
Val Tyr Gly Val Ser Leu Ala Thr His Leu Gln Glu Leu Gly Arg Glu
210 215 220
Ile Ala Leu Pro Ile Glu Ala Cys Val Met Met Leu Leu Ser Glu Gly
225 230 235 240
Met Lys Glu Glu Gly Leu Phe Arg Leu Ala Ala Gly Ala Ser Val Leu
245 250 255
Lys Arg Leu Lys Gln Thr Met Ala Ser Asp Pro His Ser Leu Glu Glu
260 265 270
Phe Cys Ser Asp Pro His Ala Val Ala Gly Ala Leu Lys Ser Tyr Leu
275 280 285
Arg Glu Leu Pro Glu Pro Leu Met Thr Phe Asp Leu Tyr Asp Asp Trp
290 295 300
Met Arg Ala Ala Ser Leu Lys Glu Pro Gly Ala Arg Leu Gln Ala Leu
305 310 315 320
Gln Glu Val Cys Ser Arg Leu Pro Pro Glu Asn Leu Ser Asn Leu Arg
325 330 335

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Tyr Leu Met Lys Phe Leu Ala Arg Leu Ala Glu Glu Gln Glu Val Asn
340 345 350
Lys Met Thr Pro Ser Asn Ile Ala Ile Val Leu Gly Pro Asn Leu Leu
355 360 365
Trp Pro Pro Glu Lys Glu Gly Asp Gln Ala Gln Leu Asp Ala Ala Ser
370 375 380
Val Ser Ser Ile Gln Val Val Gly Val Val Glu Ala Leu Ile Gln Ser
385 390 395 400
Ala Asp Thr Leu Phe Pro Gly Asp Ile Asn Phe Asn Val Ser Gly Leu
405 410 415
Phe Ser Ala Val Thr Leu Gln Asp Thr Val Ser Asp Arg Leu Ala Ser
420 425 430
Glu Glu Leu Pro Ser Thr Ala Val Pro Thr Pro Ala Thr Thr Pro Ala
435 440 445
Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Leu Ala Ser Ala
450 455 460
Ala Thr Lys Glu Arg Thr Glu Ser Glu Val Pro Pro Arg Pro Ala Ser
465 470 475 480
Pro Lys Val Thr Arg Ser Pro Pro Glu Thr Ala Ala Pro Val Glu Asp
485 490 495
Met Ala Arg Arg Ser Pro Arg Gly Ala Thr Gly Arg Lys Glu Arg Phe
500 505 510
Ala Cys Ser Tyr Gly Thr Asp Ser Ser Leu Val Asp Met Phe Phe Val
515 520 525
Arg Leu Val Asn Lys Leu Phe Trp
530 535

<210> 183

<211> 2434

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (97).. (2007)

<223>

<400> 183

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ctgcaggcct gtctgcaggg ccagagcggg gcagac atg gac aag cgg gtg aag 114

Met Asp Lys Arg Val Lys

1

5

aag ctt ccc ctc atg gct ctg tcc acc acg atg gct gag agc ttc aag 162

Lys Leu Pro Leu Met Ala Leu Ser Thr Thr Met Ala Glu Ser Phe Lys

10

15

20

gag ctg gac cct gat tcc agc atg ggg aag gcc ttg gag atg agc tgt 210

Glu Leu Asp Pro Asp Ser Ser Met Gly Lys Ala Leu Glu Met Ser Cys

25

30

35

gcc atc cag aat cag ctg gcc cgc atc ctg gcc gag ttt gag atg acc 258

Ala Ile Gln Asn Gln Leu Ala Arg Ile Leu Ala Glu Phe Glu Met Thr

40

45

50

ctg gag agg gac gtc ctg cag cca ctc agc agg ctg agt gag gag gag 306

Leu Glu Arg Asp Val Leu Gln Pro Leu Ser Arg Leu Ser Glu Glu Glu

55

60

65

70

ctg cca gcc atc ctc aaa cac aag aaa agc ctc cag aag ctc gtg tcc 354

Leu Pro Ala Ile Leu Lys His Lys Lys Ser Leu Gln Lys Leu Val Ser

75	80	85	
gac tgg aac aca ctc aag agc agg ctc agt cag gca acc aag aat tca			402
Asp Trp Asn Thr Leu Lys Ser Arg Leu Ser Gln Ala Thr Lys Asn Ser			
90	95	100	
ggc agc agt caa ggc cta gga ggc agc ccg ggt agt cac agc cat acg			450
Gly Ser Ser Gln Gly Leu Gly Gly Ser Pro Gly Ser His Ser His Thr			
105	110	115	
acc atg gcc aac aag gtg gag acg ctg aag gag gag gag gag gag ctg			498
Thr Met Ala Asn Lys Val Glu Thr Leu Lys Glu Glu Glu Glu Glu Leu			
120	125	130	
aag agg aaa gtg gag caa tgc agg gac gag tac ttg gct gac ctg tac			546
Lys Arg Lys Val Glu Gln Cys Arg Asp Glu Tyr Leu Ala Asp Leu Tyr			
135	140	145	150
cac ttt gtt acc aag gag gac tcc tat gcc aac tac ttc att cgt ctc			594
His Phe Val Thr Lys Glu Asp Ser Tyr Ala Asn Tyr Phe Ile Arg Leu			
155	160	165	
ctg gag att cag gcc gat tac cat cgc agg tca ctg agc tcg ctg gac			642
Leu Glu Ile Gln Ala Asp Tyr His Arg Arg Ser Leu Ser Ser Leu Asp			
170	175	180	
aca gcc ctg gct gag ctg agg gag aac cac ggc caa gca gac cac tcc			690
Thr Ala Leu Ala Glu Leu Arg Glu Asn His Gly Gln Ala Asp His Ser			
185	190	195	
cct tcg atg aca gcc acc cac ttc ccc agg gtg tat ggg gtg tcg ctg			738
Pro Ser Met Thr Ala Thr His Phe Pro Arg Val Tyr Gly Val Ser Leu			
200	205	210	
gca acc cac ctg caa gag ctg ggc cgg gag att gcc ctg ccc atc gag			786
Ala Thr His Leu Gln Glu Leu Gly Arg Glu Ile Ala Leu Pro Ile Glu			

215	220	225	230	
gcc tgc gtc atg atg ctg ctt tct gag ggc atg aag gaa gag ggt ctc				834
Ala Cys Val Met Met Leu Leu Ser Glu Gly Met Lys Glu Glu Gly Leu				
235	240	245		
ttc cgt ctg gct gct ggg gcc tcg gtg ctg aag cgt ctc aag cag aca				882
Phe Arg Leu Ala Ala Gly Ala Ser Val Leu Lys Arg Leu Lys Gln Thr				
250	255	260		
atg gcc tcg gac ccc cac agc ctg gag gag ttc tgc tcc gac ccg cac				930
Met Ala Ser Asp Pro His Ser Leu Glu Glu Phe Cys Ser Asp Pro His				
265	270	275		
gct gtg gca ggt gcc ctc aag tcc tat ctg cgg gag ctg cca gag cct				978
Ala Val Ala Gly Ala Leu Lys Ser Tyr Leu Arg Glu Leu Pro Glu Pro				
280	285	290		
ctg atg acc ttc gac ctc tat gat gac tgg atg agg gca gcc agc ctg				1026
Leu Met Thr Phe Asp Leu Tyr Asp Asp Trp Met Arg Ala Ala Ser Leu				
295	300	305	310	
aag gag cca ggg gcc cgg ctg cag gcc ctc caa gag gtg tgc agc cgc				1074
Lys Glu Pro Gly Ala Arg Leu Gln Ala Leu Gln Glu Val Cys Ser Arg				
315	320	325		
cta ccc ccc gag aac ctc agc aac ctc agg tac ctg atg aag ttc ctg				1122
Leu Pro Pro Glu Asn Leu Ser Asn Leu Arg Tyr Leu Met Lys Phe Leu				
330	335	340		
gca cgg ctg gcc gag gag cag gag gtg aac aag atg aca ccc agc aac				1170
Ala Arg Leu Ala Glu Glu Gln Glu Val Asn Lys Met Thr Pro Ser Asn				
345	350	355		
atc gcc ata gtc ctg gga ccc aac ttg ctg tgg cca cct gag aaa gaa				1218
Ile Ala Ile Val Leu Gly Pro Asn Leu Leu Trp Pro Pro Glu Lys Glu				

360	365	370	
ggg gac cag gcc cag ctg gat gca gcc tcc gtg tct tcc atc cag gtg	1266		
Gly Asp Gln Ala Gln Leu Asp Ala Ala Ser Val Ser Ser Ile Gln Val			
375	380	385	390
gtg ggc gtc gtc gag gcg ctg atc cag agc gca gac acc ctc ttc cct	1314		
Val Gly Val Val Glu Ala Leu Ile Gln Ser Ala Asp Thr Leu Phe Pro			
395	400	405	
gga gac atc aac ttc aac gtg tca ggc ctc ttc tca gct gtt acc ctc	1362		
Gly Asp Ile Asn Phe Asn Val Ser Gly Leu Phe Ser Ala Val Thr Leu			
410	415	420	
cag gac aca gtc agt gac agg ctg gcc tct gag gaa ctt ccg tcc act	1410		
Gln Asp Thr Val Ser Asp Arg Leu Ala Ser Glu Glu Leu Pro Ser Thr			
425	430	435	
gcc gtg ccc acc cca gcc acc acc ccg gct ccg gct ccg gct cca gct	1458		
Ala Val Pro Thr Pro Ala Thr Thr Pro Ala Pro Ala Pro Ala Pro Ala			
440	445	450	
cca gct ccg gcc cca gcc ttg gct tca gca gct acc aag gaa agg aca	1506		
Pro Ala Pro Ala Pro Ala Leu Ala Ser Ala Ala Thr Lys Glu Arg Thr			
455	460	465	470
gag tct gag gtg cct ccc aga cca gcc tcc ccc aag gtc acc agg agt	1554		
Glu Ser Glu Val Pro Pro Arg Pro Ala Ser Pro Lys Val Thr Arg Ser			
475	480	485	
ccc ccg gag aca gct gcc cca gtg gag gac atg gct cgg agg acc aag	1602		
Pro Pro Glu Thr Ala Ala Pro Val Glu Asp Met Ala Arg Arg Thr Lys			
490	495	500	
cgc ccg gcg cca gcc cgg ccc acc atg ccg ccc ccc cag gtc tcc ggc	1650		
Arg Pro Ala Pro Ala Arg Pro Thr Met Pro Pro Pro Gln Val Ser Gly			

505	510	515	
tcc cgc tcc tcc cct cca gcc ccg ccc ttg ccc cct ggc tct ggc agc			1698
Ser Arg Ser Ser Pro Pro Ala Pro Pro Leu Pro Pro Gly Ser Gly Ser			
520	525	530	
cct ggg acc ccc caa gcc ctg ccc cga cgt ctg gtt ggc agc agc ctc			1746
Pro Gly Thr Pro Gln Ala Leu Pro Arg Arg Leu Val Gly Ser Ser Leu			
535	540	545	550
cga gcc ccc aca gtg cca ccc ccg tta ccc ccc aca ccc cct cag cct			1794
Arg Ala Pro Thr Val Pro Pro Pro Leu Pro Pro Thr Pro Pro Gln Pro			
555	560	565	
gcc cgg cgc caa agc cgg cgt tca cca gcc tcc ccc agc ccg gcc tcc			1842
Ala Arg Arg Gln Ser Arg Arg Ser Pro Ala Ser Pro Ser Pro Ala Ser			
570	575	580	
cca ggt cca gcc tcc ccc agc cca gtc tct ttg agt aac cct gca cag			1890
Pro Gly Pro Ala Ser Pro Ser Pro Val Ser Leu Ser Asn Pro Ala Gln			
585	590	595	
gtg gac ctg ggg gct gcc aca gca gag gga gga gcc cct gag gct atc			1938
Val Asp Leu Gly Ala Ala Thr Ala Glu Gly Gly Ala Pro Glu Ala Ile			
600	605	610	
agt ggg gtc ccc act ccc cca gct atc ccc cct cag ccc cgc ccc agg			1986
Ser Gly Val Pro Thr Pro Pro Ala Ile Pro Pro Gln Pro Arg Pro Arg			
615	620	625	630
agc ctt gcc tca gag acc aac tgagtggctg gtttctccct aagcagccct			2037
Ser Leu Ala Ser Glu Thr Asn			
635			
cagcaccccc tccctcccca cctggccctc ccaggacagc tctcgccccc cacaagggg			2097
catgggcctc cagcctttgc ccacaagtgc ctcaagtccc actgggtcgg ccccatggc			2157

caggagggt caggacaatc ctctatttcc tgaccttttc ctcgtccacc ctgggcttgg 2217
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 gagaggtttg cctgtccta cgggactgat tcttctcttg ccgacatgtt ttttgtaagg 2337
 ctggtaaata aattattttg gacaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2397
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa actcggg 2434

<210> 184

<211> 637

<212> PRT

<213> Homo sapiens

<400> 184

Met Asp Lys Arg Val Lys Lys Leu Pro Leu Met Ala Leu Ser Thr Thr

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Met Ala Glu Ser Phe Lys Glu Leu Asp Pro Asp Ser Ser Met Gly Lys

20 25 30

Ala Leu Glu Met Ser Cys Ala Ile Gln Asn Gln Leu Ala Arg Ile Leu

35 40 45

Ala Glu Phe Glu Met Thr Leu Glu Arg Asp Val Leu Gln Pro Leu Ser

50 55 60

Arg Leu Ser Glu Glu Glu Leu Pro Ala Ile Leu Lys His Lys Lys Ser

65 70 75 80

Leu Gln Lys Leu Val Ser Asp Trp Asn Thr Leu Lys Ser Arg Leu Ser

85 90 95

Gln Ala Thr Lys Asn Ser Gly Ser Ser Gln Gly Leu Gly Gly Ser Pro

100 105 110

Gly Ser His Ser His Thr Thr Met Ala Asn Lys Val Glu Thr Leu Lys

115 120 125

613/617

Glu Glu Glu Glu Glu Leu Lys Arg Lys Val Glu Gln Cys Arg Asp Glu
130 135 140
Tyr Leu Ala Asp Leu Tyr His Phe Val Thr Lys Glu Asp Ser Tyr Ala
145 150 155 160
Asn Tyr Phe Ile Arg Leu Leu Glu Ile Gln Ala Asp Tyr His Arg Arg
165 170 175
Ser Leu Ser Ser Leu Asp Thr Ala Leu Ala Glu Leu Arg Glu Asn His
180 185 190
Gly Gln Ala Asp His Ser Pro Ser Met Thr Ala Thr His Phe Pro Arg
195 200 205
Val Tyr Gly Val Ser Leu Ala Thr His Leu Gln Glu Leu Gly Arg Glu
210 215 220
Ile Ala Leu Pro Ile Glu Ala Cys Val Met Met Leu Leu Ser Glu Gly
225 230 235 240
Met Lys Glu Glu Gly Leu Phe Arg Leu Ala Ala Gly Ala Ser Val Leu
245 250 255
Lys Arg Leu Lys Gln Thr Met Ala Ser Asp Pro His Ser Leu Glu Glu
260 265 270
Phe Cys Ser Asp Pro His Ala Val Ala Gly Ala Leu Lys Ser Tyr Leu
275 280 285
Arg Glu Leu Pro Glu Pro Leu Met Thr Phe Asp Leu Tyr Asp Asp Trp
290 295 300
Met Arg Ala Ala Ser Leu Lys Glu Pro Gly Ala Arg Leu Gln Ala Leu
305 310 315 320
Gln Glu Val Cys Ser Arg Leu Pro Pro Glu Asn Leu Ser Asn Leu Arg
325 330 335
Tyr Leu Met Lys Phe Leu Ala Arg Leu Ala Glu Glu Gln Glu Val Asn

340 345 350
Lys Met Thr Pro Ser Asn Ile Ala Ile Val Leu Gly Pro Asn Leu Leu
355 360 365
Trp Pro Pro Glu Lys Glu Gly Asp Gln Ala Gln Leu Asp Ala Ala Ser
370 375 380
Val Ser Ser Ile Gln Val Val Gly Val Val Glu Ala Leu Ile Gln Ser
385 390 395 400
Ala Asp Thr Leu Phe Pro Gly Asp Ile Asn Phe Asn Val Ser Gly Leu
405 410 415
Phe Ser Ala Val Thr Leu Gln Asp Thr Val Ser Asp Arg Leu Ala Ser
420 425 430
Glu Glu Leu Pro Ser Thr Ala Val Pro Thr Pro Ala Thr Thr Pro Ala
435 440 445
Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Leu Ala Ser Ala
450 455 460
Ala Thr Lys Glu Arg Thr Glu Ser Glu Val Pro Pro Arg Pro Ala Ser
465 470 475 480
Pro Lys Val Thr Arg Ser Pro Pro Glu Thr Ala Ala Pro Val Glu Asp
485 490 495
Met Ala Arg Arg Thr Lys Arg Pro Ala Pro Ala Arg Pro Thr Met Pro
500 505 510
Pro Pro Gln Val Ser Gly Ser Arg Ser Ser Pro Pro Ala Pro Pro Leu
515 520 525
Pro Pro Gly Ser Gly Ser Pro Gly Thr Pro Gln Ala Leu Pro Arg Arg
530 535 540
Leu Val Gly Ser Ser Leu Arg Ala Pro Thr Val Pro Pro Pro Leu Pro
545 550 555 560

Pro Thr Pro Pro Gln Pro Ala Arg Arg Gln Ser Arg Arg Ser Pro Ala
565 570 575
Ser Pro Ser Pro Ala Ser Pro Gly Pro Ala Ser Pro Ser Pro Val Ser
580 585 590
Leu Ser Asn Pro Ala Gln Val Asp Leu Gly Ala Ala Thr Ala Glu Gly
595 600 605
Gly Ala Pro Glu Ala Ile Ser Gly Val Pro Thr Pro Pro Ala Ile Pro
610 615 620
Pro Gln Pro Arg Pro Arg Ser Leu Ala Ser Glu Thr Asn
625 630 635

<210> 185

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 185

tcgagctctt cttcccagga actcaatg 28

<210> 186

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 186

tcgacattga gttcctggga agaagagc

28

<210> 187

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 187

cttctgctct aaaagctgcg

20

<210> 188

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 188

cgacctgcag ctcgagcaca

20